STIC-Biotech/ChemLib



From: Sent: To:

Fredman, Jeffrey Monday, October 01, 2001 3:42 PM

STIC-Biotech/ChemLib Lacourciere, Karen

FW: Sequence search approval 09/757100

I Approve.

Subject:

Cc:

Jeff Fredman

----Original Message-----

Fr m:

Lacourciere, Karen

Sent:

Monday, October 01, 2001 3:06 PM

T :

Fredman, Jeffrey

Subject:

Sequence search approval 09/757100

Jeff, could you approve this sequence search? Each sequence is ~20 nt's long and they are antisense targeted to one sequence. Thank-you!

Karen

Please search the following SEQ ID NO:'s for 09/757,100 in both the commercial databases and the pending files (interference)

3, 4, 6-12,14-18, 20, 23, 30, 31 and 33.

Please limit the length of oligos to less than 50 nucleotides long. Thank-you!

Karen A. Lacourciere Ph.D. ´CM1 11D09 GAU 1635 🗸 (703) 308-7523

> Point of Contact: **Toby Port** Technical Info. Specialist CM1 1E01 TEL: 308-3534

Point of Comact: Toby Port Technical Info. Specialist CM1 1E01 TEL: 308-3534

P

SEARCH REQUEST FORM

Access DB#______

Scientific and Technical Information Center

V.			_
Requester's Full Name:		Examiner # :	Date:
Requester's Full Name: Art Unit: Phone Nu Mail Box and Bldg/Room Location:	Res	alts Format Preferred (c	arcle): PAPER DISK E-MAI
If more than one search is submit	ted, please prioriti	ze searches in order o	of need.
*******	*****	*****	*******
Please provide a detailed statement of the se Include the elected species or structures, key utility of the invention. Define any terms the known. Please attach a copy of the cover sh	ywords, synonyms, acro iat may have a special n	inyms, and registry numbers neaning. Give examples or r	and combine with the concept or
Title of Invention:			
Inventors (please provide full names):			
Earliest Priority Filing Date:			
For Sequence Searches Only Please include appropriate serial number.	all pertinent information	ı (parent, child, divisional, or i	ssued patent numbers) along with the
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STAFF USE ONLY	Type of Search		d cost where applicable
Searcher: 1084 PORT	NA Sequence (#) 19	NT2	
Searcher Phone #: 308-3534	AA Sequence (#)	Dialog	
Searcher Location.	Structure (#)	Questel Orbit	
Date Searcher Picked Up	Bibliographic		
Date Completed: 10/3	Litigation	Lexis/Nexis	
Searcher Prep & Review Time	Fulltext	Sequence Systems	<u>y</u>
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PTO-1590 (1-2000)

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9b_ht915:**
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Database :

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182248	Ouery Match Query Match Best Local Similarity 87.5%; Pred. No. 6.3e+04; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Qy 2 ttcaaccagatggca 17	RESULT 3 190782 29 bp DNA PAT 01-DEC-1998 LOCUS 190782 29 bp DNA PAT 01-DEC-1998 DEFINITION Sequence 32 from patent US 5725862. ACCESSION 190782 VERSION 190782.1 GI:3935252 KEYWORDS SOURCE Unknown. ORGANISM Unknown.	REFERENCE 1 (bases 1 to 29) AUTHORS MUTPHY,T.R. JOURNAL Patent: US 5725862-A 32 10-MAR-1998; FEATURES 5 ource 1.29 Arganism="unknown" 8 to 29 ORIGIN	Query Match 64.0%; Score 12.8; DB 10; Length 29; Best Local Similarity 87.5%; Pred. No. 6.3e+04; Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Oy 2 ttcaaccagatggtca 17 	LOCUS HUMKRT10AG 45 bp DNA PRI 06-JAN-1995 DEFINITION Human keratin 10 (KRT10) gene, partial cds including polymorphism. ACCESSION L20218.1 G1:307087 VERSION KEYWORDS Keratin; keratin 10; polymorphism; suprabasal keratin. SOURCE HOMO sapiens Adult Blood DNA. ONGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthbria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 45) AUTHORS Rothnagel,J.J., Dominey,A., Fisher,M., Axtell,S., Pittelkow,M.; Anton-Lamprecht,I., Hohl,D. and Roop,D.
AR016116 Sequence AR01914 Sequence AR03405 Sequence AR034456 Sequence AR07401 Sequence AR07645 Sequence AX067989 Sequence AX067989 Sequence AX076373 Sequence AX076373 Sequence AX076373 Sequence E14337 Primer. 7/1 A42578 Sequence 95 A42579 Sequence 95 A44579 Sequence 91 A88767 Sequence 91 A88767 Sequence 91 A84757 Sequence 91 A84777 Se	APACH Sequence 68 ARO89824 Sequence D50147 A PCR prime A37961 Sequence 24 121766 Sequence 24 ARO11102 Sequence ARO738261 Sequence ARO75191 Sequence 158550 Sequence	161215 Sequence 22 AR054052 Sequence AR011107 Sequence AR075196 Sequence 15855 Sequence 20 161220 Sequence 27 E12236 Synthetic D E12234 Synthetic D	PAT 25-AUG-1993			Length 20; ; Indels 0; Gaps 0;
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RESULT 1 A1028/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL FEATURES

BASE COUNT ORIGIN

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/organism='Artificial sequences'
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                    E13249 41 bp DNA PAT
Oligonucleotide for microgene construction.
E13249
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E13249.1 GI:3252054
JP 1997154585-A/9.
unidentified.
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reads 1 to 41)
Shiba.K.
FORMATION OF RANDOM POLYMER OF MICROGENE
PREAT: JP 1997154585-A 9 17-JUN-1997;
KAĞAKU GIJUTSU SHINKO JIGYODAN
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C12N15/09,C07H21/04//C12N9/00;
strandedness: Single;
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1 (bases 1 to 30)
Wel,Y. and Sutton,G.G. III.
Human AlkB polypeptide
Patent: US 5747312-A 4 05-MAY-1998;
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/organism="unidentified"
/db_xref="taxon:32644"
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Sequence 4 from patent US 5747312.
AR004965.1 GI:3965844
                                                                                                                                                                                                                            Artificial sequences.
JP 1997154585-A/9
17-JUN-1997
06-DEC-1995 JP 1995318396
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//oce="kellix-initiation motif of lA segment of rod domain"
//ocdon_start=1
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Identification of mutational hot spots in the suprabasal keratin genes from patients with epidermolytic hyperkeratosis Unpublished (1993)
                                                                                                                                                                                                                                                                                                                                                        /gene="KRT10"
/note="polymorphism results in an Arg->His mutation at
amino acid position #10 in the HK10 rod; G00-118-828"
/phenotype="wild-type (G)"
/replace="g"
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/db_xref="taxon:9606"
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Kuhajda,F.P. and Pasternack,G.R.
Cancer related antigen
Patent: US 5665874-A 7 09-SEP-1997;
Location/Qualifiers
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Sequence 7 from patent US 5665874.
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Svendsen,A., Patkar,S.Anant, Gormsen,E., Okkels,J.Sigurd and Thellersen,M.
Lipase variants
Patent: US 5869438-A 38 09-FEB-1999;
Location/Qualifiers
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Pred. No. 1.3e+05;
0; Mismatches 3; Indels
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Pred. No. 1.3e+05;
0; Mismatches 3; Indels
First, M.Kent and Agoulnik, A.I.
Male infertility Y-deletion detection battery
Patent: US 5783390-A 4 21-JUL-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       Unknown.
Unclassified.
1 (bases 1 to 28)
Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
Achtods of assaying differential expression
Patent: US 5994076-A 1026 30-NOV-1999;
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Pred. No. 1.3e+05;
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Sequence 1026 from patent US 5994076.
AR090906.1 GI:10017661
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Sequence 38 from patent US
AR034456 AR034456.1 GI:5950061
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Matches 14; Conservative
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Location/Qualifiers
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Pred. No. 1e+05;
0; Mismatches 1;
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Pred. No. 1.3e+05;
0; Mismatches 3;
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Wei Y. and Sutton, G.G. III.

DNA encoding human Alkb
Patent: US 5618717-A 4 08-APR-1997;
Location/Qualifiers
                                                 140158 30 bp DNA
Sequence 4 from patent US 5618717.
140158.1 GI:2083163
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Sequence 4 from patent US 5776682.
AR016116 GI:3972393
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Sequence 4 from patent US 5783390.
AR019114
AR019114.1 GI:3974228
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/organism="unknown"
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Best Local Similarity 82.4%;
Matches 14; Conservative
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Unclassified.
1 (bases 1 to 20)
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Best Local Similarity 92.9
Matches 13; Conservative
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DEFINITION ACCESSION VERSION

RESULT AR016116

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RESULT 1 AR019114

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synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 29)
Levin, J.Z., Bauer, M.W. and Zheng, F.
Herbicide target genes and methods
Patent: WO 0077185-A 34 21-DEC.2000;
Novartis AG (CH); Novartis-Erfindungen Verwaltungsgesellschaft
                                                                                                                                                                                                                                                                                                      Query Match 60.0%; Score 12; DB 10; Length 29 Best Local Similarity 75.0%; Pred. No. 1.6e+05; Matches 15; Conservative 0; Mismatches 5; Indels
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligonucleotide"
a 8 c 5 g t
Sequence 34 from Patent WO0077185.
AX067989
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Job time: 14175 sec
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Fukuchi,N., Yamamoto,H., Nagano,M., Kito,M., Tanaka,A., Ishii,K., Kobayashi,T. and Yoshimoto,R.
Peptide having anti-thrombus activity and method of producing the
       Gaps
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Unclassified.
Unclassified.
1 (bases 1 to 33)
Svendsen.A. Patkar.S. Anant, Gormsen,E., Clausen,I.Groth, Okkels,J.Sigurd and Thellersen,M.
Lipase variants
Patent: US 5892013-A 38 06-APR-1999;
Location/Qualifiers
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Sequence 38 from patent US 5892013.
AR070401. GI:7221289
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Sequence 9 from patent US 5856126.
AR026654 GI:5937494
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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9b_est36.5
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9b_est40.8
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170: em_est100:*
171: em_est100:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

JOURNAL Unpublished (1997) COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo , Ph.D.	CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html	Trace considered overall poor quality Insert Length: 1015 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 1.	rce	//ab_host="DH10B" //lab_host="DH10B" //note="Vector: pT/T3D-Pac (Pharmacia) with a modified //note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories // Inc., and primed with a Not I - ollgo(dT) primer [5,	TGTTGAGGGGGGGGGCGCCCAATTTTTTTTTTTTTTTTT	BASE COUNT 5 a 8 c 4 g 8 t	Query Match 62.0%; Score 12.4; DB 17; Length 25; Best Local Similarity 92.9%; Pred. No. 4.4e+04; Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	<pre>Qy</pre>	RESULT 2 AZ429959/c LOCUS LOCUS MA2429959 39 bp DNA GSS 03-OCT-2000 DEFINITION M0214N08F mouse 10kb plasmid UUGCIM library Mus musculus genomic		OKGANISM MUS MUSCULUS UKATYOLA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE I (bases 1 to 39) AUTHORS Dun, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly	JM., KOSE, M., KOSE, K., SLOKES, K., Tingey, A., Von Niedernausern, A. and Wright, D., Weiss, R., Tille Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Unpublished (2000)	
SUMMARIES . SUMMARIES . SUMMARIES . Soore Match Length DB ID Description	1 12.4 62.0 25 17 AI208968 2 12.4 62.0 39 243 AZ429959 3 12.2 61.0 50 107 AIJ04028 4 12.2 61.0 50 107 AIJ04039 5 12 60.0 43 242 AZ888563	12 60.0 49 16 A1125432 A112543 12 60.0 49 241 A2311307 A23113 11.6 58.0 31 244 A2453622 A24356 11.6 58.0 34 247 A2653664 A266566 11.6 58.0 35 247 A2653664 A266566	11.6 58.0 35 4 AAZ66819 AAZ66819 MAZ6751720 11.6 58.0 43 2 AA075907 AA075907 ZM 11.6 58.0 34 6 249 AZ777948 AZ777948 11.2 56.0 34 16 A1096045 A1	17 11.2 56.0 44 11 AA75536 AA775536 AA775536 18 11.2 56.0 44 11 AA725427 AA700915 Z 20 11.2 56.0 49 10 AA700915 AA700915 Z 20 11.2 56.0 50 107 AU104136 AU104138 AU10	11 55.0 24 AZ41,922 AZ31,92 11 55.0 25 244 AZ449662 AZ44277 11 55.0 28 243 AZ427748 AZ4277 11 55.0 35 154 BG504713 BG5047 11 55.0 45 250 AZ821491 AZ8214 11 55.0 45 189 T80630	28 11 55.0 49 2 AA075329 22 AA075329 23 AA075329 23 AA075329 24 AA053904 AA053904 AA053904 AA053125 AA0535125 AA0535	10.8 54.0 40 14 AA296127 10.8 54.0 40 14 AA995117 10.8 54.0 42 242 AA298334 10.8 54.0 43 243 A248834	36 10.8 54.0 44 158 H55075 CH 37 10.8 54.0 50 114 AW28556 AW28556 38 10.6 53.0 26 244 AZA63718 AZA63718 39 10.6 53.0 26 249 AZ780163 AZ780163	10.6 53.0 26 249 A2783434 10.6 53.0 30 241 A2320504 10.6 53.0 34 11 AA734076 10.6 53.0 34 249 A8792647 10.6 53.0 34 249 A8792823 10.6 53.0 35 258 TAZ622824	ALIGNMENTS	A1208968/C A1208968 25 bp mRNA EST 29-NOV-1998 DEFINITION 9929711.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1836621	ACCESSION A1208968 VERSION A1208968.1 GI:3770910 KEYWORDS EST. SOURCE human.	

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AU104139.1 GI:13553660
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82.4%;
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                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with 74 DNA polymerase and 74 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 k range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 (pblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNN, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 50)

2 (Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Emall: ysuzukielms.u-tokyo.ac.j
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and
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                                                                                                                                                                                                                                                                                                                                    /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                           /sex="Male" /sex="Male" /sex="Male" /sex="Male" /sex="E. Coli strain XLI0-Gold, Tl-resistant, F-"
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                                                                                                                                                                                                                                                                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0214 row: N column: 08
Seg primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
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                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0214N08"
                                                                                                               High quality sequence stop: 39.
Location/Qualifiers
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92.9%;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata S., H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.

Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries of Department of Virology Institute of Medical Science, University of Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and sof-centiched cDNA library. Gene 200 (1-2), 149-156 (1997).
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a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997). Location/Qualifiers
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Pred. No. 6.2e+04;
); Mismatches 3; Indels 0
                                                                              /organism="Homo sapiens"
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/clone="HEP21348"
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KEYWORDS

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

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Sequencing Center
information can be
                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-remail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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100.0%; Pred. No. 7.8e+04;
ive 0; Mismatches 0;
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High quality sequence stop: 1.
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/db_xref="taxon:9606"
/clone="IMAGE:1737047"
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AI125432
AI125432.1 GI:3593946
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Best Local Similarity 100.
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//organism="musculus"
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/db_xref="taxon:10090"
/db_xref="taxon:10090"
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/clone="UGCIM0148F08"
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/note="Vector: FWD42Dr; Purified genomic DNA from M.
musculus C57BL/6J, (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gil4732114|gb]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli x110-Gold (Stratagene) cells
and selected for ampicillin resistance."

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                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E. 1 (bases 1 to 43)
E. 1 (bases 1 to 43)
S. Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0148 row: F column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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84112, US
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 (pplAEL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1M0543J20F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0543J20 F, DNA sequence.
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Dunn, D., Aoyadi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="CS7BL/6J"
/db_xref="taxon:10090"
/db_aref="UGG1M0255E08"
/clone_lib="wouse 10kb plasmid UGG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                          Mouse whole genome scaffolding with paired end reads from 10kb
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Pred. No. 1.2e+05;
0; Mismatches 4; Indels 0;
                                                                                                                                                                                                 Rm. 308, Biomedical Polymers Research Bldg., 20
84112, USA
                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 717
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0255 row: E column: 08
Seq primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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//note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/G0 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
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polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess: The
adaptored DNA was purified and size-selected for a 9.5 to
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electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
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adaptored vector DNA, and transformed into
chemically-competent E. coli Xil0-Gold (Stratagene) cells
and selected for ampicilin resistance."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mouse whole genome scaffolding with paired end reads from 10kb
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
84112, USA
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                                                                                                                                                                                                                     Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunnegenetics.utah.edu
lasert Length: 10000 Std Error: 0.00

Plate: 0026 row: K column: 11

Seq primer: CACACAGGAAACAGTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Mus musculus"
                                                  Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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/clone="UUGC1M0026K11"
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AZ453622.1 GI:10611604
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                             plasmid inserts
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COMMENT

TITLE

source

FEATURES

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/lab host-"E. Coli strain XL10-Gold, T1-resistant, F."
//note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114[gb]AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
      Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
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                                                                                                 Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@qenetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0485 row: J column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: 0485 row: J column: 13
Seq primer: CGTTGTAAAACGACGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                              Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone="UUGC1M0485J13"
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High quality sequence stop: 35.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymurlectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gii4732114 (gib1AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XIIO-Gold (Stratagene) cells and selected for amplicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1M0485J13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0485J13 F, DNA sequence.
AZ631220
AZ631220.1 GI:11753410
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host-"E. Coli strain XLI0-Gold, Tl-resistant, F-" /note-"Vector: PWD42nv; Puiffied genomic DNA from M. musculus G57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                               Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
/db.rt axon:10090"
/clone="UGGCIM054320"
/clone_lib="Mouse 10kb plasmid UGGIM library"
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                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0543 row: J column: 20
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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                                                                                                                      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 34. Location/Qualifiers
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77.8%;
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                                                                                                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
                                                                                              plasmid inserts
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Matches 14; Conserv
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DEFINITION

AZ631220

RESULT

à g ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

BASE COUNT

ORIGIN

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Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags G0704478
                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should b
kept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ777948 46 bp DNA GSS 16-FEB-2001
2M0012P13R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0012P13 R, DNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 46)
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Mouse whole genome scaffolding with paired end reads from 10kb
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 1.

Location/Qualifiers
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                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 1.2e+05;
); Mismatches 4;
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/db_xref="GDB:3920910"
/db_xref="taxon:9606"
/clone="IMAGE:531398"
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ilarity 77.8%;
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                                                                                                                                  Contact: Wilson RK
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Best Local Similarity
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84112, USA
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Hiller,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Mortis,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
                                          Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Mortis,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"Organ: lymph node; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; ist strand cDNA was primed with a Not I - oligo(dT) primer
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AA075907

BEST

23-DEC-1997

AA74608.1. Strategene neurocepithelium (#937231) Homo sapiens CDNA clone IMAGE:531398 5' similar to TR:6972436 G972436 CYCLIN DEPENDENT PROTEIN KINASE, TYPE 4 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information. MGI:446242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                           The WashU-HHMI Mouse EST Project Contact: Marra MyMouse EST Project Contact: Marra MyMouse EST Project WashU-HHMI Mouse EST Project WashIngton University School of MedicineP A444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Fax: 314 286 1810
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Pred. No. 1.2e+05;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares mouse lymph node NbMLN"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                              Trace considered overall poor quality
Seq primer: -28mil rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="lymph node"
/dev_stage="4 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:720746"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C57BL/63"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA075907.1 GI:1615777
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77.8%;
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Best Local Similarity 77.8'
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                                                                                                                                    Waterston, R.
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Gaps

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Email: genome@smith.edu
The library was constructed by Wenhong Lu. The library is available
from Dr. S.A. Williams, email genome@smith.edu When requesting this
clone from Dr. Williams, please reference the Williams lab clone id
SWOVL3CAN20F0S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Those transcores filatial nematode parasite of humans.

MRNA was prepared from third stage infective larvae of onchocerca volvulus isolated from mosquitoes 10 days after infection and converted to double stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNApol I. The library had 1.8 x 10E5 independent recombinants and average insert size was 900 base pairs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The library was constructed by Wenhong Lu. The library is available from Dr. S.A. Williams, email genome@smith.edu.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SAW94WL-OvL3)"
/lab_host="XL1-Blue MRF'"
/note="Vector: lambda UniZap XR; Site_1: EcoR I; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 42)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA936922 42 bp mRNA EST 17-JUN-1998 om55c08.sl NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1551086 3' similar to gb:M38188 OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Department of Biological Sciences, Clark Science Center, Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="onch1306"
/clone_lib="Onchocerca volvulus infective larva cDNA
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0
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Pred. No. 1.9e+05;
0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                 Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: T3 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Onchocerca volvulus"
/strain="Sierra Leone"
/db_xref="taxon:6282"
                          Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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AA936922
AA936922.1 GI:3094956
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81.2%;
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                          College, Northan
Tel: 4135853826
Fax: 4135853786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWAPA2 (gil4732114 gb]AR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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1 (bases 1 to 34)
Williams, S.A., Lizotte-Waniewski, M., Laney, S., Wenhong, L., Hillier
L., Allen, M., Bowles, L., Gelsel, S., Jost, S., Kucaba, T., Martin, J.,
Steptoe, M., Theising, B., White, Y., Wylle, T., Chappell, J., Person, B.,
Gibbons, M., Harvey, N., Pape, D., Chamberlain, A., Morales, R.,
Molecular Parasitology OvL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parameter vectors and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance." 
 8 c 11 g ^7 t
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SWOVL3CANZOFO5 Onchocerca volvulus infective larva cDNA
(SAW94WL-OVL3) Onchocerca volvulus cDNA clone onch1306 5' similar
to TR:Q25606 Q25606 LARVAL 18 KDA PROTEIN. ;, mRNA sequence.
AI096045
                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="UUGC2M0012P13"
/clone_lib="Mouse 10kb plasmid UUGClM library"
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                 Fax: 801 585 /1//
Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory Mouse DNA Resource
                                                                        Insert Length: 10000 Std Error: (Pate: 0012 row: P column: 13 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                       High quality sequence stop: 46.
Location/Qualifiers
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Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                        /strain="C57BL/6J
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Best Local Similarity 77.8%;
Matches 14; Conservative
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Gaps

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Trace considered overall poor quality
Insert Length: 753 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .42
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InhaGE:1551086"
/cl
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Gaps 0; Query Match 56.0%; Score 11.2; DB 13; Length 42; Best Local Similarity 81.2%; Pred. No. 1.9e+05; Matches 13; Conservative 0; Mismatches 3; Indels (

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3 tcaaccagatggtcat 18 ||| | ||||||||| 22 TCATCATGATGGTCAT 37 ò g

Search completed: October 2, 2001, 15:01:08 Job time: 10837 sec

Searched:

Run on:

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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gb_htg24:*
gb_htg25:*
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Match Length DB
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9b_htg16:
9b_htg17:
9b_htg18:
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9b_htg19:
9b_htg20:
                    em_ph:*
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                                                                    October 2, 2001, 12:00:36 ; Search time 3339.34 Seconds (without alignments) 92.640 Million cell updates/sec
                                                                                                                                                                                                           423528
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                     1344157 seqs, 7733874588 residues
                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                               OM nucleic - nucleic search, using sw model
                                                                                                                                    1 ccgcgggctcacagtggtcg 20
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Gapop 10.0 , Gapext 1.0
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                                                                                                             Title:
Perfect score:
Sequence:
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AX04389 Sequence 41 AX043850 Sequence AX090386 Sequence AX090365 Sequence X70713 M.musculus AX026028 Sequence E28465 Hyaluronate AR095613 Sequence

192389 AX043850 AX090386 AX090365 MMTCRAIC7 AX026028 E28465 AR095613

016666

41 23 30 40 40

Description

ΩI 10

SUMMARIES

23-NOV-2000

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synthetic construct
artificial sequence.
1 (bases 1 to 50)
Savidge, B., Lassner, M.W., Weiss, J.D. and Post-Beittenmiller, D.
Nucleic acid sequences to proteins involved in tocopherol synthesis
Patent: WO 0063391-A 57 26-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12.6; DB 10; Length 37;
Pred. No. 1e+05;
); Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide primer"
1 c 1 g 6 t
                                                                                                                                                                                                                                                                                                                                                                  PAT
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83.3%; Pred. No. 4.7e+04;
cive 0; Mismatches 3;
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="0ligonucleotide"
16 c 14 9 11 t
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synthetic construct
artificial sequence.
1 (bases 1 to 37)
Lassner, M. and van Eenennaam, A.
Plant sterol acyltransferases
Patent: WO 0116308-A 79 08-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                         AXU90386 37 bp DNA
Sequence 79 from Patent WO0116308.
AX090386
                     AX043850 50 bp DNA
Sequence 57 from Patent WO0063391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AX090365 41 bp DNA
Sequence 58 from Patent W00116308.
AX090365 GI:13444226
AX090365.1 GI:13444226
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Location/Qualifiers
                                                                                                                                             Calgene LLC (US)
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78.9%; Pred
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AR041129 Sequence
AR041130 Sequence
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119530 Sequence 7
119532 Sequence 9
186209 Sequence 6
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AR067323 Sequence
AR073339 Sequence
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Levenbook, I.S., Chumakov, K.M., Norwood, L.P. and Roninson, I.
Assay for virulent revertants of attenuated live vaccines and kits
therefor
                                                                                                                                                                                                                                      119534 Sequence 11
121731 Sequence 6
186214 Sequence 11
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I21472 Sequence 19
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121733 Sequence 8
A58772 Sequence 18
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AR078873 Sequence
                  AX090361 Sequence
AX043846 Sequence
AR041138 Sequence
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AR095535 Sequence
AX033429 Sequence
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AX042765 Sequence
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Pred. No. 5.2e+04;
); Mismatches 3;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 41 from patent US 5728519.
192389
192389.1 GI:3936859
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AX095615
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AX090361
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AR041138
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Gaps

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Length 50; Indels 21-MAR-2001

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Gaps

REFERENCE AUTHORS JOURNAL

SOURCE

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FEATURES

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synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 29)
Eshhar, Z., Bolhuis, R.L. and Willemsen, R.A.
Immune cells having predefined biological specificity, comprising
chimeric t cell receptor chimeric t cell receptor patent: WO 0031239-A 9 02-JUN-2000;
ESHHAR ZELIG (IL); YEDA RES & DEV (IL); BOLHUIS REINDER L H (NL);
WILLEMSEN RALPH A (NL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YOICHI YAMADA,NAOKI ITANO,KOJI KIMATA
C12N15/09,C12N9/00,C12Q1/68//(C12N15/09,C12R1:91),C12N15/00,
(C12N15/00,C12R1:91)
Strandedness: Single;
                                                                                 16-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 29;
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'organism='Unidentified'.
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Pred. No. 1.7e+05;
0; Mismatches 3;
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic DNA"
1 0 c 11 g 4 t
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Yolchi,Y.N.I. and Kimata.
Hyaluronate synthase promoter DNA
Patent: JP 1999196875-A 13 27-JUL-1999;
SEIKAGAKU KOGYO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .30
/organism="unidentified"
/db_xref="taxon:32644"
a 11 c 7 g 5
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Hyaluronate synthase promoter DNA.
E28465
                                                                                               Sequence 9 from Patent WO0031239.
AX026028
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JP 1999196875-A/13
27-JUL-1999
14-JAN-1998 JP 1998006191
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82.4%;
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 18 CCGCGCGCTCACAG
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Submitted (15-JAN-1993) J. Casanova, INSERM U132, Developpement
Normal et Pathologique du, Systeme Immunitaire, Necker, Pavillon
Kirmisson, 149 rue de Sevres, 75743 Paris Cedex, FRANCE
2 (bases 1 to 45)
Casanova, J.L., Martinon, F., Gournier, H., Barra, C., Pannetier, C.,
Regnault, A., Kournisky, P., Cerottini, J.C. and Maryanski, J.L.
T cell receptor selection by and recognition of two class I major
histocompatibility complex restricted antigenic peptides that
J. Exp. Med. 177 (3), 811-820 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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J-alpha gene segment; junction; T-cell receptor; V-alpha gene
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9 c 18 g 12 t
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//organism="synthetic construct"

//db_raf="taxon:32630"

//note="Synthetic oligonucleotide primer"

13 c 15 g t
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Pred. No. 9.9e+04;
0; Mismatches 4;
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             synthetic construct
artificial sequence.
1 (bases 1 to 41)
Lassner,M. and van Eenennaam,A.
Plant sterol acyltransferases
Patent: WO 0116308-A 58 08-MAR-2001;
MONSANTO COMPANY (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="DBA2"
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/db_xref="taxon:10090"
/haplotype="H2-d"
/tissue_type="T cell"
/cell_type="CTL"
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illarity 78.9%;
Conservative
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synthetic construct.
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Best Local Similarity 92.9
Matches 13; Conservative
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Mus musculus
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Best Local Similarity
Matches 15; Conserv
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Location/Qualifiers
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AX043844.1 GI:11342429
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Unclassified.
1 (bases 1 to 40)
Lunnen.K.D., Dalton,M.A., Wilson,G.G. and Xu,S.
Lunnen.K.D. balton,M.A., Wilson,G.G. and xu,S.
Method for cloning and producing the Aval restriction endonuclease
and purification of the recombinant Aval restriction
endonuclease
Patent: US 6004793-A 8 21-DEC-1999;
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Lunnen, K.D., Dalton, M.A., Wilson, G.G. and Xu,S.
Method for cloning and producing the Aval restriction endonuclease in E. coll and purification of the recombinant Aval restriction
                            Gaps
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Score 12.2; DB 10; Length 30; Pred. No. 1.7e+05; 0; Mismatches 3; Indels
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Pred. No. 1.6e+05;
0; Mismatches 3; Indels
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Pred. No. 1.6e+05;
0; Mismatches 3; Indels
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Patent: US 6004793-A 10 21-DEC-1999;
Location/Qualiflers
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                                                                                                                                    Sequence 8 from patent US 6004793.
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AR095615
AR095615.1 GI:10023644
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Best Local Similarity 82.4%;
Matches 14; Conservative (
y Match 61.0%;
Local Similarity 82.4%;
nes 14; Conservative
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Best Local Similarity 82.4%;
Matches 14; Conservative
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18 CGCGTGCTCATGGTGGT 2
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synthetic construct.
synthetic construct
artificial sequence.

1 (bases 1 to 41)
Savidge, B., Lassner, M.W., Weiss, J.D. and Post-Beittenmiller, D.
Nucleic acid sequences to proteins involved in tocopherol synthesis
Calgene LLC (US)
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 12.2; DB 9; Length 41; Pred. No. 1.6e+05; 0; Mismatches 3; Indels
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide primer"
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/db_xref="texon:32630"
/note="01jgonuclectide"
13 c 11 g 11 t
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synthetic construct
artificial sequence.

( bases 1 to 44)
Lassner, M. and van Eenennaam, A.
Plant sterol acyltransferases
Patent: WO 0116308-A 54 08-WAR-2001;
MONSANTO COMPANY (US)
Location/Qualifiers
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Sequence 54 from Patent WO0116308.
AX090361
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Sequence 53 from Patent WO0063391.
AX043846 AX043846.1 GI:11342431
AX043844 41 bp DNA
Sequence 51 from Patent WO0063391.
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Search completed: October 2, 2001, 15:56:35 Job time: 14159 sec
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Best Local Similarity
Matches 13; Conserva
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          synthetic construct.
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artificial sequence.
1 (bases 1 to 45)
Savidge, B., Lassner, M.W., Weiss, J.D. and Post-Beittenmiller, D.
Nucleic acid sequences to proteins involved in tocopherol synthesis
Calgene LLC (US)
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Nadeau, J.G., Dean, C.H., Schram, J.L., Howard, D.R., Dey, M.S. and
Wright, D.D.
Wright, D.D.
Patent: US 5811269-A 13 22-SEP-1998;
Location/Qualifiers
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Leckie, G.W., Davis, A.H., Semple-Facey, I.E., Manlove, M.T. and
Solomon, N.A.
Materials and methods for the detection of Mycobacterium
tuberculosis
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Pred. No. 1.5e+05;
0; Mismatches 3; Indels
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"
1 3 c 14 9 14 t
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Sequence 13 from patent US 5811269.
AR041138
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143055
143055.1 GI:2468299
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3 c 6 g
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Best Local Similarity 82.4%;
Matches 14; Conservative (
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Detection of mycobacteria by multiplex nucleic acid amplification Patent: US 5811269-A 3 22-SEP-1998; Location/Qualifiers
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Nadeau,J.G., Dean,C.H., Schram,J.L., Howard,D.R., Dey,M.S. and
                                                                                                                                                        Gaps
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Pred. No. 2.9e+05;
0; Mismatches 2;
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Pred. No. 2.7e+05;
0; Mismatches 2;
Patent: US 5631130-A 38 20-MAY-1997;
Location/Qualifiers
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Sequence 3 from patent US 5811269.
AR041128 GI:5961624
                                           /organism="unknown"
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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MRNAs using full-length enriched and 5'-end enriched CDNA libraries Unpublished (2001)
Contact: Yutaka Suzuki
Contact: Yutaka Suzuki
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bemail: ysuzukiélma.u-tokyo.ac.jp
Suzuki,Y...Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 46)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lery,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                       AA196905 46 bp mRNA EST 12-MAR-1998 zq09b06.rl Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:629171 5' similar to TR:E36241 E36241 PM5 PROTEIN. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="SOLR (kanamycin resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llonl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1100 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                      sapiens cDNA library"
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Pred. No. 4.8e+03;
0; Mismatches 1; Indels 0
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/organism="Homo sapiens"
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AU104386 AU104386
ALA76427 r brucei
AZ34556 1M0080114
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AZ834614 2M0117121
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Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Oda,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,H., Suyama,A. and Sugano,S.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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(http://www.fax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qi|4732114|qb|AE129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 40)
                                                                                       Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/61 (male) was obtained from the Jackson
                                                                                                                                                                                      Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0254A13"
/clone=lub="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: 0254 row: A column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 40.
Location/Qualifiers
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87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: plasmid ends
                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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       Mus musculus
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Best Local Similarity
Matches 14; Conser
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                                                                       REFERENCE
                                                                                            AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)

Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Institute of Medical Science, University of Tokyo
4-6.1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6.1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              AU107932 50 bp mRNA EST 05-APR-2001
AU107932 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
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9 t lothers
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                                                                                                                                                                                                            Length 46;
                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                         Score 13.6; DB 3;
Pred. No. 1.2e+04;
                                                                                                                                                                                                                                                             Mismatches
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/db_xref="taxon:9606"
/clone="ZRV62008"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yutaka Suzuki
Department of Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ453043.1 GI:10610442
                                                                                                                                                                                                         68.0%;
80.0%;
                                                                                                                                                                                                                                                                                                      1 ccgcgggctcacagtggtcg 20
                                                                                                                                                                                                                                                                                                                             41 CCGCCCCTCAATGTGGTCG 22
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Matches 15; Conservative
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house mouse
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COMMENT
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vp30g03.rl Barstead mouse proximal colon MPLRB6 Mus musculus cDNA clone IMAGE:1078228 5' similar to gb:U13705 Mus musculus domesticus C57BL/6J plasma glutathione (MOUSE);, mRNA sequence.
AA822940.1 GI:2892808
                                   ö
                                     Gaps
                                   .
0
Length 40;
                                   Indels
Score 12.8; DB 244;
Pred. No. 3e+04;
0; Mismatches 2; I
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VERSION
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/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECO RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and so circles were made in vitro. Pollowing HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a polo 16 5,000 clones made from the same library (cloneIDs 13223/6-1333911, 1456007-1456775, and 150552-150285). Subtraction by Bento Soares and M. Patima Bonaldo. "
                                                                                                                 CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 31)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, M., Lennon, G., Marra, M., Martin
,J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA845818 31 bp mRNA EST 04-MAR-1998 ak85f01.s1 Barstead spleen HPLRB2 Homo sapiens CDNA clone IMAGE:1414681 3' similar to SW:C1QC_HUMAN P02747 COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR. ;, mRNA sequence. AA845818 aA845818.1 GI:2931958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                   www-bio.llnī.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                               Trace considered overall poor quality Insert Length: 436 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 1. Location/Qualifiers
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t
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/clone_lib="NCI_CGAP_Kid11"

    .25
    /organism="Homo sapiens"
/db_xref="taxon:9606"

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Matches 15; Conserv
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI762402 25 bp mRNA EST 20-DEC-1999 wh65e10.xl NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385642 3' similar to TR:P78421 P78421 CHROMOSOME 16P13 BAC CLONE TIP9778.492B4 COMPLETE SEQUENCE; HTGS PHASE 3 ;, mRNA sequence. AI762402 GI:5178069
                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 25)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GGAP dancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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0
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Pred. No. 3e+04;
); Mismatches 2; Indels (
                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trace considered overall poor quality Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1. Location/Qualifiers
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Best Local Similarity 87.5%;
Matches 14; Conservative
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                             house mouse.
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AUTHORS
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AZ834614/C
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E I (bases 1 to 46)

S Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Context: Robert B. Weiss
University of Utah Genome Center
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//dev_stage="adult, 17 years"
//lab_host="DH108"
//lab_host="Lab_host="DH108"
//lab_host="Lab_host="DH108"
//lab_host="Lab_host="DH108"
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IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
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                                                                                                                                                                                                                                            1. .31
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1414681"
/clone_lib="Barstead spleen HPLRB2"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84112, USA
Fal: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Plate: 0276 row: F column: 12
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 46.
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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Best Local Similarity 78.9°
Matches 15; Conservative
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AZ465895/c
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/clone_inb='mouse lukb plasmid ouccim library"
//sex="Watle"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMP42nv; Purified genomic DNA from M.
musculus C57BL/6/ (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kp range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|aF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampliallin resistance."
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A2834614 50 bp DNA GSS 20-FEB-2001
2M0117121F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0117121 F, DNA sequence.
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0
/clone="UUGC1M0276F12"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 12.6; DB 244; Length 46;
Pred. No. 3.8e+04;
0; Mismatches 4; Indels 0
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Insert Length: 10000 Std Error: 0.00
Plate: 0117 row: I column: 21
Seq primer: GGTGTAAAAGGACGCCAGT
Class: plasmid ends
High quality sequence stop: 50.
Location/Qualiflers
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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78.9%;
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Best Local Similarity 78.9
Matches 15; Conservative
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Fax: 801 585 7177
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 50)
2 (bases I to 50)
3 (bases I to 50)
4 (bases I to 50)
5 (bases I to 50)
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
5-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
5-8-1, Shirokanedai, Minatoku, Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).

Location/Qualifiers
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AU106948 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone
AU106948 GI:13556469
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T. brucei sheared genomic DNA clone 140a04, forward sequence,
genomic survey sequence.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                           Length 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.0%; Score 12; DB 107; Length 50; 75.0%; Pred. No. 7.5e+04; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                   60.0%; Score 12; DB 258; 75.0%; Pred. No. 7.5e+04; tive 0; Mismatches 5;
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/db_xref="taxon:9606"
/clone="CAS03735"
                                   /db_xref="taxon:5691"
                                                                                                               12 g
/strain="TREU927"
                                                                           /clone="233a12"
10 c 1
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Best Local Similarity 75.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                   15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                           Similarity
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TA140A04P/C
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AU106948/c
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KEYWORDS
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                                                                                                                                                                                                                                                                                       (http://www.bax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 tjblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I (under the control of the control 
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Details of T. brucel sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                   /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 44)
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                               /clone="UUGC2M0117121"
/clone_lib="Mouse 10kb plasmid UUGClM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.0%; Score 12.6; DB 250; Length 50; 78.9%; Pred. No. 3.8e+04;
Live 0; Mismatches 4; Indels 0
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/db_xref="taxon:10090"
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AL481198
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                                                                                                           /sex="Male"
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nes 15; Conserv
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/sex="male" // dev_stage="adult, age 64" // dev_stage="adult, age 64" // dev_stage="adult, age 64" // dev_stage="adult, age 64" // dev_bost="DH108 (phage resistant)" // dev_bost="DH108 (phage resistant)" // dev_bost="DH108 (phage resistant)" // dev_stage developed resistant condition for the lost of the lost of the strand cond which a Not I - oligo(dT) primer [5' strand cond cond was primed with a Not I - oligo(dT) primer [5' strand cond cond cond was ligated to Eco RI adaptors [5' AATTCGGATCGAACT 3' and 5' GTTGGATCGG 3'], digested with Not I and cloned into the Not I and Eco RI sites of the modified pryT3 vector. Library constructed by Bob Barstead."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA466917 37 bp mRNA EST 11-JUN-1997 vf10g04.r1 Knowles Solter mouse blastocyst B3 Mus musculus cDNA clone IMAGE:835350 5' similar to SW:RS9_RAT P29314 40S RIBOSOMAL PROTEIN S9. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:835350"
/clone_lib="Knowles Solter mouse blastocyst B3"
/tissue_type="blastocyst"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                   /clone="IMAGE:2320062"
/clone_lib="Barstead aorta HPLRB6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 11.6; DB 24;
Pred. No. 1.2e+05;
0; Mismatches 4;
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t
                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:10090"
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Location/Qualifiers
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77.8%;
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Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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1 (bases 1 to 28)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                Tripings it to 22)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitssion
Submits (10-DEC-2000) Trypanosoma brucel genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI735009 28 bp mRNA EST 14-JUN-1999 as44e04.xl Barstead aorta HPLRB6 Homo sapiens CDNA clone IMAGE:2320062 3' similar to TR:Q99969 Q99969 TAZAROTENE-INDUCED
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
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Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 1.2e+05;
0; Mismatches 4; Indels 0;
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Contact: Wilson RK
Washington University School of Medicine
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/clone="140a04"
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Best Local Similarity 77.8%;
Matches 14; Conservative
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/db_xref="taxon:10090"
/clone="IxMes:1002771"
/clone="IxMes:1002771"
/clone="IxMes:1002771"
/closue_type="roel1"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: blood; Vector: pBluescript SK-; Site_1:
/note
                                                              /note="Organ: embryo; Vector: pSPORT; Site_1: NotI; Site_2: SalI; Cloned unidirectionally from mRNA prepared from 800 blastcoysts. Primer: SalI(dF): 5'-CGGTCGACCGTTCTTTTTTTTTTTTTTT.3'. CDNAS were cloned into the NotI/SalI sites of a pSPORT vector (Life Technologies). Two different size selections: B1 (larger inserts) and B3." 6 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vm61h02.rl Stratagene mouse Tcell 937311 Mus musculus cDNA clone IMAGE:1002771 5' similar to SW:RS9_RAT P29314 40S RIBOSOMAL PROTEIN AA607492
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Pred. No. 1.2e+05;
); Mismatches 4; Indels
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/dev_stage="embryo (pre-implantation)"
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The WashU-HHMI Mouse EST Project
                                         /lab_host="DH10B
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Matches 14; Conservative (
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Fax: 314 286 1810
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Search completed: October 2, 2001, 15:00:45 Job time: 10814 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Database

127712 Sequence 19 183056 Sequence 19 AX094895 Sequence A09940 oligonucleo A47740 Sequence 4 AR019411 Sequence 1.32460 Human (clon AR092516 Sequence

A09940 A47740 AR019411 HUMTCVD1DK AR092516

I27712 I83056 AX094895

Description

SUMMARIES

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 21)
Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and Mccarthy,J.J.
Single nucleotide polymorphisms in genes
Patent: WO 018250-A 73 15-WAR-2001;
WHITEHBAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
           10-JUN-1998
                                                                                                                                                                                                                                                                                                                           30-MAR-2001
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                                                                                     1 (bases 1 to 21)
Wang, C.J. and Wu, K.
Wats for detecting a target nucleic acid with blocking oligonucleotides
Patent: US 5712386-A 19 27-JAN-1998;
Location/Qualifiers
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Pred. No. 2.2e+05;
L; Mismatches 2; Indels (
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Pred. No. 8.8e+04;
; Mismatches 3;
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                   5712386
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Sequence 73 from Patent WO0118250.
AX094895.1 GI:13511098
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Location/Qualifiers
1. .21
/organism="Homo sapiens"
/db_xref="taxon:9606"
7 a 5 c 4 9 4
                                                                                                                                                               /organism="unknown"
6 c 11 g
          183056 21 bp DNA Sequence 19 from patent US : 183056 183056.1 GI:3211353
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AR029572 Sequence
AR098525 Sequence
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141940 Mus musculu
U41956 Mus musculu
U41971 Mus musculu
E10439 Primer. 9/2
AR024068 Sequence
249042 M. musculus
AR089906 Sequence
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108721 Sequence 9
155881 Sequence 11
AR004362 Sequence
AR097153 Sequence
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AR012355 Sequence
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192341 Sequence 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang, C.J. and Wu, K.
Methods for reducing non-specific priming in DNA detection
Patent: US 5567583-A 19 22-OCT-1996;
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Pred. No. 8.8e+04;
); Mismatches 3;
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MMU41956
MMU41971
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AR024068
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AR093351
AR029572
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Best Local Similarity 83.3
Matches 15; Conservative
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HUMTCVDIDK 47 bp mRNA pRI 10-FEB-1995
Human (clone: 3cpj20) T-cell receptor delta-chain (V-delta-1) mRNA.
L32460
L32460.
L32460.1 GI:497530
T-cell receptor; delta chain.
Homo sapiens intestine cDNA to mRNA.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalia; Eutheria: Primates; Catarrhini; Hominidae: Homo.
1 (bases 1 to 47)
Chowers,Y., Holtmeier,W., Harwood,J., Morzycka-Wroblewska,E. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 50)
Loosamore,S.M., Yacoob,R.Khayyam, Zealey,G.Ross and Klein,M.Henri.
Loosamore,S.M., Yacoob,R.Khayyam, Zealey,G.Ross and Klein,M.Henri.
Expression of gene products from genetically manipulated strains of
Bordeteila
Parent: US 5998168-A 46 07-DEC-1999,
Location/Qualifiers
1. 50
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Pred. No. 2.4e+05;
0; Mismatches 3;
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J. Exp. Med. 180 (1), 183-190 (1994)
94275371
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AR092516.1 GI:10019270
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/db_xref="taxon:9606"
/tissue_type="intestine"
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/organism="unknown"
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                        unclassified.

1 (bases 1 to 22)

Moureau,P., Derclaye,I., Delor,I. and Cornelis,G.

Nucleic acid probes useful for detecting specifically different
bacterial species of the genus Campylobacter
Patent: EP 0350392-A 2 10-JAN-1990;
IRE-MEDGENIX S.A

Location/Qualifiers
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Pred. No. 2.7e+05;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M unidentified
unclassified.
1 (bases 1 to 38)
Wood, P.C. and Quirk, A.V.
YEAST STRAINS
PATENT: WO 953833-A 4 14-DEC-1995;
DELTA BIOTECHNOLOGY LTD (GB)
Other publication AU 2626295 960104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 38)
Wood,P.Carolyn and Quirk,A.Victor.
Yeast strains
Patent: US 5783423-A 4 21-JUL-1998;
Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
? a 9 c 13 g 9
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AR019411
AR019411.1 GI:3974525
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/organism="unidentified"
/db_xref="taxon:32644"
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Sequence 4 from Patent W09533833.
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82.4%;
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
1 (bases 1 to 20)
1 (bases M. P. and David, G. J.
New members of the 91ypican gene family
Patent: WO 9937764-A 49 29-JUL-1999;
VEUGELERS MARK PALL DITTMAR (BE); VLAAMS INTERUNIV INST BIOTECH
(BE); DAVID GUIDO JOSEPH FRANS (BE)
Location/Qualifiers
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synthetic construct
artificial sequence.
1 (bases 1 to 25)
Botstelin,D., Goddard,A., Gurney,A.L., Hillan,K.J., Roy,M.A. and
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide Probe"
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Pred. No. 5.1e+05;
0; Mismatches 4;
AAV020035 20 bp DNA Sequence 49 from Patent WO9937764.
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Sequence 58 from Patent WO0105836.
AX076946
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Sequence 32 from patent US 5817495.
AR044492.1 GI:5965957
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/organism="Homo sapiens"
/db_xref="taxon:9606"
3 c 6 g 2
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Matches 13; Conserv
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Knappik, A. Pack, P., Ilag, V., Ge, L., Moroney, S. and Plueckthun, A. PROTEIN (POLY) PEPTIDE LIBRARIES
PATEIN. (POLY) PEPTIDE LIBRARIES
PATEIN: WO 9708320-A 157 06-MAR-1997;
MORPHOSYS PROTEINOPTIMIERUNG (DE)
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        Score 12.2; DB 9;
Pred. No. 2.3e+05;
0; Mismatches 3;
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75.0%; Pred. No. 3.4e+05;
iive 0; Mismatches 5.
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1 (bases 1 to 20)
Wallace,R.Bruce and Ugozzoli,L.
Manchyping of multiple allele systems
Patent: US 5521301-A 4 28-MAY-1996;
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Sequence 157 from Patent WO9708320.
AG0848
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Sequence 4 from patent US 5521301.
121584 GI:1601938
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/db_xref="taxon:32644"
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        Ouery Match 61.0%;
Best Local Similarity 82.4%;
Matches 14; Conservative
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I (bases 1 to 36)
Dahm, M.W.
METHOD OF QUANTIFYING TUMOUR CELLS IN A BODY FLUID AND A SUITABLE
                                 (bases 1 to 27)
Pedersen, A. Hjelholt, Vind, J., Svendsen, A., Cherry, J.R., Lamsa, M., Schneider, P. and Jensen, B. Kostgaard.
H.sub. 2 O.sub. 2 - stable peroxidase variants
Patent: US 5817495-A 32 06-OCT-1998;
                                                                                                                                                                                                                  Gaps
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Unknown.
Unclassified.
1 (bases 1 to 43)
Tal,R., Wong,H.C., Casipit,C., Chavaillaz,P. and Wittman,V.
Tal,R., Worghtide synthesis and purification
Patent: US 5763284-A 46 09-JUN-1998;
Location/Qualifiers
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Pred. No. 5e+05;
0; Mismatches 4; Indels
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Pred. No. 4.7e+05;
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Sequence 46 from patent US 5763284.
AR012355 AR012355.1 GI:3970345
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Sequence 13 from Patent WO9718322.
A93959
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18 GGCGACGGGAATCGATGG 1
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 50)

2 Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S.

Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched CDNA libraries on Unpublished (2001)

Contact: Yutaka Suzuki
Department of Virology Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library, Gene 200 (1-2), 149-156 (1997).
mRNAs using full-length enriched and 5'-end enriched CDNA libraries Unpublished (2001)
Contact: Yutaka Suzuki
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki.Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).
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AU105195 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
REC06645, mRNA sequence.
AU105195 GI:13554716
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/db_xref="taxon:9606"
/clone="HRC0645"
/clone_lib="Sugano Homo sapiens cDNA library"
/ 13 c 24 g 5 t
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Pred. No. 9.5e+03;
0; Mismatches 4; Indels 0
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/clone="CoLF6124"
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
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AU105197 AU105197
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AU103598 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
COLF6124, mRNA sequence.
AU103598.1 GI:13553119
                                           Description
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AZ816650.1 GI:12986558
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Best Local Similarity 80.0°
Matches 16; Conservative
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Mammalla; Euteria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
1 (bases 1 to 50)
2 Suzuki,Y., Tsunoda,T., Tanaka,T., Makamura,Y., Morishita,S., Okubo,Y., Suyama,A. and Sugano,S.
1 (Nota) T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,Y., Suyama,A. and Sugano,S.
1 (Pupublished (2001)
1 Contact: Yutaka Suzuki
1 Department of Virology
1 Contact: Yutaka Suzuki
1 Department of Virology
2 Medical Science, University of Tokyo
3 Medical Science, University of Tokyo
4 foll Shrokanedai, Minatoku, Tokyo 108-8639, Japan
5 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
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Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
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Location/Qualifiers
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AU105198 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HSIO1637, mRNA sequence.
AU105198 GI:13554719
                                      AU105197 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@lms.u-tokyo.ac.jp
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                                                                                                                        AU105197.1 GI:13554718
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Department of Virology
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Best Local Similarity 80.0%
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,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997). Location/Qualifiers
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2M0085D03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0085D03 R, DNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 47)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Jann, B., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb
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/db_xref="taxon:9606"
/clone="HSIQ1637"
/clone_lib="Sugano Homo sapiens cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                   50;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0085 cow: D column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/db_xref="taxon:10090"
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1. (badas 1 to 2)

Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Taira, H., Nakamura, Y., Morishita, S., Okubo, H., Suyama, A. and Sugano, S.

Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)

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Email: ysuzukiejims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library, Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 50)
2 (bases I to 50)
3 (bases I to 50)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Bach: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukiteins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,R., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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AU103768 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP12651, mRNA sequence.
AU103768
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="HEP11908"
/clone_lib="Sugano Homo sapiens cDNA library"
14 c 12 g 13 t
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/clone="HEP12651"
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   AU103765
AU103765.1 GI:13553286
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Matches 14; Conservative
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27 GCCCAGGGAAGCGAA 12
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AU103768/c
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SOURCE
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                              electrophoresis. Vector DNA was prepared from a derivative of pWN42 (qil4732114 |qb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplicillin resistance."
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Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan
5-5-1, Syazukitélins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
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AU103765 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP11908, mRNA sequence.
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Pred. No. 1.5e+04;
0; Mismatches 3; Indels 0
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Pred. No. 1.5e+04;
); Mismatches 3; Indels 0
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21 c 15 g 12 t
   10.5 kb range using preparative agarose gel
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/db_xref="taxon:9606"
/clone="HEP15178"
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AU105437
AU105437.1 GI:13554958
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83.3%;
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Best Local Similarity 83.3%;
Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserv
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RESULT 6 AU105437/c LOCUS DEFINITION

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

BASE COUNT

ORIGIN

AU103765/c LOCUS DEFINITION

RESULT

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BASE COUNT

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FEATURES

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ACCESSION

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SOURCE

JOURNAL

COMMENT

TITLE

FEATURES

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Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata, H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries uppublished (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries (npublished (2001)
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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AU103791 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone
HEP16708, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
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/db_xref="taxon:9606"
/clone="HEP15173"
/clone=lib="Sugano Homo sapiens cDNA library"
1 3 c 11 g 20 t
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18 t
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Pred. No. 2.4e+04;
); Mismatches 2; I
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Pred. No. 2.4e+04;
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/db_xref="taxon:9606"
/clone="HEP16708"
/clone_lib="Sugano Homo sapa 13 c 13 g 18
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ilarity 87.5%;
Conservative (
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87.5%;
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1 (bases 1 to 50)
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Suzuki, Mirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitcmo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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AU103787.1 GI:13553308
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AU103787/c
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Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki(elms.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).
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Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ott,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Brail: Suzuki@ims.u-tokyo.ac.jp
Suzuki,Y. Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-enclentiched CDNA library. Gene 200 (1-2), 149-156 (1997).
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AU103977 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP17580, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 2.4e+04;
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/db_xref="taxon:9606"
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/clone_lib="Sugano Homo
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Best Local Similarity 87.5
Matches 14; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
Unpublished (2001)
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Institute of Medical Science, University of Tokyo
Shirokanedai, Minatcku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitcone Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
A.S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA_library. Gene 200 (1-2), 149-156 (1997).
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Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.

Fine Structural and Sugano,G.

mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)

Contact: Yutaka Suzuki
Department of Virology
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AU103975 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HER10657, mRNA sequence.
AU103975 GI:13553496
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AU103974 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone
HEP00461, mRNA sequence.
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20 c 14 g 10 t
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/db_xref="taxon:9606"
/clone="HEP00461"
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AU103974.1 GI:13553495
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87.5%;
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                            1 ggcgccgtgaagcgaa 16
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AU103980 50 bp mRNA EST 05-APR-2001
AU103980 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT01573, mRNA sequence.
AU103980. GI:13553501
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                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="KAT01573"
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Search completed: October 2, 2001, 15:00:46 Job time: 10815 sec

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Run on:

Title:

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S77087 T-cell rece
AF195645 Erythroce
AF195643 Semopith
A69037 Sequence 25
AR018055 Sequence
E05905 Primer. 9/1
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      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                    1344157 seqs, 7733874588 residues
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Maximum Match 100%
Listing first 45 summaries
                                          OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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14-AUG-2000

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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 42)
Jorgensen,J.L., Esser,U., de St Groth,B.F., Reay,P.A. and
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red guenon.
Erythrocebus patas
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 38)
Karanth, P. and Stewart, C.B.
Direct Submission
Submitted (16-OCT-1999) Biological Sciences, State University of
New York, 1400 Washington Avenue, Albany, NY 12222, USA
1.38
                                                                                                                                                                                                                                                                                                                    <1. >42
/note="This sequence comes from FIG. 4 c; conceptual
translation presented here differs from translation in
publication"
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1 (bases 1 to 38)
Karanth, P., Stewart, C. B., Holt, R. A., deKoning, J. and Messier, W. Positive Darwinian selection on the lineage leading to humans Unpublished
                                                                                                                                                                                                                          GenBank staff at the National Library of Medicine created this GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 77087] from the original journal article. This sequence comes from FIG. 4 c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPPROTII2 38 bp DNA PRI 23-DEC-2000
Erythrocebus patas protamine P2 gene, exon 2 and complete cds
ARI95645.1 GI:11990583
                                                                                                                                                                                        Mapping T-cell receptor-peptide contacts by variant peptide immunization of single-chain transgenics Nature 355 (6357), 224-230 (1992)
                                 S77087 42 bp mRNA ROD 14-AUG-20
T-cell receptor beta chain V-J region {CDR3 region} {mice, transgenic, mRNA Partial, 42 nt}.
                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/product."T-cell receptor beta chain V-J region"
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/db_xref="G1:9800659"
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Pred. No. 2.1e+04;
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/organism="Mus sp."
/db_xref="taxon:10095"
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Mus sp.
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Best Local Similarity 88.2
Matches 15; Conservative
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            RESULT 2
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                                                         A08097 Synthetic o
A08101 Synthetic o
A08100 Synthetic o
A62490 Sequence 5
A69043 Sequence 1
L139593 Homo sapien
AR011280 Sequence
117918 Sequence 14
AR066368 Sequence
                                                                                                                                                                  S80826 gamma delta
AR003624 Sequence
A08096 Synthetic o
179231 Sequence 4
AR101074 Sequence
AX068306 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chandy.K.G., Kalman,K., Chandy,G. and Gutman,G.A.
Chandy,K.G., Kalman,K., Chandy,G. and Gutman,G.A.
Voltage-gated potassium channel gene, KV1.7, vectors and host cells comprising the same, and recombinant methods of making potassium channel proteins
Patent: US 5559009-A 3 24-SEP-1996;
Location/Qualifiers
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AR078949 Sequence
A36503 Sequence 44
AR080136 Sequence
AX097533 Sequence
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179830 Sequence 15
AR052426 Sequence
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191198 Sequence 39
             E04313 PCR primer
A45762 Sequence 19
AR069418 Sequence
                                               143148 Sequence 1
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A46142 Sequence 37
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 36;
                                                                                                                                                                                                                               1 (bases 1 to 36)
Budu,P., Rivierc,M., Audonnet,J. and Bouchardon,A. FELINE POLYNCLECTIDE VACCINE FORMULA Patent: WO 9803660-A 25 29-JAN-1998;
BAUDU PHILLIPEE (FR)
Other publication FR 2751223 19980123.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
         Indels
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          4;
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Pred. No. 3.4e+04;
0; Mismatches 1;
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Dillon, P.J. and Vockley, J.G.
Arginase II
Patent: US 5780286-A 12 14-JUL-1998;
         Mismatches
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                                                                                                                     Sequence 25 from Patent WO9803660.
A69037
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/organism="unidentified"
/db_xref="taxon:32644"
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10 c 8 g
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                                               19 GAAGATGCAGAAGGTACTAA 38
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Best Local Similarity 93.3%;
Matches 14; Conservative
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Best Local Similarity 93.3%;
Matches 14; Conservative
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      16; Conservative
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AR018055/c
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AR071945/c
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/product="protamine 2"
/protein_id="AAG42202.1"
/db_xref="G1:119905800"
/translation="WMYRMRSLSERPHEWHGQOVYGOEGGHNGQEEGGLSPEHVEVY
ERTHQGYSHHRRRRCSRRRLYRIHRRRHRSCRRRRRRSCRHRRRRRRGCRTRRRRCRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Semnopithecus entellus.
Semnopithecus entellus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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2 (bases 1 to 38)
Raranth,P. and Stewart,C.B.
Direct Submission
Submitted (16-OCT-1999) Biological Sciences, State University of
New York, 1400 Washington Avenue, Albany, NY 12222, USA
                                                                                                                                                                                                                                                                                                                                                                                                   SEPROTII2 38 bp DNA PRI 23-DEC-2000 SEPROTIILL SAGMODILHecus entellus protamine 2 gene, exon 2 and complete cds AF195643 GI:11990579
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1 (bases 1 to 38)
Karanth, P., Stewart, C.B., Holt, R.A., deKoning, J. and Messier, W. Positive Darwinian selection on the lineage leading to humans Unpublished
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                                                                                                                                                                                                                                                         Length 38;
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/organism="Semnopithecus entellus"
/db_xref="Laxon:88029"
/note="Common name:Hanuman langur"
join(AF195642.1:<1. .274,1. .>38)
/product="protamine 2"
join(AF195642.1:1. .274,1. .38)
                                                                                                                                                                                                                                                      Score 13.6; DB 91;
Pred. No. 2.7e+04;
0; Mismatches 4;
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80.0%;
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Best Local Similarity 80.0%;
Matches 16; Conservative (
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/number=2
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C12N9/22,C12N1/21,C12N15/55,(C12N9/22,C12R1:19),(C12N1/21, PC
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                                                                                                                                                                                                                                                                                                                                                                                 66.0%; Score 13.2; DB 10; Length 27; 83.3%; Pred. No. 4.4e+04; Live 0; Mismatches 3; Indels (
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                                                                                                                    1 (bases 1 to 27)
Cimino,G.D. and Lin,L.
Quality control assay for platelet decontamination
Patent: US 5565320-A 13 15-OCT-1996;
Location/Qualifiers
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JP 1993038286-A/3.
synthetic construct.
m synthetic construct
artificial sequence.
1 (bases 1 to 44)
Kimura, S.
VARIANT TYPE ESCHERICHIA COLI RIBONUCLEASE H
PATENT TYPE ESCHERICHIA COLI RIBONUCLEASE H
PATENT WOOGAKU KENKYUSHO:KK
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/db_xref="taxon:32630"
10 c 12 g 7 t
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Artificial sequence; Genes.
JP 1993038286-A/3
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07-AUG-1991 JP 1991197703
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topology: Linear;
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  I27338.1 GI:1818114
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Best Local Similarity 83.3
Matches 15; Conservative
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                                                                          Unknown.
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PD 19-FEE
PF 07-AUG
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Synthetic construct.

SM synthetic construct.

artificial sequence.

E 1 (bases 1 to 44)

S Kimura,S., Ishikawa, H. and Nakamura, H. .

KHILISAN SABILIZING PROTEIN MOLECULE

L Patent: JP 1993308963-A 3 22-NOV-1993;

ARTIFICIAL Sequence; Genes.

OS Artificial sequence; Genes.

PN JP 1993308963-A/3

PD 22-NOV-1993

PD 22-NOV-1993

PD 12-NOV-1993

PD 22-NOV-1993

PD 22-NOV-1993

PD 22-NOV-1993

CC Strandedness: Single;

CC topology: Linear; C. .

CC topology: Linear; C. .
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/db_xref="taxon:32630"
9 c 11 g 7 t
                                                                                                                    Unknown.
Unclassified.
1 (bases 1 to 43)
Vockley,J.G and Dillon,P.J.
Arghase II
Patent: US 5912159-A 12 15-JUN-1999;
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Sequence 13 from patent US 5565320.
127338
Sequence 12 from patent US 5912159.
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Location/Qualifiers
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10 c 8 g
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                                               AR071945.1 GI:7222833
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Matches 14; Conservative
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Serine protease inhibitor proteins, medicaments containing them, DNA sequences coding for these proteins and methods for producing Phase proteins, medicaments and DNA sequences Patent: EP 0373335-A 19 20-JUN-1990; Gruenenthal GmbH
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synthetic construct
artificial sequence.
1 (bases 1 to 28)
Heinzel-Wieland, R., Ammann, J., Steffens, G.J. and Flohe, L.
Serine protease inhibitor proteins, medicaments containing them,
DNA sequences coding for these proteins and methods for producing
                                                                                  Reaction-based selection for expression of and concentration of catalytic moieties
Patent: US 5631137-A 1 20-MAY-1997;
Location/Qualifiers
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1 (bases 1 to 28)
Heinzel-Wieland, R., Ammann, J., Steffens, G.J. and Flohe, L.
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Martin,M.T., Smith,R.G., Darsley,M.J., Simpson,D.M. and
Blackburn,G.F.
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Cerutti,M., Chaabihi,H., Devauchelle,G., Gauthier,L., Kaczorek,M.,
Lefranc,M. and Poul,M.
RECOMBINANT BACULOVIRUS AND USE THEREOF IN THE PRODUCTION OF
MONOCLONAL ANTIBODIES
PARTENT: WO 9520672-A 19 03-AUG-1995;
PROTEINE PERFORMANCE (FR)
Other publication FR 2715664 9508015
Other publication FR 2715664 950804.
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Marthi,M.T., Smith,R.G., Darsley,M.J., Simpson,D.M. and
Blackburn,G.F.
Reaction-based selection for expression of and concentration of
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Patent: US 5891648-A 1 06-APR-1999;
          Sequence 19 from Patent W09520672.
A45762
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Sequence 1 from patent US 5631137.
143148 1 GI:2468392
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/db_xref="taxon:32644"
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these proteins, medicaments and DNA sequences
Patent: EP 0373335-A 23 20-JUN-1990;
Gruenenthal GmbH
Location/Qualifiers
1. 28
//organism="synthetic construct"
//db_xref="taxon:32630"
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                      JOURNAL
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source

BASE COUNT ORIGIN

Gaps ö Query Match
Best Local Similarity 87.5%; Pred. No. 7.1e+04;
Matches 14; Conservative 0; Mismatches 2; Indels

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Search completed: October 2, 2001, 15:56:39 Job time: 14163 sec

67.0 43 18 AAV00587 67.0 43 19 AAV17634 67.0 43 20 AAX77316 67.0 43 21 AAA08070 67.0 44 14 AAQ40649 67.0 44 15 AAO53496	13.4 67.0 44 13.2 66.0 27 13.2 66.0 27 13.2 66.0 27	13 65.0 44 14 AAQJ87/11 13 65.0 44 14 AAQJ6640 13.65.0 44 20 AAXJ4253 12.8 64.0 21 16 AAQJ5681	12.8 64.0 35 19 AAV49413 12.8 64.0 35 22 AAC90404	12.8 64.0 36 20 AAX56/35 12.8 64.0 36 21 AAC55237	12.6 63.0 21 13 AAQJS5015 12.6 63.0 21 AAQJS5338 13.6 63.0 35 30 38 30710064	12.6 63.0 26 18 AAT81543	12.6 63.0 26 19 AAV21769 . 12.6 63.0 36 20 AAV08912 . 12.6 63.0 36 21 AAZ95630 . 12.6 63.0 39 21 AAZ955133	12.6 63.0 43 21 12.4 62.0 25 18 12.4 62.0 28 21	12.4 62.0 29 19 AAV34689 12.4 62.0 30 21 AAA30159 12.4 62.0 35 21 AAZ59858	Constitution to	ALIGNMENTS	SULT 1 265538	ID AAC65538 standard; DNA; 20 BP. KX	AAC65538; **	77 12-FEB-2001 (first entry)	DE Human focal adhesion kinase antisense sequence #4.	KW Human; focal adhesion kinase; FAK; signal transduction; cancer; KW embryonic development disorder; angiogenic disorder; wound healing;	Homo sapiens.	US613	KX pp 17-0CT-2000.	KX PF 19-AUG-1999; 99US-0377310.	KX PR 19-AUG-1999; 99US-0377310.	XX PA (ISIS-) ISIS PHARM INC.	XX PI Monia BP, Gaarde WA;	XX DR WPI; 2001-006141/01.	New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal	
	i n n n n i			N m c	n min	n chi chi c		4 4				RESUL AAC65	0 X														PT X
4.5 Compugen Ltd.	Search time 876.95 Seconds (without alignments) 14.320 Million cell updates/sec				:s: 854978			seqn/NA1980.DAT:*	geneseqn/NA1981.DAT:* geneseqn/NA1982.DAT:* geneseqn/NA1983.DAT:*	segn/Na1984.DaT:* egn/Na1985.DaT:*	eeqii/ nalago . Dal: * eeqii/ nalago . Dal: * eeqii/ nalago nam: *	seqn/NA1989.DAT:* :seqn/NA1989.DAT:*	sseqn/NA1991.DAT:* \seqn/NA1992.DAT:*	seqn/Na1993.DAT:* seqn/Na1994.DAT:*	.seqn/NA1995.DAT:* .seqn/NA1996.DAT:*	genesegn/NA1997.DAT:*		Juywezoot by chanc	the result being pr e distribution.			Description	Human rocal adhesi Human focal adhesi	Dystropnin gene sp Neisseria species	# E C	HIV-1 fragment PCR PCR primer used to	Primer AB067 for F PCR primer 5R used
GenCore version 4.5 Copyright (c) 1993 - 2000 Com nucleic search, using sw model	2001, 16:18:35 ;	US-09-757-100B-6 20 1 gaaactgcagaaggcactga 20	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	730101 seqs, 313950809 residues	hits satisfying chosen parameters	length: 0 length: 50	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Geneseq_0601:* /SIDS8/gcgdata/geneseg/	 /SIDSB/gcgdata/geneseq/geneseqn/NA1981.DAT.* /SIDSB/gcgdata/geneseq/geneseqn/NA1982.DAT.* /SIDSB/gcgdata/geneseq/geneseqn/NA1983.DAT.* 	5: /SIDS8/gcgdata/geneseq/genes 6: /SIDS8/gcgdata/geneseq/genes	/: /SIDSB/gcgdata/geneseq/gene: 8: /SIDSB/gcgdata/geneseq/gene: 9: /SIDSB/gcgdata/geneseg/genes	o. //SIDS8/gcgdatta/geneseq//genesequ/.na.200.Lbal.* 11: /SIDS8/gcgdatta/geneseq//geneseqn/.NA1980.DbAl.* 11: /SIDS8/gcgdatta/geneseq//geneseqn/.NA1990.DbAl.*	12: /SIDS8/gcgdata/geneseq/gene 13: /SIDS8/gcgdata/geneseg/gene	14: /SIDS8/gcgdata/geneseg/gene 15: /SIDS8/gcgdata/geneseg/gene	16: /SIDS8/gcgdata/geneseg/gene 17: /SIDS8/gcgdata/geneseg/gene	18: /SIDS8/gcgdata/geneseq/gene	/SIDS8/gcgdata/geneseq/ /SIDS8/gcgdata/geneseq/ /SIDS8/gcgdata/geneseq/ /SIDS8/gcgdata/geneseq/	the number of results pre	r than or equal to the score ed by analysis of the total	SUMMARIES		Length DB	15 22	33 21	40 17	68.0 42 21 AA256558 67.0 20 20 AA204825	36 19 43 18
OM nucleic - nucl		Title: Perfect score: Sequence:	Scoring table:	Searched:	Total number of }	Minimum DB seq le Maximum DB seq le	Post-processing:	Database :		•	0	,				. 16		Pred. No. i	score great and is deri		, ,	Score	-1 0 1	J 4 n	n 40 r	c 8 13.6 c 9 13.4	10 13.4 c 11 13.4

adeno-associated virus; AAV;

98JP-0142134 98JP-0142134.

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encoding a shortened dystrophin - useful for the treatment of
                                                                                                                                                                                                                                                                                                                                                                  (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
(KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO
                                                                                                                                                                                                Muscular dystrophy; rod domain; adeno-assodystrophin gene; truncated; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 10; 44pp; Japanese.
                                                                                                                                                                       Dystrophin gene specific primer R5.
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AAZ48582 standard; DNA; 40 BP.
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                       The present invention describes a number of phosphorothicate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a number of phosphorothicate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated
                                                             in cancer, particularly colon, breast and oral tumours, embryonic development disorders, anglogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                   Human; focal adhesion kinase; FAK; signal transduction; cancer;
embryonic development disorder; angiogenic disorder; wound healing;
antisense; phosphorothioate; ss.
                                                                                                                                                                                                ö
                                                                                                                                                                     ; DB 22; Length 20;
                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Human focal adhesion kinase antisense sequence #24.
                                                                                                                               Sequence 20 BP; 8 A; 4 C; 6 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15 BP; 6 A; 4 C; 4 G; 1 T; 0 other;
                                                                                                                                                                                                Mismatches
                                                                                                                                                                       Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Column 25; 30pp; English
Claim 3; Column 23; 30pp; English
                                                                                                                                                                                                ö
                                                                                                                                                                     100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                      99US-0377310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0377310.
                                                                                                                                                                                                                                                                                                                AAC65558 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaarde WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-006141/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6133031-A.
                                                                                                                                                                                                                                                                                                                                                                  12-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monia BP,
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& X C C C C C C X X
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The invention provides a gene for the treatment of muscular dystrophy having at least one rod repeat structure of hinge 1, hinge 4 and rod domain of dystrophin gene and having a base sequence of 4.5 kb. The gene and a gene-introducing medium consisting of an adeno-associated virus (AAV) vector or lentivirus vector containing the rod shortened dystrophin genes can be used for the genetic treatment of muscular dystrophy of low immune reaction. Sequences AAZ48572-584 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; PCR primer; ss.
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                  Length 40;
                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                Score 14.8; DB 21;
Pred. No. 4.6e+02;
0; Mismatches 2;
                                                                                                                                                                                                   Sequence 40 BP; 4 A; 13 C; 12 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria species ORF cloning PCR primer #60.
                                                                                                                                                       dystrophin gene specific primers.
                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                74.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                        2 aaactgcagaaggcactg 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ54675 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                             21 AGACTGCAGAAGGCCCTG 4
                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 16; Conserv
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Gaps

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75.0%; Score 15; DB 22; Length 15; 100.0%; Pred. No. 3.3e+02; ive 0; Mismatches 0; Indels

Conservative

Query Match Best Local Similarity Matches 15; Conserv

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Genomic sequences AAT04954-55 of mouse Kv1.7 voltage-gated potassium channel (see AAT04953) show the splice donor and acceptor sites which form the boundaries of the single intervening sequence (see Fig 1A). These sequences are compared with that of mouse (mKv1.7 and hamster (haKv1.7) cDNAs. The potassium channel may be used in drug screening for identification of therapeutics which modulate the channel and, therefore, modulate insulin secretion. Selective antagonists increase insulin release and thereby reduce hyperglycemia associated with non-insulin-dependent diabetes
                                                                                                                                                                                                                                                                                                                                                                          New voltage-gated potassium channel gene - used to identify material(s) which can increase insulin release e.g. for treating non-insulin dependent diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fas ligand; transplant rejection; autoimmune disease; diabetes; inflammation; graft rejection; rheumatoid arthritis; allergy; cystic fibrosis; multiple sclerosis; polymerase chain reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 13.8; DB 16; Length 25;
Pred. No. 1.3e+03;
0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25 BP; 2 A; 11 C; 5 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                  Gutman GA, Kalman K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soluble mouse Fas ligand gene 5' DNA primer.
                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 20; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT09688 standard; DNA; 40 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.0%;
88.2%;
                                                                                                                                                                    95WO-US02221.
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Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 GGAACTGCAGAAGGGAC 1
                                                                                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA.
                                        14..25
/*tag=
                                                                                                                                                                                                                                                                                                  Chandy KG,
                                                                                                                                                                                                                                                                                                                                     WPI; 1995-320573/41.
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                                                                                            WO9523858-A1
                                                                                                                                                                                                         LO-AUG-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JAN-1995;
                                                                                                                                                                    23-FEB-1995;
                                                                                                                                                                                                                            04-MAR-1994;
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                                                                                                                               08-SEP-1995
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                                                                                                                                                                                                                                                                                                  Chandy G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT09688;
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                     Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54578 to AAZ54576 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention
                                                                                                                                                                                                                                                                                                                                                                                           Masignani V, Mora M;
Scalato E, Scarselli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse Kv1.7 voltage-gated potassium channel splice site;
insulin antagonist drug screening; insulin agonist drug screening;
non-insulin-dependent diabetes mellitus; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Splice site for mouse Kv1.7 voltage-gated potassium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.0%; Score 14; DB 21; Length 33; 100.0%; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                           Hickey E,
Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 33 BP; 14 A; 5 C; 9 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 16; Page 141; 1453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           Galeotti C, Grandi G,
, Pizza M, Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT04955 standard; DNA; 25 BP
                                                                                                                                                              98US-0083758.
98US-0098894.
98US-0099094.
98US-0103749.
98US-0103796.
99US-0103796.
                                                                                                                             99WO-US09346
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                                                                                                                                                                                                                                                                                                                                                      (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Petersen J, Pizza M,
Tettelin H, Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 aaactgcagaaggc 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 aaactgcagaaggc 14
                                                                                                                                                                                                                                                                                                                                     (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-062150/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 14; Conserv
                   Neisseria sp.
                                                    WO9957280-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                             30-APR-1999;
                                                                                                                                                                                                                                                         09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-APR-1996
                                                                                           11-NOV-1999
                                                                                                                                                                                                       02-SEP-1998
                                                                                                                                                                                                                        02-SEP-1998
                                                                                                                                                                                                                                            09-OCT-1998
Synthetic
                                                                                                                                                                                                                                                                                                                                                                                           Fraser C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT04955;
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RESULT 5 AAT04955/C

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Length 42; Indels

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The present invention describes a gene amplification system comprising a transducing vector, a packaging vector and a suitable host. The lentiviral vectors are useful to transform suitable host. The certification of the vectors are useful to transform suitable host. The certification of a dividing human cells (e.g. neuronal cells and hemantopoietic stem on-dividing human cells (e.g. neuronal cells and hemantopoietic stem colls) e.g. in gene therapy. The vector system is also useful to produce polypeptides in cells (e.g. TE671 and HeLa cells) in vitro and in vov, and to produce transgenic animals e.g. animals expressing human proteins. Use of modified lentiviral packaging vectors reduces the risk of generating replication-competent virus through recombination with the transducing vector or a defective provirus endogenous to the vector system provides increased long-term gene expression compared with prior art lentivirus packaging vectors. The vector system provides increased long-term gene expression compared with prior art lentivirus packaging vectors. The vector system provides increased long-term gene expression compared with other viral vectors (e.g. could remain transduced for at least 120 days), so it may be possible for the vector to remain transduced for the necessary time course of a particular treatment. AAZ55538 to AAZ5578 represent nucleotide sequences used in the exemplification of
express specific genes at high levels, e.g. for gene therapy. The improved vectors are safer, yet permit increased efficiency of packaging the recombinant viral genome and increased long-term gene expression. These properties are required for gene therapy as a means of treating infectious and non-infectious diseases. Unlike other retroviruses, the lentiviruses are able to infect non-dividing cells. The present sequence represents an HIV VPx C-terminal and Tat N-terminal PCR primer which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New gene amplification system, useful to express a target gene in cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene amplification system; gene therapy; packaging;
                                                                                                                                                                                                                                                                                             Score 13.6; DB 21;
Pred. No. 1.6e+03;
); Mismatches 4;
                                                                                                                                                                                                                         Sequence 42 BP; 4 A; 15 C; 5 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 98; 197pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                68.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HÎV-1 fragment PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                                                                                                            23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US11634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ56558/c
ID AAZ56558 standard; DNA; 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           GAAAGAGCAGAAGACAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                    gaaactgcagaaggcactga
                                                                                                                                                                                                                                                                                             Query Match 68.0
Best Local Similarity 80.0
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.g. in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-072617/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lentiviral vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               42
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     888888888
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(a) its major splice donor site is either deleted or is sufficiently different from the reference lentivirus so that it is not a potential site for homologous recombination; and (b) it lacks a functional major packaging signal so that the introduced vector causes the host cell to produce packaging vector particles comprising functional Gag and Pol proteins. The vectors are useful for transforming (eukaryotic) cells to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New packaging vector comprising a nucleotide sequence encoding Gag and Pol proteins of a reference lentivirus useful for the delivery of non-lentiviral genes to target cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lentiviral vector; packaging; gag; pol; gene therapy; infection; gene expression; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                          the full-length
                                                                                                                                                                                            Use of Fas ligand - for suppressing lymphocyte-mediated immune responses, e.g. transplant rejection or auto-immune conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                   soluble mouse Fas ligand gene. It is used in conjunction with the 3' DNA primer (AAT07687).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV Vpr C-terminal and Tat N-terminal PCR primer SEQ ID NO:15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.0%; Score 13.8; DB 17; 88.2%; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 40 BP; 9 A; 13 C; 11 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 148; 311pp; English.
                                                                                                                                                                                                                                                                      Disclosure; Page 32; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ88079 standard; DNA; 42 BP
  94US-0250478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US11516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0086635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 aactgcagaaggcactg 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 acctgcagaaggaactg 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                          Use of Fas ligand - for
                                                (COLS ) UNIV COLORADO
                                                                                                 Duke RC;
                                                                                                                                              WPI; 1996-030252/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-137067/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHAN/) CHANG
  27-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-APR-2000
                                                                                                 Bellgrau D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ88079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chang L;
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BP.

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Multivalent vaccine; cat; pathogen; respiratory disease; FeLV; FPV; FCV digestive disease; Feline leukademia virus; feline palleukopaenia virus; feline calcivirus; feline immunodeficiency virus; FTV; rabies virus; vector; envelope glycoprotein; primer; PCR; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multi-valent polynucleotide vaccines against feline pathogens -consist of at least 3 plasmids able to express protective antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 17; Page 16; 42pp; French.
                                                                                                                                                                                                                                                                                    for FIV env gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Feline immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96FR-0009337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96FR-0009337.
                                                                                                                                             AAV49285 standard; DNA; 36
                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INMR ) RHONE MERIEUX SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baudu P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                consist of at least 3 press from specified viruses
       WPI; 1998-112823/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Audonnet JCF,
                                                                                                                                                                                                                                                                                    Primer AB067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FR2751223-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUL-1996;
                                                                                                                                                                                                                                     28-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                         AAV49285;
                                                                                               10
                                                                                                                  AAV49285
                                                                                                 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR primers AAZ01426-206209 were used to amplify open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs encode polypeptides (see AAX36754-Y37949) which can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diseases such as conventional trachom, nonendemic trachom, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and veneraal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eye disease; conventional trachoma; nonendemic trachoma;
                                                                                                                                                                   ö
                                                                                                                       Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR primer used to amplify an ORF of Chlamydia trachomatis.
                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.4; DB 20;
Pred. No. 1.9e+03;
0; Mismatches 1;
                                                                                                                  Score 13.6; DB 21;
Pred. No. 1.6e+03;
0; Mismatches 4;
                                              Sequence 42 BP; 4 A; 15 C; 5 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 1720; 1755pp; English.
                                                                                                                                                              0;
                                                                                                                  68.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                             1 gaaactgcagaaggcactga 20
                                                                                                                                                                                                                                          42 GAAAGAGCAGAAGACAGTGA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97FR-0015041,
97FR-0016034,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-IB01939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0107077
                                                                                                                                                                                                                                                                                                                                                                            AAZ04825 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-OCT-1999 (first entry)
                                                                                                                  Query Match 68.0°
Best Local Similarity 80.0°
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 67.0
Best Local Similarity 93.3
Matches 14; Conservative
the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-371125/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ04825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccine;
                                                                                                                                                                                                                                                                                                                                                      AAZ04825/c
                                                                                                                                                                                                                                                                                                                             RESULT
SXC
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Riviere MEA;

Bouchardon A,

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The invention relates to a multivalent vaccine for protecting cats against several pathogens, especially pathogens associated with respiratory and digestive diseases. The pathogens are especially selected from feline leukaemia virus (FeLV), feline panleukopaenia virus (FPV), feline calcivirus (FCV), feline immunodeficiency virus (FIV), or rabies virus. The vaccines are preferably composed of polynucleotide sequences encoding 3 antigens, all as part of vectors. Primers AAV49285-V49286 were used to PCR amplify the feline immunodeficiency virus (FIV) petaluma strain gene encoding the envelope glycoprotein. The sequence sub-cloned into the plasmid pVR1012 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  67.0%; Score 13.4; DB 19;
93.3%; Pred. No. 2e+03;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                         generate plasmid pAB030 for use in the vaccine.
                                                                                                                                                                                                                                                                                                                                                  Sequence 36 BP; 14 A; 6 C; 11 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT84971 standard; DNA; 43 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 aaactgcagaaggca 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT84971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
AAT84971/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DXXXE
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Gaps

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Indels

Length 20;

67.0%; 93.3%;

4 actgcagaaggcact 18

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(first entry)

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Arginase II; proline production; glutamate production; hyperarginaemia; nitric oxide biosynthesis; arginase activity; urea cycle disease; hypertension; hypotension; hyperammonaemia; prostate disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding human arginase II - useful for treating, diagnosing and monitoring e.g. urea cycle disorders, hypotension, nitric oxide-mediated immune and nervous diseases, etc
                                                                      PCR primer 5R used to amplify arginase II from a cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC. (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 3; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-470868/43.
                                                                                                                                                                                                  PCR primer; ss.
                                                                                                                                                                                                                                                                                             WO9733986-A1.
                                                                                                                                                                                                                                                                                                                                                                                              20-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAR-1996;
                      25-MAR-1998
                                                                                                                                                                                                                                                                                                                                                18-SEP-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dillon PJ,
                                                                                                                                                                                                                                                Synthetic.
Turkat cell line cDNA library. The cDNA sequence of Arginase I was used as a probe sequence for a computer search of cDNA databases. Several expressed sequence for a computer search of cDNA databases. Several expressed sequence tags with 50-60% sequence. The above PCR primers were designed to the extreme 3' and 5' ends of the consensus sequence, and used to isolate arginase II. In addition to a hypothetical role in the production of proline and glutamate, it is postulated that arginase II. In addition to a hypothetical role in the production of proline and glutamate, it is postulated that arginase II, or its agonists, antagonists and fragments, are used to treat conditions associated with lack of arginase activity. Compounds that inhibit activation of the protein are used to treat conditions associated with excess arginase activity. Typical conditions that can be treated are diseases of the urea cycle, hypertension, hypotension (caused by sepsis or cytokines), episodic hyperammonaemia, defective synthesis of proline, glutamate, nitric oxide or ornithine.

Caused by sepsis or cytokines), episodic hyperammonaemia, defective synthesis of proline, glutamate, nitric oxide or ornithine.

Pyperarginaemia and related spasiticity, prostate or kidney damage, also nitric oxide associated immune and nervous system diseases. The arginase II cDNA is used to produce recombinant protein and for chromosome in the contract arginase II-encoding sequences and to diagnose the above
                                                                    Arginase II; proline production; glutamate production; hyperarginaemia; nitric oxide biosynthesis; arginase activity; urea cycle disease; hypertension; hypotension; hyperammonaemia; prostate disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primers AAT84962-74 were used to amplify human arginase II from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide encoding human arginase II - useful to treat, diagnose and monitor, e.g. urea cycle disorders, prostatic disease, hypotension and nitric oxide mediated immune and nervous diseases
                      PCR primer 5R used to amplify arginase II from a cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 43 BP; 8 A; 10 C; 8 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 3; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                              96WO-US03561.
                                                                                                                                                                                                                                                                                                                                                                                              96WO-US03561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dillon PJ, Vockley JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-470867/43.
                                                                                                                                                PCR primer; ss
                                                                                                                                                                                                                                             WO9733985-A1
                                                                                                                                                                                                                                                                                                                                              14-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                              14-MAR-1996;
                                                                                                                                                                                                                                                                                             18-SEP-1997.
                                                                                                                                                                                             Synthetic.
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NAME OF THE PROOF OF THE PROOF

96WO-US13455. 96WO-US03561.

Vockley JG;

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                                                                                                                                                                                                                                                                                                                                                  through the production of ornithine as a precursor of glutamate.
Arginase II, or its agonists, antagonists and fragments, are used to treat conditions associated with lack of arginase activity. Compounds that inhibit activation of the protein are used to treat conditions associated with excess arginase activity. Typical conditions that treated are diseases of the urea cycle, hypertension, hypotension (caused by sepsis or cytokines), episodic hyperammonaemia, defective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthesis of proline, glutamate, nitric oxide or ornithine, hyperarginaemia and related spasticity, prostate disease (e.g. cancer, prostatitis and benign hypertrophy), prostate or kidney damage, also nitric oxide associated immune and nervous system diseases. The arginase II CDNA is used to produce recombinant protein and for chromosome
PCR primers AAV00578-90 were used to amplify human arginase II from a Jurkat cell line cDNA library. The cDNA sequence of Arginase I was used as a probe sequence for a computer search of CDNA databases. Several expressed sequence tags with 50-60% sequence homology were identified. These were combined to give a 1075 bp sequence. The above PCR primers were designed to the extreme 3' and 5' ends of the consensus sequence, and used to isolate arginase II. In addition to a hypothetical role in the production of proline and glutamate, it is postulated that arginase II may play an important role in nitric oxide biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        identification, while its fragments are used (as primers and probes) to detect arginase II-encoding sequences and to diagnose the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 13.4; DB 18;
Pred. No. 2e+03;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 43 BP; 8 A; 10 C; 8 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ő
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AAV17634/c
ID AAV17634 standard; DNA; 43 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.0%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 actgcagaaggcact 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 ACTGCAGAAGGCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches
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Gaps

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Length 43; Indels

Score 13.4; DB 18; Pred. No. 2e+03;); Mismatches 1;

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67.0%; 93.3%;

Query Match 67.0 Best Local Similarity 93.3 Matches 14; Conservative

4 actgcagaaggcact 18

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16 ACTGCAGAGGCAAT

AAV00587 standard; cDNA; 43 BP.

RESULT 12 AAV00587/ AAV00587;

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The invention relates to a polypeptide with Arginase II activity. The Arginase II polypeptides may be used in gene therapy for the treatment of type I arginase disorders resulting in hyperargininemia. The polypeptide sequences may also be used as immunogens to produce antibodies, these antibodies may then be used to treat numerous diseases e.g. urea disorders, hypertension, hypotension, prostate cancer, benign prostatic hyperplasia. Sequences AAXY7307-319 represent PCR primers used for cloning the Arginase II cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uropathic; cytostatic; neuroprotective; gene therapy; hypertension; nitric oxide biosynthesis modulator; urea cycle disease; hypotension; episodic hyperammonaemia; hyperargininaemia; spasticity; prostatitis; growth retardation; progressive mental impairment; prostate disease; prostate cancer; benign prostatic hyperplasia; hypertrophy; prostate damage; kidney disease; kidney damage; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arginase II; arginase I; diagnosis; hypotensive; hypertensive;
                                                                                                                                                                                                                                                        Polypeptides with Arginase activity, useful for treating type arginase and disorders resulting in hyperargininemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 43 BP; 8 A; 10 C; 8 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 13.4; DB 2
Pred. No. 2e+03;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human arginase II PCR primer SEQ ID NO:12.
                                                                                                                             (HUMA-) HUMAN GENOME SCI INC. (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC. (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ő
                                                                                                                                                                                                                                                                                                                  Examples; Fig 3; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA08070 standard; DNA; 43 BP.
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97US-0914981.
96US-0700186.
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93.3%;
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Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                   Vockley JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 ACTGCAGAAGGCAAT 2
                                                                                                                                                                                                                      WPI; 1999-357201/30.
                                    20-AUG-1997;
                                                                                          20-AUG-1996;
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                                                                         20-AUG-1997;
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20-AUG-1997;
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15-JUN-1999
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ID AAA08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human arginase II protein – useful for treating, e.g. diseases associated with defect in arginase II gene such as episodic
                                                                                                                                          diagnosis; susceptibility; urea cycle; hypertension; hypotension; episodic; proline; blosynthesis; defect; glutamate; nitric oxide; ornithine; hyperargininaemia; spasticity; growth retardation; mental impairment; prostate; cancer; prostatis; benign prostatic; hyperplasia; hypertrophy; damage; kidney; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arginase II; gene therapy; hyperargininemia; immunogen; human; urea cycle disorder; hypertension; hypotension; prostate cancer; benign prostatic hyperplasia; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 43;
                                                                                                                             human; arginase II; disease; gene defect; hyperammonaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 2e+03;
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                                                                                        Homo sapiens arginase II gene PCR primer.
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                                                     (first entry)
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RESULT 14

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Gaps

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Dillon PJ, Vockley JG;
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WPI; 2000-328355/28

Novel human arginase II polypeptides useful for treating urea cycle diseases, hypertension, hypotension, episodic hyperammonemia, to control nitric oxide formation and kidney damage -

Example 1; Fig 3; 37pp; English

The present invention describes human arginase II. Arginase II has hypertensive, hypertensive, uropathic, cytostatic and neuroprotective activities, and can be used in gene therapy and as an intric oxide activities, and can be used in gene therapy and as an intric oxide activities modulator. Human arginase II proteins can be used to treat diseases associated with or caused by a defect in the arginase II gene expression, such as, for e.g. urea cycle diseases, hypertension, hypotension, episodic hyperammonaemia, defects in biosynthesis of proline, glutamate, nitric oxide and ornithine, as well as hyperargininaemia and its related spasticity, growth retardation, and progressive mental impairment, and prostate disease, particularly prostate cancer, prostatitis and benign prostatic hyperplasia or prostate to montrol nitric oxide formation in an original and its also used to control nitric oxide formation in an individual. Arginase II or its fragments, variants or derivatives can be used as diagnostic reagents for diagnosing arginase II are used in an individual having or suspected of having a defect in the nitric oxide pathway and the urea cycle. The genes encoding arginase II are used in also used to deplace systemic arginine levels in an individual. AAA08061

Sequence 43 BP; 8 A; 10 C; 8 G; 17 T; 0 other;

Gaps ; 0 67.0%; Score 13.4; DB 21; Length 43; 93.3%; Pred. No. 2e+03; 1ve 0; Mismatches 1; Indels (Query Match 67.0 Best Local Similarity 93.3 Matches 14; Conservative

4 actgcagaaggcact 18 ð

16 ACTGCAGAAGGCAAT 셤 Search completed: October 2, 2001, 16:18:36 Job time: 15480 sec

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TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Unpublished (2000) COMMENT Contact: Robert B. Weiss University of Utah Genome Center	PENTURES FEATURES FEATURES FOLDOR—"Water and the properties and the profit of properties and the profit of profit	Oy 5 ctgcagaaggcactga 20 Db 18 CAGCATAAGGCACTGA 3	RESULT 2 A2759899 34 bp DNA GSS 16-FEB-2001 LOCUS DEFINITION IM0553A10F Mouse 10kb plasmid UUGCIM library Mus musculus genomic ACCESSION A2759899 1 GI:12867159 KEYWORDS SOURCE Names mouse. ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. AUTHORS Ito 34) AUTHORS Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Result Query No. Score Match Length DB ID Description	C 1 12.8 64.0 33 250 AZ809687 AZ809687 2M0073M14 2 12.8 64.0 34 24 AZ809687 AZ809687 2M0073M14 3 12.8 64.0 37 139 139 139 139 139 139 4 12.6 63.0 63.0 46 129 140 464 47 44 4246457 AA016378 AA016378 AA016378 5 12.6 63.0 63.0 40 120 40 40 40 40 40 6 12.6 63.0 63.0 40 40 40 40 40 7 12.6 63.0 63.0 63.0 40 40 40 40 8 12.6 63.0 63.0 63.0 40 40 40 9 12.2 61.0 31 24 AZ44647 AA016378 AA010278 AA010278 10 12.2 61.0 31 24 AZ43216 AA013617 AA010615 AA010278 AA010278 AA010278 11 12.2 61.0 31 24 AZ43216 AA010278 AA010278 AA010278 12 12.2 61.0 31 24 AZ43216 AA010278 AA010278 13 12.2 61.0 31 24 AZ43216 AA010278 AA010278 14 12.2 61.0 31 24 AZ43216 AA010278 AA010278 15 12 60.0 46 11 AA9716 AA0187 AA0187 AA0187 15 12 60.0 46 11 AA787 AA0187 AA0187 AA0187 15 12 60.0 46 12 AZ43216 AA0187 AA0187 AA0187 15 16 60.0 46 24 AZ43216 AA0187 AA0187 AA0187 16 17 60.0 40 40 40 AZ447 AA0187 AA0187 AA0187 18 19 60.0 40 40 AZ447 AA0187 AA0187 AA0187 AA0187 19 10 60.0 40 40 AZ447 AA0187	ALIGNMENTS	RESULT 1 A2809697/C AZ809697 33 bp DNA GSS 20-FEB-2001 DEFINITION 2M0073M14R Wouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZW0073M14 R, DNA sequence. AZE09697 1 G1:1297622 KEYWORDS GSS 20-FEB-2001 AZE09697 1 G1:1297622 SOURCE house mouse. Normalias musculus ENKARYOCIA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutherla; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 33) AUTHORS 1 to 33) AUTHORS 1 to 33, AUTHORS 1 to 34, AUTHORS 1 kose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (q1|4732114|q1b|AFL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
      Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Unpublished (2000)
University of Utah Genome Center
University of Utah
Fin. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hehl, A., Manger, I., Marra, M., Parmley, S., Sibley, L.D., Hillier, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/G1 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Toxoplasma.
1 (bases 1 to 37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.0%; Score 12.8; DB 249; Length 34; 87.5%; Pred. No. 6.6e+04; ive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0553 row: A column: 10
Seg primer: cGTTGTAAAACGACGCCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="UUGC1M0553A10"
                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 34.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="C57BL/6J
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and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Matches 14; Conserv
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LOCUS
DEFINITION
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VERSION
KEYWORDS
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AUTHORS
                                                              JOURNAL
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                    TITLE
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/note="Vector: Bluescript II SK-; Site_1: EcoRI; Site_2:
NotI; Mature bradyzoites were obtained from infected mouse
brains by percoll density centrifugation. The original
library was constructed by Steve Parmiey, Palo Alto
Medical Foundation. cDNAs were synthesized by priming with
oligo d(T) and directionally cloned into the EcoRI/NotI
sites of lambda gill. Warning: the library contains a
small percentage of host cDNAs derived from mouse cells.
Inserts from this cDNA library were excised with Notl and
EcoRI, size selected in a range of 0.7 - 2.0 kb and
subcloned into Bluescript II SK- (Adrian Hehl, Ian Manger
and John Boothroyd, Stanford University)"
Allen, M., Bowles, L., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, N., Jost, S., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, Freising, B., Bowers, Y., Wylie, T., Ajioka, J.A., Aslett, M.A., Wan, K.L., Wilson, R., Waterston, R. and Boothroyd J.C.
Wash U. Stanford - PAMF-NIH Toxoplasma EST project
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I (bases 1 to 33)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="tgzz35g06.rl"
/clone_lib="TgME49 invivo Bradyzoite cDNA size selected"
/dev_stage="Bradyzoite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE739126 33 bp mRNA EST 15-SEP-2000 601556265F1 NIH_MGC_58 Homo sapiens CDNA clone IMAGE:3826072 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Email: cgapbs remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                          Email: toxo@watson.wustl.edu
Contact John Boothroyd (jboothr@leland.Stanford.EDU) for
information on clone and library availability.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 6.6e+04;
0; Mismatches 2;
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/organism="Toxoplasma gondii"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host-"DH10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
;
                                                                                                                                                                      Unpublished (1997)
Contact: Marra M
WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="ME49"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE739126.1 GI:10153118
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Best Local Similarity 87.5%;
Matches 14; Conservative C
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
TH: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 4)

Dunn, D., Aoyaqi A.)

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1M0274A02F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0274A02 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/clone="UUGC1M0274A02"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.0%; Score 12.6; DB 159; Length 46; 78.9%; Pred. No. 8.4e+04; Live 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Std Error: 0.00
                                 /organism="Homo sapiens"
/db_xref="GDB:3888014"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Prosect Trow: A column: 02
Seq primer: GGTPGTAAAACGAGGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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Class: plasmid ends
High quality sequence stop: 47.
Location/Qualifiers
                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:258404"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="C57BL/6J
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1 (Dases 1 to 46)

4 Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hullman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

The Washuf Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
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clone IMAGE:258404 5' similar to gb:J00117 CHORIOGONADOTROPIN BETA
CHAIN PRECURSOR (HUMAN);, mRNA sequence.
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High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Frace considered overall poor quality
Seq primer: T7
High quality sequence stop: 1.
Location/Qualifiers
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.a column: 17
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Location/Qualifiers
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N40673.1 GI:1164270
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Best Local Similarity 78.9
Matches 15; Conservative
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/tissue_type="placenta"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="DHIOB"
/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
fist strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                    retraccaatcraactgaactgaccgcccggaaattrittrittrittrit

T 1; J; double-stranded cDNA was ligated to Eco R adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pr773 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M.Fatima Bonaldo."
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Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Suzuki, Manatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a S'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \begin{array}{lll} \text{mRNA} & \text{EST} & \text{O5-APR-2001} \\ \text{sapiens cDNA library Homo sapiens cDNA clone} \end{array}
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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       /clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
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18 c 15 q 15 t
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/db_xref="taxon:9606"
/clone="KAT06002"
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                                                                                                   (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (qil4732114 (pilAFL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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mh10d05.rl Soares mouse placenta 4NbMp13.5 14.5 Mus musculus cDNA
clone IMAGE:442089 5' similar to WP:F35G12.9 CE00978 ;, mRNA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
WashU-HMI Wash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 12.6; DB 244; Length 47;
Pred. No. 8.4e+04;
); Mismatches 4; Indels 0;
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Possible reversed clone: similarity on wrong strand
Seq primer: ETPrimer
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="IMAGE:442089"
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13; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 50)

Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata, H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.

Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries uppullished (2001)

Contact: Yutaka Suzuki
Department of Virology Institute of Medical Science, University of Tokyo
1 institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Makagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukiéims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama K., Suyama,A. and Sugano
'S. Construction and characterization of a full length-enriched and
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                                     AU102796 50 bp mRNA EST 05-APR-2001
AU102796 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS11037, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
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/db_xref="taxon:9606"
/clone="CAS11037"
/clone=lib="Sugano Homo sapiens cDNA library"
1 5 c 21 g 5 t
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AU102800.1 GI:13552321
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AU102796.1 GI:13552317
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Department of Virology
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92.9%;
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Best Local Similarity 92.9
Matches 13; Conservative
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A2779631 31 bp DNA GSS 16-FEB-2001
2M0016K13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0016K13 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dunn, D., Ayyadi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
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5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997). Location/Qualifiers
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/db_xref="taxon:10090"
/clone="UUGC2M0016K13"
/sex="Male"
                                                                                                                                                                     sapiens cDNA library"
6 t
                                                                                                                                                                                                                                                                                                                   Length 50;
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84112, USA
                                                                                                                                                                                                                                                                                                                   Score 12.4; DB 107;
Pred. No. 1.1e+05;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0016 row: K column: 13
Seq primer: CGTTGTAAAACGACGCCAGT
                                                   /clone_lib="Sugano Homo sapiens"
/db_xref="taxon:9606"
/clone="Tax11356"
/clone_lib="Sugano Homo se a B c 16 g 6
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/organism="Mus musculus"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 31.
Location/Qualifiers
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92.9%;
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Gaps

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/note="Organ: pooled: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NHL19W, testis NHT, and B-cell NCI_CGAP_CGAP. CASP. and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hypridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M. A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. " 8 a 8 c 12 g 15 t
10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732141 gblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli %110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 43)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 429 Efform. 0.00
Seq primer: -40013 fwd. ET from Amersham
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA971669 43 bp mRNA EST 07-JUL-1
0955c10.s1 Soares_NFL_T_GBG_S1 Homo sapiens CDNA clone
IMAGE:1583634 3' similar to SW:PWPZ_HUMAN Q15269 PERIODIC
TRYPTOPHAN PROTEIN 2 HOWOLOG.; mRNA sequence.
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Pred. No. 1.3e+05;
0; Mismatches 3; Indels 0;
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/clone="IMAGE:1583634"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH108"
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82.4%;
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Unpublished (1997)
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Best Local Similarity
Matches 14; Conserv
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electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qi|4732114|gb|RF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. L (bases 1 to 39)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 bp DNA GSS CONTROL OF SELECTION OF SELECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Vector: PWD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host-"E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 12.2; DB 249; Length 31; Pred. No. 1.2e+05; 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0219 row: A column: 01
Seg primer: CGTTCTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1M0219A01F Mouse 10kb plasmid UUGC1M
clone UUGC1M0219A01 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0219A01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 38. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.0%;
82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 82.4°
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 actgcagaaggcactga 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 ACTGCTGAAGGCAACGA 7
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ORIGIN
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ433216
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Gaps

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

ACCESSION

TITLE JOURNAL

COMMENT

LOCUS

RESULT 14 AI048043

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/crous_lib_rouse_low_pissmin_coccin library
/sex="Male"
//lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
//note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1. 1 (bases 1 to 32) (b
AZ826678 32 bp DNA GSS 20-FEB-2001
2M0102P06R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0102P06 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0102P06"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 32;
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100.0%; Pred. No. 1.6e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: 0102 row: P column: 06
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .32 /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0102 row: P column. 06
                                                                                                                                                      AZ826678.1 GI:12996586
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                            house mouse.
Mus musculus
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DEFINITION
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ORIGIN
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                                                                                                                    ACCESSION
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                                                                                                                                                                                     KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae, Murinae; Mus.

1 (bases 1 to 43)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,R., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Materston,R.

The washU-HMM Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note—"Organ: embryo; Vector: pSPORT; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally from mRNA prepared
from 800 blastcoysts. Primer: SalI(dT):
5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTTTTT.3'. CDNAs were
cloned into the NotI/SalI sites of a pSPORT vector (Life
Technologies). Two different size selections: B1 (larger
inserts) and B3:
16 9 t
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                                                                                                                                                                                                                                                                                              AIO48043 43 bp mRNA EST 08-JUL-1998 v021E12.1 Knowles Solter mouse blastocyst B1 Mus musculus cDNA clone IMAGE:1021871 5' similar to WP:T13H5.2 CE03653 RETINAL-BINDING LIKE PROTEIN; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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/strain="B6D2 F1/J"
/db_xref="taxon:10090"
/clone_1tb="Knowles Solter mouse blastocyst B1"
/tssue_type="blastocyst"
/dev.stage="embryo (pre-implantation)"
/lab_host="B108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Possible reversed clone: similarity on wrong strand
Seq primer: -40RP
High quality sequence stop: 1.
Location/Qualifiers
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Pred. No. 1.3e+05;
0; Mismatches 3;
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AI048043.1 GI:3296330
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82.4%;
                                      2 aaactgcagaaggcact 18
                                                                                 34 AAAATGCAGTACGCACT 18
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Best Local Similarity 82.4'
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
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FEATURES

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Gaps

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RESULT 15 AZ826678

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BASE COUNT

Search completed: October 2, 2001, 15:00:48 Job time: 10817 sec

Run on:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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gb_sts2:*
gb_sts3:*
           em_pat:*
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em_ro:*
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gb_ro2:*
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gb_pr10:*
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gb_un:*
gb_vi1:*
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Match Length
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                                                                            October 2, 2001, 15:56:39 ; Search time 3339.34 Seconds (without alignments) 92.640 Million cell updates/sec
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                   1344157 seqs, 7733874588 residues
                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                         - nucleic search, using sw model
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Maximum DB seq length: 50
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Perfect score:
Sequence:
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Database

AX060862 Sequence AR109090 Sequence A81012 Sequence 64 A95391 Sequence AR004745 Sequence AR008231 Sequence 177015 Sequence 75 I81010 Sequence 75

A95391 AR004745 AR008231 I77015 I81010

00000001

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AX060862 AR109090 A81012

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DB

Description

SUMMARIES

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
Kahn,A. and Chelly,J.
A gene called XLIS and the XLIS gene product, called doublecortin and their applications
Patent: EP 0918091-A 64 26-MAY-1999;
INST NAT SANTE RECH MED (FR)
                    Gaps
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                                                                                                                 14-FEB-2001
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Score 13.8; DB 9;
Pred. No. 1.2e+04;
                                                                                                                                                                                    Unclassified.

1 (bases 1 to 41)

1 (bases 2 to 41)

1 (bases 3 to 41)

Branieux, B., Landry, B.S. and Sapolsky, R.J.

Brassica polymorphisms

Patent: US 6114116-A 49 05-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 12.6; DB 9;
Pred. No. 4.9e+04;
); Mismatches 4;
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Pred. No. 1.2e+04;
1; Mismatches 3;
          Pred. No. 1.2e
0; Mismatches
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Sequence 49 from patent US 6114116.
AR109090.1 GI:12825366
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/db_xref="taxon:9606"
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Sequence 64 from Patent EP0918091.
A81012
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166695 Sequence 35
184789 Sequence 35
A04979 Artificial
A04980 Artificial
AR036378 Sequence
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AR104422 Sequence
A46535 Sequence 9
A18117 Oilgonucleo
A82690 Sequence 35
A82705 Sequence 50
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151986 Sequence 20
AR039578 Sequence
AR089681 Sequence
AR030029 Sequence
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AR022302 Sequence
AR066394 Sequence
AR084122 Sequence
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                                       AX043897 Sequence
AX059414 Sequence
AX043901 Sequence
AR3876 Sequence 11
AR061353 Sequence
AR108252 Sequence
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/note="Mutated complementarity determining region (CDR)"
                                                                      Sequence 11
                                                                                                                                                                             AX080565 Sequence
                                                                                                                                                                                                                                                             I34292 Sequence 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthetic construct
artificial sequence.
1 (bases 1 to 3)
Huse, W.D. and Wu.H.
Anti-g(a) v?_g(b)3? recombinant human antibodies, nucleic acids encoding same and methods of use
Patent: WO 0078815-A 83 28 -DBC-2000;
Applied Molecular Evolution (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                          A64833 Sequence 9
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    .33
/organism="synthetic construct"
/db_xref="taxon:32630"

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/transl_table=11
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/db_xref="GI:12406241"
/translation="LINRYSSOSIS"
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AR061353
AR108252
116209
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AN036378
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AX080565
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AR104422
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JOURNAL

FEATURES

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REFERENCE

TITLE

KEYWORDS

RESULT AX060862

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1 (bases 1 to 30)
Schlick, W.H., Goldgar, D.E., Miki, Y., Swenson, J., Kamb, A.,
Harshman, K. D., Shattuck-Eidens, D.M., Tavtigian, S.V., Wiseman, R.W.
and Futreal, P. Andrew.
170-linked breast and ovarian cancer susceptibility gene
Patent: US 5753441-A 75 19-MAY-1998;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unclassified.

1 (bases 1 to 30)
Shattuck-Eidens, D.M., Simard, J., Durocher, F., Emi, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 30)
Shattuck-Eidens, D.M., Simard, J., Durocher, F., Emi, M. and
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Linked breast and ovarian cancer susceptibility gene
Patent: US 5693473-A 75 02-DEC-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Distriction ovarian cancer susceptibility gene Linked breast and ovarian cancer susceptibility gene Patent: US 570999-A 75 20-JAN-1998;
Location/Qualifiers
1. .30
                                                                                                                                                                                                                               9; Length 30;
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Pred. No. 5e+04;
0; Mismatches 4;
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Pred. No. 5e+04;
0; Mismatches
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Sequence 75 from patent US 5693473.
177015 177015.1 GI:3013169
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Sequence 75 from patent
IB1010
IB1010.1 GI:3209300
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Best Local Similarity 78.9%;
Matches 15; Conservative
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                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 20)
Francis,F. and Kahn,A.
A GENE CALLED XLIS AND THE XLIS GENE PRODUCT, CALLED DOUBLECORTIN
AND THEIR PREPARATIONS
Patent: WO 9927089-A 64 03-JUN-1999;
INST NAT SANTE RECH MED (FR); FRANCIS FIONA (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 30)
Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,
Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,
Harshman,K.D., Shattuck-Eidens,D.M., Tavtigian,S.V., Wiseman,R.W.
and Futreal,P.Andrew.
170-linked breast and ovarian cancer susceptibility gene
Patent: US 5747282-A 75 05-MAY-1998;
Location/Qualifiers
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Pred. No. 5e+04;
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Pred. No. 4.9e+04;
0; Mismatches 4.
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Sequence 75 from patent US 5753441.
AR008231 GI:3967340
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Sequence 75 from patent US 5747282.
AR004745.1 GI:3965624
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                          A95391 20 bp DNA
Sequence 64 from Patent W09927089.
A95391
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/db_xref="taxon:9606"
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03-APR-1998
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Unclassified.
1 (bases 1 to 22)
North, M., Nishina, P. and Naggert, J.
Genes associated with retinal dystrophies
Patent: US 5686598-A 4 11-NOV-1997;
Location/Qualifiers
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Pred. No. 7.9e+04;
0; Mismatches 3;
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Pred. No. 7.8e+04;
0; Mismatches 3;
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Inouye,M. and Nakamura,K.
Plasmid cloning vehicles
Patent: EP 0055942-A2 11 14-JUL-1982;
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103808
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Sequence 10 from Patent WO0049166.
AX043897
                                                                 173726 22 bp DNA
Sequence 4 from patent US 5686598.
173726
173726.1 GI:3009867
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Matches 14; Conservative
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Best Local Similarity 82.4
Matches 14; Conservative
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Unknown.
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Unclassified.
1 (bases 1 to 30)
Skolnick,M. H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,
Harshman,K.D., Shattuck-Eidens,D.M., Tavtigian,S.V., Wiseman,R.W.
and Futreal,P.Andrew.
17q-linked breast and ovarian cancer susceptibility gene
Patent: US 5710001-A 75 20-JAN-1998;
Location/Qualifiers
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Pred. No. 5e+04;
0; Mismatches 4; Indels
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North, M., Nishina, P., Naggert, J. and Noben-Trauth, K. Gene family associated with neurosensory defects
Patent: US 6114502-A 38 05-SEP-2000;
Location/Qualifiers
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Pred. No. 5e+04;
0; Mismatches 4;
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Sequence 38 from patent US 6114502.
AR110286.1 GI:12826562
/organism="unknown"
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78.9%;
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Best Local Similarity 78.9%;
Matches 15; Conservative
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bugnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 26)
Preuss, D., Copenhaver, G. and Keith, K.
Plant chromosome compositions and methods
Patent: WO 0055325-A 147 21. SEP-2000;
The University of Chicago (US)
Location/Qualifiers
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1 (bases 1 to 26)
Graham,F.L., Ng,P., Parks,R., Bacchetti,S. and Anglana,M.
A system for production of helper dependent adenovirus vectors bas ed on use of endonucleases
Patent: WO 0049166-A 10 24-AUG-2000;
Merck & Co., Inc. (US)
Location/Qualifiers
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A system for production of helper dependent adenovirus vectors bas
ed on use of endonucleases
Patent: WO 0049166-A 14 24-AUG-2000;
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/db_xref="taxon:3702" 2 t
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Sequence 147 from Patent WO0055325.
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AX043901
AX043901.1 GI:11342484
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/organism="synthetic cor
/db_xref="taxon:32630"
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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em_gss_hum3:* em_gss_hum4:* em_gss_hum5:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk COMMENT CONSTRUCTED at the Institute for Genomic Research (TTGR).	Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).	Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/. FEATURES Location/Qualifiers 1. 35 Location/Qualifiers 1. 35 Location/Qualifiers 1. 35 //Outine="Trypanosoma brucei" //Strain="TREU927" //db_xref="taxon:5691" //db_xref="taxon:5691" //clone="124f02" //clone="124f02" //clone="124f02"	Query Match 71.0%; Score 14.2; DB 258; Length 35; Best Local Similarity 84.2%; Pred. No. 7.1e+03; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy 2 tetecettecgttattett 20	RESULT 2 AZ810736 AZ810736 LOCUS LOCUS DEFINITION 2M0076B05R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZM0076B05 R, DNA sequence. ACCESSION AZ810736 VERSION AZ810736.1 GI:12978289 KEYWORDS SOURCE house mouse. ORGANISM Mus musculus	Eukaryota Metazoa Mammalia: Eutheria CE 1 (bases 1 to 49) RS Dunn,D., Aoyagi,A., Islam,H., Longacre, 'M., Rose,M., Rose, and Wright,D.,Weiss Mouse Whole genome plasmid inserts The Country of the country of t	COMMENT Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: adunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0076 row: B column: 05 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends Insert Length: 10000 std 89. FEATURES Location/Qualifiers Location/Qualifiers //strain="CS7BL/6J" //db_xref="taxon:10090"
SUMMARIES RESUlt Query No. Score Match Length DB ID Description	14.2 71.0 35 258 TA124F02Q AL46335 13.6 68.0 49 250 AZ810736 AZ810731 12.8 64.0 37 8 AA500031 12.6 63.0 30 244 AZ447206 AZ447201 12.6 63.0 50 249 AZ776590 AZ776590 12.2 61.0 39 242 AZ357911 AZ35791. 12.2 61.0 46 189 T45694 T45694	9 12.2 61.0 49 24 A1747625 A7747625 A7747625 U 10 12 60.0 31 19 A1355496 A1355496 11 12 60.0 31 250 A2850974 A1355496 13 12 60.0 34 242 A2551509 A1355791 A1351509 A1355791 A1351509 A2577613 15 12 60.0 34 242 A257513 A2575791 A2575791 A257796 A25777 A25777 A25777 A257777 A257777 A257777 A257777 A257777 A257777 A257777 A257777 A2577777 A257777 A2577777 A257777 A25777	12 00.0 50 249 AC105595 AC107380 AC1073	29 11.6 58.0 37 258 HAMCOSALO X888437 H.Saplens D	11.2 56.0 24 A1148505 11.2 56.0 34 16 A1130467 11.2 56.0 38 258 TA72G01Q 11.2 56.0 43 20 A4242931 11.2 56.0 45 244 A2452742	TAI24F02Q/C TAI24F02Q TY

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/organism="Mus musculus"
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                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynuclectide kinase. Adaptor oligonuclectides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gal
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicial in resistance."
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Eukaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Matazoa; Chordata; Sclurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 37)
Marta M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Marta M., Hillier, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                       /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.0%; Score 13.6; DB 250; Length 49; 80.0%; Pred. No. 1.4e+04; 1ve 0; Mismatches 4; Indels 0;
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Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
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The WashU-HHMI Mouse EST Project
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/clone="UUGC2M0076B05"
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AA500031.1 GI:2234998
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Fax: 314 286 1810
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly
, M., Rose, M., Rose, R.,
and Wright, D., Welss, R.
Mouse Whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A2447206 30 bp DNA GSS 04-OCT-2000 1M0244J07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0244J07 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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/db_xref="taxon:10090"
/clone="UGGIM0244J07"
/sex="Male"
/lab_host="E. Coli strain XLI0-Gold, Tl-resistant, F-/note="Vector: PWD42nv; Purlfied genomic DNA from M.
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/db_xref="taxon:10090"
/clone="IMAGE:920108"
/clone="IMAGE:920108"
/clone="IMAGE:920108"
/sex="mixed"
/tissue_type="pooled organs"
/dev.stage="7 day"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 12.8; DB 8; Length 37; Pred. No. 3.3e+04; 0; Mismatches 2; Indels
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Fax: 801 585 7177
Fax: 801 585 7177
Fax: 801 585 7177
Fax: 801 585 7177
Fax: 1 ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0244 row: J column: 07
Seq primer: CGTFGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (qi|4732114|qib|ARD20072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
WR. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus subtracts, Craniata; Vertebrata; Euteleostomi; Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 37)
1 (ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ404740 37 bp DNA GSS 03-OCT-2000 1M0173D10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0173D10 F, DNA sequence.
                                     musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
   /note="Vector: PWD42nv; Purified genomic DNA from M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Mouse 10kb plasmid UUGC1M library"
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Insert Length: 10000 Std Error: 0.00
Plate: 0173 row: D column: 10
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Seg primer: CGTTGTAAAACGACGCCCAGT
Class: plasmid ends
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/db_xref="taxon:10090"
/clone="UUGC1M0173D10"
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AZ404740.1 GI:10528753
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Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  house mouse.
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Best Local Similarity
Matches 15; Conserv
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                                                        (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114) plaRt29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chaptors competent E. coli XL10.Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 50)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
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2M0010A23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0010A23 F, DNA sequence.
AZ776590
musculus C57BL/6J (male) was obtained from the Jackson
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0
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                                     Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
Plate: 0010 row: A column: 23
Seq primer: CGTTGTAAAACGACGCCAGT
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/strain="C57BL/6J"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Rese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="UUGC2M0010A23"
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Location/Qualifiers
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 15; Conserv
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KEYWORDS
SOURCE
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Gaps

us-09-757-100b-7.szlim50.rst

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gilq19219072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (base 1 to 46)

Hillier, L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chissoe, S., Dietrich, N., Dubuque, T., Fevello, A., Gish, W., Hawkins

M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore

M. Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,

Schellenberg, K., Wohldman, P., Waterston, R., Wilson, R. and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T49694 46 bp mRNA EST 06-FEB-1995 7478911.81 Extragene placenta (#937225) Homo sapiens CDNA clone IMAGE:67844 3' similar to similar to 9b:M24194 GUANINE NUCLECTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (HUMAN), mRNA
                                                      /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                              /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 12.2; DB 242; Length 39;
Pred. No. 6.4e+04;
0; Mismatches 3; Indels 0;
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High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
Insert Size: 711
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Contact: Wilson RK
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      /sex="Male"
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Best Local Similarity 82.4
Matches 14; Conservative
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                                                                                                       (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qi|4732114 qiplat129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Nose,M., Rose,N., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A2357911 39 bp DNA GSS 02-OCT-2000 1M0099L13R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0099L13 R, DNA sequence.
/lab_host-"E. Coli strain XLIO-Gold, T1-resistant, F-"
/note-"Vector: PWD42nv: Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/clone="UUGC1M0099L13"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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Pred. No. 6.3e+04;
0; Mismatches 3; Indels 0;
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Seq primer: CACACAGGAAACAGCTATGACC
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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High quality sequence stop: 39.
Location/Qualifiers
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Insert Length: 10000 Std Erro
Plate: 0099 row: L column: 13
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82.4%;
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Matches 14; Conservative
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Fax: 801 585 7177
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Gaps

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plasmid inserts
Unpublished (2000)
Confect: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCTARCTG6], digested and clonned into distinct DraIII sites of the pME185-FL3 vector [5' site CACTGTGTG, 3' site CACCATGTG). Xhol should be used to isolate the cDNA insert. Size selection was performed to exclude fragments clists. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). CUTCTGCTCTTAAAGCTGGG and 3' end primer CGACCTGCAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt endrrepaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were
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Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ385263 29 bp DNA GSS 02-OCT-2000 IM0143109R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0143109 R, DNA sequence.
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/sex="Male"
                                                                                                                                                                                                                                                                                               Length 49;
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Pred. No. 6.6e+04;
0; Mismatches 3;
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Seq primer: CACACAGGAAACAGCTATGACC
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0143109"
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Insert Length: 10000 Std Erro
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Fax: 801 585 7177
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Best Local Similarity
Matches 14; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 49)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,

Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Glibons,M., Pape,D., Harvey,N., Schurk,R., Ritter

Weterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ul19d03.x1 Sugano mouse embryo mewa Mus musculus cDNA clone
IMAGE:2088005 3' similar to TR:089050 089050 MUSKELIN. ;, mRNA
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
T=1: 314 286 1800
Fax: 314 286 1810
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0
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Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
                       1.46
/organism="Homo sapiens"
/db_xref="GDB:489509"

    .49
    /organism="Mus musculus"

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Best Local Similarity
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ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel. electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114[gb]AF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
MAS Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
ound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A1355496 31 bp mRNA EST 15-FEB-1999 qu15c07.xl NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:1964844 3' similar to TR:Q60501 Q60501 PPREINSERTION DNA.; contains element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 31)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Bmall: gapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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/db_xref="taxon:9606"
/clone="IMAGE:1964844"
/clone_lib="NCI_CGAP_Ov23"
/tisus_type="tumor, 5 pooled (see description)"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                          Score 12; DB 242; Length 29; Pred. No. 7.6e+04;
                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TARI repetitive element;, mRNA sequence.
AI355496
AI355496.1 GI:4095649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                www-bio.llni.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trace considered overall poor quality
Insert Length: 234 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                          60.0%;
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| ||||||| || |||||||
27 rccrccrccrrcrrr 8
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Unpublished (1997)
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Best Local Similarity
watches 15; Conserv
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//doce="Vector: PWASING: Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114) gblak129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplian resistance.
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                                                                                                                                                                                                                                                                                                                                    2M0153109F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0153109 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 32)
Unun,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
'M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert B. Welss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse whole genome scaffolding with paired end reads from 10kb
                                                          Gaps
                                                                                                                                                                                                                                                                                                            21-FEB-2001
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  Length 31;
                                                        Indels
Score 12; DB 19; I
Pred. No. 7.6e+04;
); Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="UUGC2M0153I09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          row: I column: 09
                                                                                                                                                                                                                                                                                                                  DNA
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60.0%;
75.0%;
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                                                                                                          Unpublished (2000)
                                                        Conservative
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Fax: 801 585 7177
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Query Match
Best Local Similarity
Matches 15; Conserv
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1 ttctcccttccgttattctt 20
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Best Local Similarity
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                                                                                                             RESULT 14
AZ357613/c
                                                                                                                                                                   DEFINITION
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KEYWORDS
SOURCE
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Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Théising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Ritter,Materston,R. and Wilson,R.

The Washungton Oniversity School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI551509 34 bp mRNA EST 23-MAR-1999 vo54h02.x1 Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone IMAGE:1053747 3' similar to TR:Q33559 Q33559 NH2 TERMINUS UNCERPAIN ;, mRNA sequence.
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Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .34
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:1053747"
/clone_lib="Barstead mouse irradiated colon MPLRB7"
/dev_stage="8 weeks"
/lab_host="DH10B"
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0
                                                       Length 32;
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Pred. No. 7.7e+04;
0; Mismatches 5; Indels
                                                                                        5; Indels
                                                   Score 12; DB 250;
Pred. No. 7.7e+04;
                                                                                        0; Mismatches
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                                                   60.0%;
                                                                                                                            1 ttctcccttccgttattctt 20
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75.0%;
                                                                                                                                                 24 TCCTCCCTACCTTTCCTCTT 5
                                               Query Match 60.0°
Best Local Similarity 75.0°
Matches 15; Conservative
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Best Local Similarity 75.0°
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
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ORIGIN
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                                                                                                                                                                                                                      RESULT 13
AI551509
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JOURNAL
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AUTHORS
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ORIGIN
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114) [glaffar23072.1], a copy number inducible derivative of plasmid R1. The vector was ligated purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Uppublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance." 1\ c 15\ g 0 t
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 34)
Dunn,D., Aoyagi,Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly and Wright,D.,Weiss,R., Stokes,R., Tingey,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                             A2357613 34 bp DNA GSS 02-0CT-2000
1M0099K18F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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/clone="UUGCIMO099K18"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 12; DB 242; Length 34; Pred. No. 7.7e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: K column: 18
                                                                                                                                                                                                                                                               clone UUGC1M0099K18 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 34.
Location/Qualifiers

    . 34
    /organism="Mus musculus"
    /strain="C57BL/6J"

                                                                                                                                                                                                                                                                                                                         AZ357613.1 GI:10471313
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75.0%;
                        21
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2 TTTTCTCTTTATTCTT
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rm.\ 308 , Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112 , USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 35)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedérsen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                             AZ829796 35 bp DNA GSS 20-FEB-2001
2M0107H11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
   Gaps
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/strain="C57BL/6J"
/db_xref="taxon:10H00"
/clone="UGC2M0107H11"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
   Indels
   5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0107 row: H column: 11
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
   Mismatches
                                                                                                                                                                                                                                                                                                                          clone UUGC2M0107H11 R, DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 35.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                   AZ829796
AZ829796.1 GI:12999704
                                                          1 ttctcccttccgttattctt 20
                                                                                                             22 rccrrccrrrcGrcrrcrr 3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
                                                                                                                                                                                                      RESULT 15
AZ829796/c
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ORIGIN
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
COMMENT
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60.0%; Score 12; DB 250; Length 35;

Query Match

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Search completed: October 2, 2001, 15:00:51 Job time: 10820 sec

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Sequence

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Sequence 7, Application US/09377310B
Patent No. 6133031
GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
APPLICANT: Garde, William A.
TITLE OF INVENTION: Attisense Modulation of Focal Adhesion Kinase;
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 15
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         US-08-133-629-6

US-08-133-629-6

US-08-470-179-201

US-08-823-516-158

US-08-123-516-158

US-08-123-516-128

US-08-123-518-25

US-08-955-138-25

US-08-955-138-25

US-08-972-4178-1

US-08-972-4178-1

US-08-172-19-9

US-08-172-19-9

US-08-172-113-9

US-08-172-113-9

US-08-172-113-9

US-08-172-113-9

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US-08-172-113-9

US-08-172-113-9

US-08-172-113-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 20; DE 100.0%; Pred. No. 0.3; ive 0; Mismatches
                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTHER INFORMATION: antisense sequence US-09-377-310-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 27, Application US/09377310B
; Patent No. 6133031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 20; Conservative
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US-09-377-310-27
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US-09-377-310-7
FEATURE:
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9.071 Million cell updates/sec
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                                                                                      Search time 417.38 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
            4.5
Compugen Ltd.
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US-08-813-507-49
US-08-481-07-49
US-08-481-022-75
US-08-483-5548-75
US-08-483-5548-75
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US-08-412-110-35
US-08-413-110-35
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                                                                                                                                                                                                                                 324599 seqs, 94655562 residues
          GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                                                                      2001, 16:03:46
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length: 50
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Perfect score:
Sequence:
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Maximum DB seq
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                                                                       APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Harshman, Keith D.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Wiseman, Roger W.
APPLICANT: Witceal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                            ADDRESSEE: Venable, Baetjer, Howard & Civiletti,
STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,784
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 12.6; DB 1;
Pred. No. 8.5e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Theory 16FFONT
                  Skolnick, Mark H.
Goldgar, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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ilarity 78.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 202-502-8300
                                                          Miki, Yoshio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 30 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                    STREET: 1202
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Matches 15; Conserv
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US-08-480-784-75
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Pred. No. 2.4e+02;
1; Mismatches 3; Indels
                                                                                             DB 3; Length 15;
61;
                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lendeux, Bertrand
APPLICANT: Lendry, Benoit S.
APPLICANT: Landry, Benoit S.
APPLICANT: Sapolsky, Ronald J.
TITLE OF INVENTION: Brassica Polymorphisms
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/813,507
FILING DATE: 07-MAR-1997
                                                                                           Score 15; DB 3; Pred. No. 61; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    018547-030100US
                ; OTHER INFORMATION: antisense sequence US-09-377-310-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,069
FILING DATE: 02-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                             75.0%; Scur.
100.0%; Pre
                                                                                                                                                                                                                                                                                                          Sequence 49, Application US/08813507 Patent No. 6114116 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 75, Application US/08480784 Patent No. 5693473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 0185
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 576-0200
TELEFAX: 415 576-0200
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78.9%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                           Query Match 75.C
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 78.9
Matches 15; Conservative
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TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY:
US-08-813-507-49
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FEATURE:
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63.0%; Score 12.6; DB 1; Length 30; 78.9%; Pred. No. 8.5e+02; Live 0; Mismatches 4; Indels
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APPLICANT: Simard, Jacques
APPLICANT: Bin, Mitsuru
APPLICANT: Bai, Mitsuru
APPLICANT: Nakamura, Yusuke
APPLICANT: Durocher, Francine
APPLICANT: Durocher, Francine
TITLE OF INVENTION: 179-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, N.W., Suite 1000 CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/487,002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24 MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29 NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION NUMBER: US 08/209,221
FILING DATE: 12-AUG-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                  Sequence 75, Application US/08487002
Patent No. 5710001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2488
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
  INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERESTICS:
1.F.NGTH: 0.0 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 63.0
Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
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US-08-487-002-75
                                                                                                                    RESULT 6
US-08-487-002-75
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APPLICANT: Kamb, Alexander
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Hartuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 179-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.0%; Score 12.6; DB 1; Length 30; 78.9%; Pred. No. 8.5e+02; Live 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, N.W., Suite 1000 CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NDTA: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NDTA: BC-DOS/MS-DOS
FILING DATE: CLASSIFICATION ADATA: APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 16-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 12-AUG-1994
PRIOR APPLICATION NUMBER: US 08/209,221
ATORNEY/AGENT INFORMATION: APPLICATION NUMBER: 22-406-1994
ATTORNEY/AGENT INFORMATION: NUMBER: 20-962-4810
FILING DATE: 12-AUG-1994
TELECOMMUNICATION NUMBER: 20-962-4810
TELECOMMUNICATION NUMBER: 20-962-4810
TELEPHAN: 202-962-4810
TELEPHAN: 202-962-4810
INPORMATION FOR SEQ ID NO: 75: SEQUENCE CHARGEREITSTICS:
                                         Sequence 75, Application US/08483553
Patent No. 5709999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                               Skolnick, Mark H.
Goldgar, David E.
Miki, Yoshio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 78.9°
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: "CZTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
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US-08-483-553-75
RESULT 5
US-08-483-553-75
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APPLICANT: Goldgar, David E.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Swenson, Jeff
APPLICANT: Harshman, Keith D.
APPLICANT: Tavigian, Keith D.
APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 179-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, N.W., Suite 1000 CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY UGA

ZIP: 20005

COUNTRY UGA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,554B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/409,305

FILING DATE: 24-MAR.1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/38,044

FILING DATE: 16-SEP-1994

PRIOR APPLICATION NUMBER: US 08/300,266

FILING DATE: 16-SEP-1994

PRIOR APPLICATION NUMBER: US 08/300,266

FILING DATE: 12-MO-1994

APPLICATION NUMBER: US 08/289,221

FILING DATE: 12-MO-1994

APPLICATION NUMBER: US 08/289,221

FILING DATE: 12-MO-1994

APPLICATION NUMBER: US 08/289,221

FILING DATE: 12-MO-1994

APPLICATION NUMBER: 28/957

REERRENCE/POCKET NUMBER: 24884-109347

TELECOMMUNICATION INFORMATION:

PELEPHONE: 202-962-4810
                                                                                                                                                                     Sequence 75, Application US/08483554B
Patent No. 5747282
GENERAL INFORMATION:
APPLICANT: Skolnick Mark H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
2 totocottocottattott 20
                         8 TCTCTTCCTCTTCTT 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202-962-8300
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ORGANISM: HOM
US-08-483-5548-75
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Gaps
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                      Length 30;
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APPLICANT: Harshman, Keith D.
APPLICANT: Abstruck-fidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 179-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: 85
NUMBER OF SEQUENCES: 85
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Venable, Baetjer, Howard & Civiletti, STREET: 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.30
                    Score 12.6; DB 1;
Pred. No. 8.5e+02;
); Mismatches 4;
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PAPLICATION NUMBER: US/08/486,011B
FILING DATE: 07-3UN 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24 WAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION NUMBER: US 08/289,221
APPLICATION NUMBER: US 08/289,221
                                                                                                                                                                                                                                                             ; Sequence 75, Application US/08488011B
; Patent No. 575341
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                      63.0%;
78.9%;
                                                                                                                                                                                                                                                                                                                           Skolnick, Mark H.
Goldgar, David E.
Miki, Yoshio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 12-AUG-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                            2 tetecettecgttattett 20
                                                                                                                                                     8 TCTCTTCTTCTTTT 26
                                                                                                                                                                                                                                                                                                                                                                                          Swenson, Jeff
Kamb, Alexander
                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                           US-08-488-011B-75
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APPLICANT:
APPLICANT:
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Gaps
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APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Simard, Jacques
APPLICANT: Nakamura, Yusuk
APPLICANT: Nakamura, Yusuk
APPLICANT: Durocher, Francine
TITLE OF INVENTION: In Vivo Mutations and Polymorphisms
TITLE OF INVENTION: in the 1/q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADRESS:
                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                    63.0%; Score 12.6; DB 4; Length 30; 78.9%; Pred. No. 8.5e+02; ive 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILLING DATE: PCI/US95/10202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24884-109347
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FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
FILON PERPLICATION DATA: US 08/289,221
APPLICATION NUMBER: US 08/289,221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 08-308,104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 75, Application PC/TUS9510202 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
                                                                                                        MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
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                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                    Query Match 63.0
Best Local Similarity 78.9
Matches 15; Conservative
      SEQUENCE CHARACTERISTICS:
                                           nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: UFILING DATE: 16-SEP-1
                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                           TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: line
                                                                                                                                                  ORIGINAL SOURCE:
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PCT-US95-10202-75
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US-08-850-727-75
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                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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STATE:
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                                                                                                                                           63.0%; Score 12.6; DB 1; Length 30;
llarity 78.9%; Pred. No. 8.5e+02;
Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Howard & Civiletti, LLP
1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 2484-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Swenson, Jeff
Kamb, Alexander
Harshman, Keith D
Shattuck Eidens, Donna M.
Tavtigian, Sean V.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,554
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
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FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
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; Sequence 75, Application US/08850727
; Patent No. 6162897
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HYDOTHETICAL: NO Genomic)
HYDOTHETICAL: NO ORIGINAL SOURCE:
ORIGINAL HOMO Sapiens
US-08-488-011B-75
                                                                                                                                                                                                                                                                                                                                                                                                                                           Skolnick, Mark H.
Goldgar, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 12-AUG-1994 ATTORNEY/AGENT INFORMATION:
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TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Miki, Yoshio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1201 NO. CITY: Washington STATE: DC COUNTRY: USA 7TP: 2005
                                                                                                                                             Query Match
Best Local Similarity
Matches 15; Conserv
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Gaps
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Futreal, P. Andrew
NVENTION: Method for Diagnosing a
NVENTION: Predisposition for Breast and Ovarian Cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                     63.0%; Score 12.6; DB 5; Length 30; 78.9%; Pred. No. 8.5e+02;
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1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/10220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                  24884-109347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION NUMBER: US 08/48,824
PRIOR APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
  US 08/289, 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 75, Application PC/TUS9510220 ; GENERAL INFORMATION:
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Shattuck-Eidens, Donna
Tavtigian, Sean V.
                                                       NAME: Thnen, Jeffrey L.
REGISTRATION UNDRER: 28,957
REFRENCE/CDCKET NUMBER: 2488
TELECOMMUNICATION INFORMATION:
TELEFAM: 202-962-4810
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goldgar, David E.
Miki, Yoshio
Swenson, Jeff
Kamb, Alexander
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                    FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 tetecettecgttattett 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 TCTCTCTTCCTCTTTT 26
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1201 Ne.
                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UZIP: 20005
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                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM:
PCT-US95-10203-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
PCT-US95-10220-75
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Wiseman, Roger W.
APPLICANT: Witeman, Poper W.
APPLICANT: Putreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Venable, Baetjer, Howard & Civiletti, LLP 1201 New York Avenue, N.W., Suite 1000
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CUBRENT APPLICATION DATA:
PPLICATION NUMBER: PCT/US95/10203
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRICE APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07-UN-1995
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24 MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,104
FILING DATE: 16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Swenson, Jeff
Kamb, Alexander
Harshman, Keith D.
Shattuck-Eidens, Donna M.
Tavttglan, Sean V.
Wiseman, Roger W.
Futreal, P. Andrew
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APPLICATION NUMBER: US 08/300,266
FITING DATE: 02.SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 75, Application PC/TUS9510203 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: HOMO sapiens
PCT-US95-10202-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skolnick, Mark H.
Goldgar, David E.
Miki, Yoshio
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202-962-4810
          TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                            Query Match 63.0
Best Local Similarity 78.9
Matches 15; Conservative
                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy.
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PRIOR APPLICATION DATA
                                                                                                                                 linear
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STATE: DC
COUNTRY: US
ZIP: 20005
TELEPHONE:
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APPLICANT:
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                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 38, Application US/09032365A
Patent No. 6114502
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: No. 6114502th, Michael
APPLICANT: Nishina, Patsy
APPLICANT: No. 6114502en-Trauth, Konrad
TITLE OF INVENTION: GENE FAMILY ASSOCIATED WITH
TITLE OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.0%; Score 12.2; DB 3;
82.4%; Pred. No. 1.3e+03;
tive 0; Mismatches 3;
                                                                                                                                                                                                               Score 12.2; DB 1;
Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Discrete
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,365A
FILIG DATE:
                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Avenue, Suite 200
                                      | LENGTH: 22 base pairs
| TYPE: nucleic acid
| STRANDEDNESS: single
| TOPOLOGY: linear
| MOLECULE TYPE: other nucleic acid
| DESCRIPTION: /desc = "primers"
| US-08-701-380-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36,677
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3400
TELEFAX: 650-327-3231
                                                                                                                                                                                                               61.0%;
82.4%;
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ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,
  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                           Query Match
Best Local Similarity 82.4 Matches 14; Conservative
                                                                                                                                                                                                                                                                                            2 tetecetteegttatte 18
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SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
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Best Local Similarity 82.4
Matches 14; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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EDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-09-032-365A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA
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STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08701380
Patent No. 568558
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
NISHINA, Patsy
APPLICANT:
INGERT, Juergen
TITLE OF INVENTION:
GENES ASSOCIATED WITH RETINAL
TITLE OF INVENTION:
DYSTROPHIES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/701,380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.0%; Score 12.6; DB 5; 78.9%; Pred. No. 8.5e+02;
            PRIOR APPLICATION UNMBER: US 08-308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
FELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECHAN: 202-962-4810
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REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: A-63565/PJS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-8701
TELEFAX: 415-494-8771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
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ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 63.0°
Best Local Similarity 78.9°
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                              LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        linear
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60.0%; Score 12; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                    RESULT 15
US-07-931-473B-35/C

Sequence 35, Application US/07931473B
Sequence 35, Application US/07931473B
Sequence 35, Application US/07931473B
Sequence 35, Application US/07931473B
Sequence 35, Application US/07063
SEQUENCE INVEMITON: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beaton & Swanson, P.C.
STREET: 4582 South UIster Street Parkway, #403
CTIT': Denver
STREET: 4582 South UIster Street Parkway, #403
COUNTRY: DENver
STREET: 4582 South UISter Street Parkway, #403
CONNUTR: DISKETTE DISKETTE, 5.25 inch, 360 Kb storage
CONNUTR: IBM compatible
COMPUTR: TRADABLE FORM:
MEDICATION TYPE: US/07/931,473B
FILING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURSIFICATION NUMBER: US/07/931,473B
FILING APPLICATION DATA:
APPLICATION NUMBER: 33,215
FRIENG APPLICATION NUMBER:
STELEPHONE: (303) 850-9900
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9901
TELECOMMUNICATION:
TELEPHONE: (303) 850-9901
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Search completed: October 2, 2001, 16:03:47 Job time: 14591 sec

Run on:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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gb_sts2:*
gb_sts3:*
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gb_htg2:*
                    em_ph: *
em_pl: *
em_ro: *
em_sts: *
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gb_pr9:*
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                                                                               October 2, 2001, 15:56:41; Search time 3339.34 Seconds (without alignments) 92.640 Million cell updates/sec
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                   1344157 segs, 7733874588 residues
                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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                                                         OM nucleic - nucleic search, using sw model
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Maximum Match 100%
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em_htg_hum2:*
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em_htgo_inv:*
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Maximum DB seq length: 50
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Perfect score:
Sequence:
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AR079693 Sequence
AR081223 Sequence
AR01344 Sequence
AR062804 Sequence
AR062804 Sequence
AR087882 Sequence
AR097852 Sequence

AR037524 AR062804 AR087882 AR091352

AR079693 AR081223 A63162 AR001344

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                                                                                             1 (bases 1 to 43)
Pavlakis,G.N. and Felber,B.K.
Nucleic acid constructs containing HIV genes with mutated inhibitory/instability regions and methods of using same Patent: US 5972596-A 17 26-00T-1999;
Location/Qualifiers
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Pred. No. 4.4e+03;
0; Mismatches 1;
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FAS LIGAND FUSION PROTEIN
PASENT: WO 9718307-A 5 22-MAY-1997;
SANDOZ LTD (CH)
Other publication AU 7684896 19970605.
    аки81223 43 bp DNA
Sequence 17 from patent US 5972596.
AR081223
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/db_xref="taxon:32644"
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A63162
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Sequence 34 from patent US SAR001344
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Best Local Similarity 87.5%;
Matches 14; Conservative
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AR03315 Sequence
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AR07271 Sequence
AR082328 Sequence
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AR054989 Sequence
AR036477 Sequence
AR069436 Sequence
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178374 Sequence 17
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I41178 Sequence 34
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AX100369 Sequence
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AR063784 Sequence
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AR020665 Sequence
A41626 Sequence 35
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AR012083 Sequence
AR030753 Sequence
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AX060907 Sequence
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Pavlakis,G.N. and Felber,B.K.
Method of eliminating inhibitory/ instability regions of mRNA
Patent: US 596726-A 17 12-OCT-1999;
Location/Qualifiers
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AR053115
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A80185
MMU232757
AR072271
AR082328
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I26382
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AX008785
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11 c 5 g
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A39180
A39239
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                    Conservative
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Unknown. Unclassified.

ORGANISM

Unknown.

AR079693

RESULT 1 AR079693/c LOCUS

DEFINITION

ACCESSION VERSION

KEYWORDS

Query Match Best Local Similarity Matches 14; Conserv

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FEATURES

TITLE JOURNAL REFERENCE AUTHORS

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Skolnick,M.H., Cannon-Albright,L.A. and Kamb,A.
Methods for detecting predisposition to cancer at the MTS gene
Patent: US 5989015-A 34 23.NOV-1999;
Location/Qualifiers
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(bases 1 to 21)

Kamb, A.

MarE2 gene

Patent: US 5994095-A 34 30-NOV-1999;
                                                                                                            AR087882 21 bp DNA
Sequence 34 from patent US 5989815.
AR087882.1 GI:10014645
  Mismatches
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AR091352
AR091352.1 GI:10018107
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Sequence 34 from patent US 5624819.
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Kamb, A.
Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes
Patent: US 5801236-A 34 01-SEP-1998;
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Pred. No. 1.3e+04;
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Pred. No. 1.3e+04;
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# Unknown.
Unclassified.

# 1 (bases 1 to 21)
# Stone, S., Jiang, P. and Kamb, A.

Mouse WISI gene
Mouse I US 5843756-A 34 01-DEC-1998;

I Location/Qualifiers

Location/Qualifiers

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     Tamly.
MTS1E1.beta. gene
Patent: US 5739027-A 34 14-APR-1998;
Location/Qualifiers
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Sequence 34 from patent US 5801236.
AR037524 GI:5955380
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Sequence 34 from patent US 5843756.
AR062804 GI:5990495
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/organism="unknown"
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78.98;
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78.9%;
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3 CTAGAGGCGAATTATCTGT 21
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Best Local Similarity 78.93
Matches 15; Conservative
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Best Local Similarity 78.9°
Matches 15; Conservative
1 (bases 1 to 21)
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Patent: US 5763190-A 7 09-JUN-1998;
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 27)
Weiner, D.B. and Refaell, Y.
Methods for the identification of compounds capable of inducing the nuclear translocation of a receptor complex comprising the glucocoticoid receptor type II and viral protein R interacting
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                      Unchassified.
Unclassified.
1 (bases to 21)
Skollock, M.H., Cannon-Albright, L.A. and Kamb, A.
Germline mutations in the MTS gene
Patent: US 5624819-A 34 29-APR-1997;
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Pred. No. 1.3e+04;
0; Mismatches 4;
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Sequence 6 from patent US 5763190.
AR012082
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Sequence 7 from patent US 5763190.
AR012083.1 GI:3970073
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6 c 8 g
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78.9%;
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Best Local Similarity 78.9
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unknown.
Unclassified.
1 (bases 1 to 35)
Terman, B.Israel and Carrion, M.Eduardo.
Terman, Bane insert domain containing receptor and gene encoding same insert domain containing receptor and gene encoding same
Patent: US 5861301-A 2 19-JAN-1999;
Location/Qualifiers
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                                                                                                                              Score 12.6; DB 9;
Pred. No. 1.3e+04;
); Mismatches 4;
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65.0%; Pred. No. 1.7e+04;
Live 3; Mismatches 4;
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Jiao, S., Habben, J.E. and Niu.X.
Seed-preferred promoter from maize
Patent: WO 0121783-A 5 29-MAR-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
                                                                                                                                                                                                                                                                                                                                      AR030753 35 bp DNA
Sequence 2 from patent US 5861301.
AR030753
AR030753.1 GI:5943967
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/db_xref="taxon:4577"
a 10 c 7 g
Location/Qualifiers 1. .27
                                    /organism="unknown"
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Best Local Similarity 65.0°
Matches 13; Conservative
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Matches 15; Conserv
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Search completed: October 2, 2001, 15:56:42 Job time: 14166 sec
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Wolf,D., Tomlinson,J.E., Fretto,L.J., Giese,N.A., Escobedo,J.A. and
Williams,L.Thomas.
Human platelet-derived growth factor receptor extracellular domain
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                                                                                                                                                                                                                                     Unknow...
Unclassified.
1 (bases 1 to 42)
Capon,D. and Petropoulos,C.J.
Capon,D. and methods for determining anti-viral drug susceptibility and resistance and anti-viral drug screening Patent: US 58374(4.A. 2 17-NOV-1998;
Location/Qualifiers
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Score 12.4; DB 10; Length 37; Pred. No. 1.7e+04; 0; Mismatches 1; Indels
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Pred. No. 2.3e+04; 
0; Mismatches 3; Indels
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Location/Qualifiers
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Sequence 10 from patent US 5872218.
AR036477 GI:5953145
                                                                                                                                                  AR054989 42 bp DNA
Sequence 2 from patent US 5837464.
AR054989.1 GI:5980566
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13 c 11 g
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82.4%;
 62.0%;
92.9%;
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Best Local Similarity 82.4%;
Matches 14; Conservative
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Matches 14; Conservative
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Matches 13; Conservative
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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 	150. 9b_est89:* 151. 9b_est90:* 153. 9b_est190:* 154. 9b_est100:* 155. 9b_est100:* 155. 9b_est100:* 156. 9b_est103:* 157. 9b_est103:* 158. 9b_est103:* 159. 9b_est105:* 160. 9b_est67:* 161. 9b_est67:* 162. 9b_est67:* 163. 9b_est77:* 164. 9b_est71:* 165. 9b_est71:* 166. 9b_est71:* 167. 9b_est71:* 168. 9b_est71:* 169. 9b_est71:*	169: 9b_est92:* 170: 9b_est93:* 171: 9b_est94:* 172: 9b_est96:* 173: 9b_est96:* 174: 9b_est96:* 175: em_esthum20:* 177: em_esthum30:* 177: em_esthum31:* 179: em_esthum31:* 180: em_esthum33:* 181: em_esthum33:* 181: em_estrum33:* 182: em_estrum33:* 183: em_estrum33:* 184: em_estrum33:* 185: em_estrum33:* 186: em_estrum33:* 187: 9b_est100:* 188: 9b_est100:*

9b_est110:* 9b_htc:* 9b_htc:* 9b_htc:* em_gss_hum1:* em_gss_hum2:* em_gss_hum3:* em_gss_hum5:* em_gss_hum6:* em_gss_hum6:* em_gss_hum6:* em_gss_hum6:* em_gss_hum8:* em_gss_hum8:* em_gss_hum8:* em_gss_hum8:* em_gss_hum8:* em_gss_nod1:* em_gss_nod2:* em_gs_nod2:* em_	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Unpublished (2000) COMMENT Contact: Robert B. Weiss University of Utah Genome Center	### 1308 ### 10 #### 10 ### 10 #### 10 #### 10 ### 10 ### 10 #### 10 #### 10 ########		RESULT 2 A1545803 A1546803 A15
summaries Result Query No. Score Match Length DB ID Description	1 12.8 64.0 49 251 AZ686456 AZ686456 AZ686456 AZ68645 AZ68647 AZ	ALIGNMENTS	RESULT 1 A2868456 A2868456 A8 bp DNA GSS 21-FEB-2001 LOCUS LOCUS LOCUS A2868456 A2868456 A8 bp DNA GSS 21-FEB-2001 DEFINITION 200180LilF Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0180Lil F, DNA sequence. A2668456 GSS. A2668456 GI:13071791 A2668456 GSS. SOURCE A2668456 A2668456 GI:13071791 KEYWORDS GSS. SOURCE Mammalia: Eutheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Mus. REFERENCE I (bases I to 48) A0THORS Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

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                       Mus musculus
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                                                                                                                                          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Email: 2brafish@watson.wustl.edu
CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
Info@egenomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact:
Info@economesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@esegen.com) and
RessourcenZentrumPrimarbatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA797125 49 bp mRNA EST 10-FEB-1998 vn43e06.rl Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:1023970 5' similar to SW:TRHY_RABIT P37709 TRICHOHYALIN. [1]
,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
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                                                                                                                                                                                                                                                                                                                                                                      Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: T3 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/organism="Danio rerio"
/db_xref="taxon:7955"
/clone_lib="zebrafish WashU MPIMG EST"
/sex="mixed"
                                                                    Washu Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
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AA797125
AA797125.1 GI:2860080
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Matches 14; Conservative
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                                                      and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                             www.rzpd.de)
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE900863 44 bp mRNA EST 29-SEP-2000 601673838F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956864 5',
                                                                                                                                                                                                                                                           Contact: Marka Mydouse EST Project
Washington University School of MedicineP
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 44)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1023970"
/clone_lib="Stratagene mouse skin (#937313)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:574746
Possible reversed clone: similarity on wrong strand Seq primer: -20ml3 rev1 ET from Amersham High quality sequence stop: 1.

Location/Qualifiers
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    .49
    /organism="Mus musculus"

                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project Unpublished (1996)
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Gaps

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Length 49;

03-OCT-2000

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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                               Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 50)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1M0203P22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0203P22 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/G1 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Mouse 10kb plasmid UUGClM library"
                                                                                                                                                            /lab_host="SOLR cells (kanamycin resistant)"
                                                         Score 11.8; DB 189; Length
Pred. No. 5.6e+04;
0; Mismatches 3; Indels
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0203 row: P column: 22
Seq primer: CGTTGTAAAACGACGGCCAGT
                                        /organism="Homo sapiens"
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University of Utah
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/db_xref="taxon:10090"
/clone="UUGC1M0203P22"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                   59.08;
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                                                                                                                                           /sex="male"
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Contact: Robert B.
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                                                                                                                                                                    4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 446
Insert Size: 446
Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)
Insert Length: 446 Std Error: 0.00
Seq primer: M13RP1
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(basso 1 to 49)

Hiller, L. Lennon, G., Becker, M., Bonaldo, M. F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Fullman, M., Kucaba, T., Legy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M. B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ya95b09.rl Stratagene placenta (#937225) Homo sapiens cDNA clone MAGE:69401 5' similar to similar to gb:M22995 RAS-RELATED PROTEIN RAP-1A (HUMAN), mRNA sequence.
              CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM833 row: k column: 09.
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Pred. No. 5.5e+04;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
Washington University School of Medicine
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86.7%;
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Best Local Similarity 86.7
Matches 13; Conservative
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide Kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil47321141gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP Clone distribution information can be
found through the I.M.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/Amage/image.html
Seq primer: -40UP from Gibco
High quality sequence stops: 1.
Location/Qualifiers
was hydrodynamically sheared by repeated passage through a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 40)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A1499269 40 bp mRNA EST 11-MAR-1999 to09c08.xl NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2178542 3' similar to TR:Q12803 Q12803 LEUKOPHYSIN. ;contains element MER40 repetitive element ;, mRNA sequence.
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/db_xref="taxon:9606"
/clone="IMAGE:2178542"
/clone=lib="NCI_cGAP_ut2"
/tissue_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"
/lab_host="DH108"
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0
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86.7%;
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//doc=woctor: PWAZINY; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Labotatory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was preparative agarose gel electrophoresis. Vector DNA was prepared from a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qi|473211qi|pb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplcillin resistance."
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1M0285119R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0285119 R, DNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Slam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                                                        Gaps
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  Length 40;
                                                        Indels
Score 11.6; DB 21;
Pred. No. 6.9e+04;
); Mismatches 4;
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Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
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/db_xref="taxon:10090"
/clone="UUGC1M0285119"
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58.08;
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Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
Query Match
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Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama.K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Suzukl,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
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Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata
                                                                                                                                                                                                                                                                                                                                             AU102832 50 bp mRNA EST 05-APR-2001
AU102832 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS01996, mRNA sequence.
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AU102838 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CASO9268, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 7.2e+04;
0; Mismatches 4; Indels 0
                                                                                           Length 45;
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m c} 12 g 8 t
                                                                                                                                        Indels
                                                                                           DB 250;
                                                                                                                Pred. No. 7e+04;
0; Mismatches
  13
                                                                                        Score 11.6;

    .50
    /organism="Homo sapiens"
/db_xref="taxon:9606"
    /clone="CAS01996"

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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/G1 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114[gb]AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., Mand Mright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                     AZ827171 45 bp DNA GSS 20-FEB-2001
2M0103P19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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                                                                                                                   Gaps
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/strain="C57BL/6J"
/db.xref="taxon:10090"
/clone="UGGC2M0103P19"
/clone=lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
                                                                DB 244; Length 41;
                                                                                                              Indels
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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: P column: 19
Seq primer: CGTTGTAAACGACGCCCAGT
Class: plasmid ends
                                                              Score 11.6; DB 244
Pred. No. 6.9e+04;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                               clone UUGC2M0103P19 F, DNA sequence. AZ827171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                              58.0%;
77.8%;
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                                                                                                                                                                                      41 AGATGCCAGTTTTCTGCC 24
                                                              Query Match
Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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3 agatgctaggtatctgtc 20
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'H., Ota,T., Isogal,T., ianuaw,...
'K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries of Unpublished (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Emall: ysuzukialms.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,R., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

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AU102843 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS11158, mRNA sequence.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CAS11158"
/clone=ltb="Sugano Homo sapiens cDNA library"
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Pred. No. 7.2e+04;
0; Mismatches 4; Indels 0
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11 c 12 g 8 t
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/db_xref="taxon:9606"
/clone="CAS09268"
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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (base: 1 to 50)
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.

Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
Contact: Yutaka Suzuki
Department of Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Bmail: ysuzukiéins.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakaqawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
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AU102844
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/db_xref="taxon.9606"
/clone="CAS11168"
/clone_lib="Sugano Homo sapiens cDNA library"
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Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                       mRNA
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48 AGAGGTTTGGTATCTGCC 31
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completed: October 2, 2001, 15:00:53 ne: 10822 sec
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Musili (bases 1 to 39)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ422252 39 bp DNA GSS 03-OCT-2000 1M0202H18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0202H18 F, DNA sequence. AZ422252 GI:10547265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicinep
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fal: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
MGI.667001
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 31.
Location/Qualifiers
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/sex="mixed"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Reseau
                                                                                                                                                                                                                                                        1. .36 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                /strain="BALB/c"
/db_xref="taxon:10090"
/clone="IMAGE:766081"
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/dev_stage="6 weeks"
/lab_host="DH10B"
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WashU-HHMI Mouse EST Project
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Best Local Similarity 92.3%;
Matches 12; Conservative C
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Fax: 801 585 7177
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                                                                                                                                                                                                                                    FEATURES
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (qil4732114 |qblAR123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                   /lab_host-"E. Coli strain XLIO-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 39.
Location/Qualifiers
                                                                                                                                                                /organism="Mus musculus"/strain="C57BL/6J"
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/clone="UUGC1M0202H18"
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Matches 12; Conserv
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APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antibanse Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT APPLICATION NUMBER: US/09/377,310B
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 20
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APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT FILING NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 15
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             US-08-460-490-10
PCT-US92-00730-10
PCT-US92-00730-10
PCT-US92-0730-10
US-08-277-803B-21
US-08-271-880A-174
US-08-271-880A-172
US-08-271-880A-172
US-08-271-880A-189
US-08-910-408-189
US-08-910-408-189
US-08-910-408-189
US-08-910-408-189
US-08-910-49-215-189
US-09-249-215-189
US-08-876-885-21
US-08-464-531-59
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ilarity 100.0%; Pred. No. 0.049;
Conservative 0; Mismatches 0
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US-09-377-310-8

Sequence 8, Application US/09377310B

Patent No. 6133031

GENERAL INFORMATION:
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9.071 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-850-049-17
US-08-747B-17
US-09-342-749-15.
US-08-474-177-34
US-08-478-17-34
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US-08-481-352-34
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US-09-120-130-34
US-09-120-130-34
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Match Length
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                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2026-4006US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)758-4800
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 BASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/858,747
FILING DATE: 27-MAR-1992
CLASSIFICATION: 435
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,478
FILING DATE: 26-OCT-1994
CLASSIFICATION DATA:
RPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
FILING DATE: 29-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 27-MAR-1992
CLASSIFICATION: 435
                     US 08/050,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/08050478; Patent No. 5972596; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.0%;
93.3%;
                                    26-OCT-1994
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 GAAGCTAGGTATCTG 5
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: NUCLEIC ACID
                   APPLICATION NUMBER: FILING DATE: 26-OC CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                             LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Expression
FILE REPERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METHOD OF ELIMINATING INHIBITORY/INSTABILITY REGIONS OF MRNA
                                                                                  DB 3; Length 15; 20;
                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 20;
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100.0%; Pred. No. 20;
ive 0; Mismatches
                                                                                      75.0%; Score 15; DB 100.0%; Pred. No. 20; Live 0; Mismatches
       ; OTHER INFORMATION: antisense sequence US-09-377-310-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: antisense sequence US-09-377-310-9
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FILING DATE: 02-MAY-1997
CLASSIFICATION: 435
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09377310B Patent No. 6133031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/08850049
Patent No. 5965726
GENERAL INFORMATION:
APPLICANT:
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APPLICANT:
TITLE OF INVENTION: METHOD OF ELI
TITLE OF INVENTION: INHIBITORY/IN
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
21P: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                        Query Match 75.0
Best Local Similarity 100.
Matches 15; Conservative
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Matches 15; Conservative
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                                                                                                                                                                                                                                                           RESULT 3
US-09-377-310-9
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FEATURE:
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; OTHER INFORMATION: 3392-3434 OF C-FOS, HUMCFOT, ACC #V01512
US-07-858-747B-17
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Pred. No. 3e+02;
0; Mismatches 2; Indels
                                                                                                                                               1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Wong, Alexander K.C.
APPLICANT: Tavtigian. Sean V.
APPLICANT: Tavtigian. Sean V.
APPLICANT: Tavtigian. Sean V.
APPLICANT: Tavtigian. David H.-F.
ITLE OF INFORTION: TWRRS2 is a Tumor Suppressor
ITLE REFERENCE: 2318-20.
CURRENT APPLICATION NUMBER: US/09/342,749
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: US 60/091,044
EARLIER APPLICATION NUMBER: US 60/091,044
EARLIER APPLICATION NUMBER: US 60/091,044
SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 39
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MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATINS: YENEM: PC DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                  Score 13.4; DB 4;
Pred. No. 1.5e+02;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 34, Application US/08474177
Patent No. 5624819
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/474,177
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                    ; Sequence 15, Application US/09342749
; Patent No. 6166194
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                                                                                                  67.0%;
93.3%;
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87.58;
                                                                                             Ouery Match
Best Local Similarity 93.3
Matches 14; Conservative
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-342-749-15
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Best Local Similarity
Matches 14; Conserv
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APPLICANT: K.
TITLE OF INVENTION: METHOD OF ELIMINATING
TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF MRNA
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                    Length 43;
                                                                                                                                                                                                                                                                                                                                                                         Indels
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IDENTIFICATION METHOD:
OTHER INFORMATION: OLIGONUCLEOTIDE FOR MUTATING NT
                                                                                                                                                                                                                                                                                                                                Score 13.4; DB 2;
Pred. No. 1.5e+02;
0; Mismatches 1;
                                REGISTRATION NUMBER: 34,398
REFERENCE/ZOCKET NUMBER: 2026-4006US1
FELECOMMUNICATION INFORMATION:
TELEPHONE: (212)758-4800
FELEFRAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 BASE PARS
LENGTH: 43 BASE PARS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/858,747B
FILING DATE: 19920327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: MARY J. MORRY
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2026-4006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)751-6849
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/07858747B Patent No. 6174666 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                67.08;
93.38;
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Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                 MORRY, MARY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SINGLE
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US-08-050-478-17
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Score 12.6; DB 1; Length 21;
Pred. No. 3.7e+02;
); Mismatches 4; Indels
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Sequence 3.3. **
Sequen
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COMPUTER: IBM PC COMPatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,810
FILING DATE: 07-JUN-1995
CLASSFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24884-109348-C
                           FILING DATE: 01-00N-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US.08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US.08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US.08/214,582
APPLICATION NUMBER: US.08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 17-MAR-1995
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957 REFERENCE/DOCKET NUMBER: 24, TELECOMMUNICATION INFORMATION: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 63.0
Best Local Similarity 78.9
Matches 15; Conservative
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APPLICATION NUMBER: F
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US-08-487-033-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
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Pred. No. 3.7e+02;
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TYTLE OF INVENTION: MISIEL-Beta GENE
TYTLE OF INVENTION: MISIEL-Beta GENE
CORRESPONDENCE 336
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Cliviletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/487,033
FILING DATE: 01-JUN 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 28-957
REGISTRATION NUMBER: 28-957
REGISTRATION NUMBER: 28-957
REGISTRATION NUMBER: 24-109348-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
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APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
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Patent No. 5739027
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ctagatgctaggtatctgt 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 15; Conservi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ANTI-SENSE:
US-08-474-177-34
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Gaps

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TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS TITLE OF INVENTION: GENE NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS: ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 21;
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COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/848,251
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 12.6; DB 2;
Pred. No. 3.7e+02;
0; Mismatches 4;
  28,957
ER: 24884-109348
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CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US 08/474,083
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
APPLICATION NUMBER: US 08/251,938
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FILING DATE: 01-UN1-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
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FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34, Application US/08848251
Patent No. 5989815
GENERAL INFORMATION:
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 2486
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
INFORMATION: 202-962-8300
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        63.0%;
78.9%;
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3 CTAGAGGCGAATTATCTGT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 63.0
Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                                                                                            LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                            linear
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US-08-508-735-34
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US-08-848-251-34
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APPLICANT: Stone, Steven
APPLICANT: Stone, Ping
APPLICANT: Jing, Ping
APPLICANT: Mamb; Alexander
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
*ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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APPLICATION NUMBER: US/08/508,735
             PRIOR APPLICATION NOMER: US UG/213,007
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY AGENT INFORMATION:
NAME: Theo. Jeffrey L.
REGISTRATION NUMBER: 28,957
REJEPHONE OF SEQ 1D NO: 34:
FELECOMMUNICATION INFORMATION:
TELEFONDE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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RICOR APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 08/215,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-508-735-34

Sequence 34, Application US/08508735

Patent No. 5843756

GENERAL INFORMATION:
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78.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ihnen, Jeffrey L.
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Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20005
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US-08-480-810-34
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; Sequence 34, Application US/09120130
; Patent No. 6037462
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APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                       REFERENCE/DOCKET NUMBER: 24:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
      28,957
                                                                                                                                                                                                                                                                                                                                                                                     63.0%;
78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ctagatgctaggtatctgt 19
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match 63.0 Best Local Similarity 78.9 Matches 15; Conservative
                                                                                                                                                            LENGTH: 21 base pairs
                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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HYPOTHETICAL: 1
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                                                                                                                                                                                                                                                                                               ; ANTI-SENSE:
US-08-486-047-34
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US-09-120-130-34
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Patent No. 5994095

GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: WT22 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
STREET: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Fidopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAMRE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,047
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 18-MRR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MRR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MRR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 18-MRR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-MRR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
PRIOR APPLICATION NUMBER: US 08/227,369
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APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-ARR-1994
ATTORNEY/AGENT INPORMATION:
NAME: Ihnen, Jeffrey L.
                                                                                     REFERENCE/DOCKET NUMBER: 2486
TELECOMMUNICATION INFORMATION:
TELEPRONE: 202-962-4810
TELEPAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ctagatgctaggtatctgt 19
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                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDRES: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
TYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-848-251-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 78.9°
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-08-486-047-34
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 12.6; DB 2;
Pred. No. 3.7e+02;
); Mismatches 4;
24884-109348-B
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APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-UNN-1994
PRICATION NUMBER: US 08/251,938
FILING DATE: 18-MAR-1994
FILING DATE: 18-MAR-1994
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRICA APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
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FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/120,130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Gaps

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Pred. No. 3.7e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: October 2, 2001, 16:03:47 Job time: 14591 sec
                                                                   34:
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78.9%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 63.0
Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                                                                                    LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 11:05 TOPOLOGY: 11:05 TOPOLOGY: 11:05 TOPOLOGY: 11:05 TOPOLOGY: 10:05 TOPOLogy: 10:0
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TITLE OF INVENTION: MTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMBUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/09/115,252
FILING DATE:
CLASSIFICATION:
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FILING DATE: 18-ARR-1994
ATORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
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APPLICATION NUMBER: US/08/480,810
APPLICATION NUMBER: US/08/480,810
FILING DATE: U7-UN-1995
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICAT
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Patent No. 6060301
GENERAL INFORMATION:
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                                             TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANUEDNESS: single
TOPOLLGY: linear
MOLECULE TYPE: CDNA
     202-962-4810
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Best Local Similarity 78.9°
Matches 15; Conservative
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     TELEPHONE:
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US-09-115-252-34
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Run on:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AX100491
A25775
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AR050806
AR053811
AR091592
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Match Length DB
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9b_htg13::*
9b_htg13::*
9b_htg16::*
9b_htg16::*
9b_htg18::*
9b_htg19::*
9b_htg21::*
9b_htg22::*
9b_htg22::*
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                                                                October 2, 2001, 15:56:42; Search time 3339.34 Seconds (without alignments) 92.640 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                  1344157 seqs, 7733874588 residues
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Maximum Match 100%
Listing first 45 summaries
                                             OM nucleic - nucleic search, using sw model
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                                                                                                                  Title:
Perfect score:
                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                           Sequence:
                                                                                                                                                                                                  Searched:
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AX100491 Sequence A25775 antisense o AR034285 Sequence AR035391 Sequence AR050806 Sequence AR053811 Sequence AR091592 Sequence

124252 Sequence 39

Description

10-APR-2001

PAT

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                     Score 12.4; DB 10;
Pred. No. 4.8e+04;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 12.2; DB 9;
Pred. No. 6.1e+04;
); Mismatches 3;
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/organism="synthetic construct"
/db_xref="taxon:32630"
8 c 7 g 12 t
                                                                                                  1 (bases 1 to 37)
Jiao, S., Habben, J. E. and Niu, X.
Seed-preferred promoter from maize
Paten: WO 0121783-A 5 29-MAR-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                             BIOCIDAL PROTEINS
Patent: WO 9304586-A 8 18-MAR-1993;
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          AX100491 37 bp DNA
Sequence 5 from Patent W00121783.
AX100491 GI:13619505
                                                                                                                                                                                                                                                                                                                         antisense oligonucleotide OWB22.
A25775
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/organism="2ea mays"
/db_xref="taxon:4577"
a 10 c 7 g
                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                     62.0%;
                                                                                                                                                                                                                                                                                                                      38 pb
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1 (bases 1 to 38)
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Best Local Similarity 92.9
Matches 13; Conservative
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Best Local Similarity
Matches 14; Conserv
                                                       Sea mays.
                                                                Zea mays
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AX100491/c
LOCUS
DEFINITION
                                                                                                                                                          source
                                                     SOURCE
ORGANISM
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ORIGIN
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VERSION
KEYWORDS
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ORIGIN
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                                                                                                            AUTHORS
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A25775/c
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KEYWORDS
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AR034285
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KEYWORDS
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A71632 Sequence 65
A43390 Sequence 34
AR054989 Sequence
A19662 Nucleotide
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AR014421 Sequence
I11864 Sequence 30
                                                                M60145 Human/HIV 3
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E60316 Identificat
                                             I87238 Sequence 64
I90213 Sequence 39
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146138 Sequence 11
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876309 PTPH1=cytos
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AX097355 Sequence
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A22305 oligonucleo
AR053115 Sequence
  Sequence 18
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AR030753 Sequence
AR075961 Sequence
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A98431 Sequence 15
AX021032 Sequence
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A17046 oligonucleo
A17446 oligonucleo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 31)
Gold,L. and Tasset,D.
DNA ligands of thrombin
Patent: US 5542393-A 39 06-AUG-1996;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                    124252 31 bp DNA
Sequence 39 from patent US 5543293.
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HUMAIDSC2
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AX097355
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S76309
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A17446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unknown.
Unclassified.
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Best Local Similarity
Matches 16; Conserv
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JOURNAL
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SOURCE
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Gaps

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Length 37;

22-MAR-1995

PAT

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Indels

Length 38;

FEATURES

VERSION

RESULT 124252

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29-SEP-1999

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Unknown.

RESULT

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Gaps

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Unclassified.
Unclassified.
1 (bases 1 to 41)
Crabtree,G.R., Schreiber,S.L., Spencer,D.M., Wandless,T.J. and
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Unclassified.
1 (bases 1 to 41)
Crabtree,G.R., Schreiber,S.L., Spencer,D.M., Wandless,T.J. and
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                                                               Score 12.2; DB 9; Length 41;
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0; Mismatches 3; Indels
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Belblaw, P.
Regulated apoptosis
Regulated apoptosis
Patent: US 5994313-A 8 30-NOV-1999;
Location/Qualifiers
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Patent: US 5834266-A 8 10-NOV-1998;
Location/Qualifiers
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Sequence 8 from patent US 5834266.
AR053811 GI:5978673
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Sequence 8 from patent US 5994313.
AR091592.1 GI:10018347
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13 c 9 g
 /organism="unknown"
13 c 9 g
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Best Local Similarity 82.4%;
Matches 14; Conservative
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Crabtree, G.R., Schreiber, S.L., Spencer, D.M., Wandless, T.J.,
Belshaw, P. and Ho, S.
Regulated transcription of targeted genes and other biological
events
            1 (bases 1 to 41)
Crabtree, G.R., Schreiber, S.L., Spencer, D.M., Wandless, T.J. and
                                      Belshaw,\mathbf{P}. Regulated transcription of targeted genes and other biological events
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Crabtree, G.R., Schreiber, S.L., Spencer, D.M., Wandless, T.J. and
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Patent: US 5830462-A 8 03-NOV-1998;
                                                                          Patent: US 5869337-A 8 09-FEB-1999;
Location/Qualifiers
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Sequence 8 from patent US 5830462.
AR050806
AR050806.1 GI:5974170
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Sequence 8 from patent US 5871753.
AR035391
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A83432 LOCUS ACCESSION

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REFERENCE AUTHORS JOURNAL

TITLE

FEATURES

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1 (bases 1 to 35)
Thastrup.O., Tullin.S.slashed.ren, Poulsen.L.Kongsbak and Bj.o
Slashed.rn.S.Petersen.
Method of detecting biologically active substances by using green
                                                                          Unclassified.
1 (bases 1 to 35)
Terman, B.Israel and Carrion, M.Eduardo.
Recombinant kinase insert domain containing receptor and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAR-1997
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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                                                                                                                                                                                                                                                                                    Score 12; DB 9; Pred. No. 7.9e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fluorescent protein
Patent: US 5958713-A 22 28-SEP-1999;
Location/Qualifiers
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Sequence 22 from patent US 5958713.
AR075961
                                                                                                                                           encoding same
Patent: US 5861301-A 2 19-JAN-1999;
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64 from Patent W09503412.
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7 c 3 g
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Mabilat,C. and Christen,R.
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                GI:5943967
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Best Local Similarity 63.2%;
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unclassified.
1 (bases 1 to 26)
Goebel, W. and Demuth, A.
USE OR A SECRETION VECTOR FOR FERTILITY CONTROL BY ORAL VACCINATION
USE OR A SECRETION VECTOR FOR FERTILITY CONTROL BY ORAL VACCINATION
USE OR A SECRETION VECTOR (DE):
GOEBEL WERNER (DE): SCHERING AG (DE)
Location/Qualifiers
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synthetic construct
artificial sequence.
1 (bases 1 to 33)
Hentze,M.W. and Paraskeva,E.
Method of isolation of rna-binding compounds
Patent: WO 9937807-A 2 29-JUL-1999;
EUROP MOLECULAR BIOLOGY LAB (DE); HENTZE MATTHIAS W (DE); PARASKEVA
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/db_xref="taxon:32630"
/note="Primer for amplification
4 c 4 q 18 t
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                                                                          A83432 26 bp DNA
Sequence 18 from Patent W09850067.
A83432 GI:6732770
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/db_xref="taxon:32644"
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PRAGMENT: WO 9503412-A 64 02-FEB-1995;
BIO MERIEUX (FR)
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1 (bases 1 to 39)
Mabilat,C. and Christen,R.
Nucleotide fragment of the 23S ribosomal RNA of mycobacteria, derived probes and primers, reagent and detection method Patent: US 5703217-A 64 30-DEC-1997;
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Thompson, G.A. and Knauf, V.C.
Plant desaturases-compositions and uses
Patent: US 5723595-A 39 03-MAR-1998;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Unpublished (2000) COMMENT University of Utah Genome Center University of Utah Genome Center Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00	Plate: Outob row: G column: U/ Seq primer: CGTTGTAAACGACGCCAGT Class: plasmid ends Location/Qualifiers 1. 0.3 Location/Qualifiers 1. 0.3 Location-C57BL/6J" //Orde="UGCIMO066607" //Clone="UGCIMO066607" //Lone="UGCIMO066607" //Lone="Vector: PW042nv; Purified genomic DNA from M. //Note="Vector: PW042nv; Purified genomic DNA from M. //Note="Vector: PW042nv; Purified genomic DNA from M. //Lote-"Vector: PW042nv; Purified genomic DNA from M. //Note="Vector: PW042nv; Purified genomic DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through was hydrodynamically sheared by repeated DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The	Query Match Query Match Query Matches Query Matc	Oy 2 tttgctagatgctagg 17 Bb 19 TTGCTAGATCCAAGG 4 RESULT 2 AU104064/c LOCUS LOCUS LOCUS LOCUS AU104064 50 bp mRNA EST 05-APR-2001 BEFINITION AU104064 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone ACCESION AU104064.1 GI:13553585 KEYWORDS EST. NUMBAN: ORGANISM HOMO sapiens BUKATYOCA: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; MAMMANIA: Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 50) AUTHORS Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogal,T., Taira,H., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
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Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Rastlute of Medical Science, University of Tokyo
Beal: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzukieims.u-tokyo.ac.jp
Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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AZ841152 GI:13011060
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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/sex="Matle"
/lab host=E. Coli strain XL10-Gold, T1-resistant, F.
/note="Vector: PWD42nv; Purified genomic DNA from M.
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84112, USA
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/db_xref="taxon:9606"
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Class: plasmid ends
High quality sequence stop: 35.
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/clone="UUGC2M0139D06"
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Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 15; Conserv
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qil4732114) gblar129072. 1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 49)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, J.M., Rose, M., Rose, M., Rose, M., Rose, M., Bose, M., Bose, M., Bose, M., Grose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1M0200D22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0200D22 F, DNA sequence.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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//db_xref="taxon:10090"
/clone="UGCIM0200022"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
//sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 12.2; DB 250; Length 35; Pred. No. 4e+04; 0; Mismatches 3; Indels 0;
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Insert Length: 10000 Std Error: 0.00
Plate: 0200 row: D column: 22
Seg primer: CGTTGTAAAACGACGCCCAGT
Class: plasmid ends
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University of Utah
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82.4%;
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Fax: 801 585 7177
Email: ddunn@genet
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Gaps

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Indels

Length 37;

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/note="Organ: breast; Vector: pCMV-SPORT4; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.2 kb. Life Technologies catalog #:10985-018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                            AGASIG137 46 bp mRNA EST 14-APR-1998 0932c10.s1 NCI_CGAP_BR7 Homo sapiens cDNA clone IMAGE:1441554 3's sinflar to SW.NU2M_HUMAN P03891 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2'; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inclination of the control of the co
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T. brucei sheared genomic DNA clone 383e12, reverse sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trypanosoma brucei.
Trypanosoma brucei
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma
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Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
                                                                Score 11.8; DB 258;
Pred. No. 6.5e+04;
0; Mismatches 2; 1
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86.7%; Pred. No. 6.7e+04;
ive 0; Mismatches 2;
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Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1441554"
/clone=lib="NCI_GGAP_Br7"
/lab_host="DH108"
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AL497988.1 GI:11873710
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                                                            59.0%;
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Matches 13; Conserv
                                                                   Query Match
Best Local Similarity
Matches 13; Conserv
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AUTHORS
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                                                                                        (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymerlectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114) plaR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRE027/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kD). The v +i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
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Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/
Location/Qualifiers
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Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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T. brucei sheared genomic DNA clone 254h02, reverse sequence,
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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/strain="TREU927"
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Best Local Similarity
Matches 15; Conserv
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Indels

Length 46;

13-DEC-2000

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Indels

Length 44;

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Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAGGG. Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                                                                                                                                                                                                                                                                                                                          AU104334 50 bp mRNA EST 05-APR-2001
AU104334 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ESC00112, mRNA sequence.
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Pred. No. 8.4e+04;
); Mismatches 4; I
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Pred. No. 8.5e+04;
); Mismatches 4; I
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/db_xref="taxon:9606"
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/clone_lib="Sugano Homo
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Best Local Similarity 77.8
Matches 14; Conservative
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Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submission
Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CBIO 18A, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAt 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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I (bases 1 to 44)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: ArCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM813 row: k column: 09.
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Pred. No. 8.2e+04;
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/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
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/db_xref="taxon:9606"
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/clone="383e12"
                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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ilarity 77.8%;
Conservative
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Gaps

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Length 50;

31-MAR-1997

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (qi|4732114 qib|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the linsert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1M0327J11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                           Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Puiffied genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                       Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
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                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0160 row: J column: 20
Seq primer: CACACAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"/strain="C57BL/6J"
                                            plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="UUGC1M0160J20"
                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 25.
Location/Qualifiers
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  and Wright, D., Weiss, R.
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Not I and Eco RI sites of the modified pT7T3 vector.

Library constructed by Bob Barstead."
                                                                                                                    Marra, M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                            Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:467001
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Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 1e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project
Unpublished (1996)
Orditact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
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High quality sequence stop: 31.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:766081"
/clone_lib="Barstead MPLRB1"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="BALB/c"
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/dev_stage="6 weeks"
/lab_host="DH10B"
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92.3%;
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Best Local Similarity 92.3°
Matches 12; Conservative
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                                                                                                                                                              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
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Pred. No. 1.3e+05;
0; Mismatches 3; Indels 0;
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1 (bases 1 to 39)
                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                             Plate: 0327 row: J column: 11
Seg primer: CGTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0327J11"
                                                                                  Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualiflers
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Schizosaccharomyces pombe
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81.2%;
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Best Local Similarity 81.2
Matches 13; Conservative
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11 TGTGCTACATGCCAGG 26
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Schizosaccharomyces pombe was prepared by cloning cDNA into the Smal site of Ml3mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"
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                                                                                                                                                                                                                                                                             /organism="Schizosaccharomyces pombe"
/strain="972"
/db_xref="taxon:4896"
/clone="spc00499"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/sex="h minus"
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Dun,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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Morimyo, M. and Mita, K. Identification of expressed sequence tags of Schizosaccharomyces
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                                                                                                                                  Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
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Pred. No. 1.3e+05;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: M13mp19; The cDNA library of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Std Error: 0.00
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Insert Length: 10000 Std Error: (
Plate: 0363 row: P column: 15
Seq primer: CACACAGGAAACAGCTATGACC
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/strain="C57BL/6J"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
                                                                                                                                                                                                                     Email: morimyo@nirs.go.jp.
Location/Qualifiers
                                                                                                             Contact: Mitsuoki Morimyo
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81.2%;
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                                                                             Unpublished (1998)
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Matches 13; Conservative
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Fax: 801 585 7177
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Search completed: October 2, 2001, 15:00:54 Job time: 10823 sec
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                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with 74 DNA polymerase and 74 polymerase about end repaired with 74 DNA polymerase and 74 polymerase to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114 (pbl.AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptore competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ588937 47 bp DNA GSS 13-DEC-2000 1M0397M06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0397M06 R, DNA sequence.
                                                                              /lab_host="E. Coli strain XLI0-Gold, Tl-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
/clone="UUGCIM0363P15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.0%; Score 11.2; DB 246; Length 41; 81.2%; Pred. No. 1.3e+05; Live 0; Mismatches 3; Indels 0
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Seq primer: CACACAGGAAACAGCTATGACC
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with TH DNA polymerase and TH polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil4732114)gblAR129072.1), a copy.number inducible derivative of pRDA2 (gil4732114) and preparative adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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October 2, 2001, 15:56:44; Search time 3339.34 Seconds (without alignments) 92.640 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	AR084719 Sequence	A84595 Sequence 5	AR079892 Sequence	A97844 Sequence 12	I44719 Sequence 45	I52125 Sequence 45	AX096725 Sequence	E04774 Synthetic D
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Unknown.
Unclassified.
Inclassified.
I (bases I to 30)
Weinrich, S. L., Atkinson, E. M. III, Lichtsteiner, S. P., Vasserot, A. P., Pruzan, R.A. and Kealey, J. T.
Purified telomerase
Purified telomerase
Patent: US 5968506-A 5 19-OCT-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                               68.0%; Score 13.6; DB 9; Length 30; 80.0%; Pred. No. 6.6e+03; ive 0; Mismatches 4; Indels
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Pred. No. 6.6e+03;
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unclassified.
1 (bases 1 to 30)
Atkinson,E.M. and Kealey,J.T.
PURIFIED TELOMERASE
Patent: WO 9845450-A 5 15-OCT-1998;
GERON CORP (US)
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Sequence 121 from Patent W09914377.
A97844
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Sequence 5 from patent US 5968506.
AR079892. GI:10006645
                                                                                                                           /organism="unidentified"
      A84595 30 bp DNA
Sequence 5 from Patent W09845450.
A84595 1 GI:6733511
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AR075530 Sequence
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AX087933 Sequence
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A81398 Sequence 28
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1 (bases 1 to 30)
S Melssner, P.S. and Coleman, T.A.
Human criptin growth factor
AL Patent: US 5981215-A 6 09-NOV-1999;
Location/Qualifiers
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A82505
A82526
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AR084719
AR084719.1 GI:10011489
30 bp
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Location/Qualifiers
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/organism="unknown"
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JP 1993091876-A/13.
synthetic construct.
synthetic construct
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Walsh, T.A., Hey, T.D. and Morgan, A.E.R.
Ribosome-inactivating proteins, inactive precursor forms thereof, a
process for making and a method of using
Patent: US 5635384-A 45 03-JUN-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 18)
Walsh,T.A., Hey,T.D. and Morgan,A.E.R.
Ribosome-inactivating proteins, inactive precursor forms thereof, a
process for making and a method of using
Patent: US 5646026-A 45 08-JUL-1997;
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                     1 (bases 1 to 18)
Quint, W and Kleter, B
Quint, W and Kleter, B
DETECTION AND DEMTIFICATION OF HUMAN PAPILLOMAVIRUS BY PCR AND
TYPE-SPECIFIC REVERSE HYBRIDIZATION
Patent: WO 9914377-A 121 25-MAR-1999;
INNOGENETICS NV (BE); DELFTS DIAGNOSTIC LAB B V (NL)
Location/Qualifiers
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                                                                                                                                                                                                                                      Length 18;
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Pred. No. 8.4e+03;
0; Mismatches 2;
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Sequence 45 from patent US 5635384.
114719 GI:2469432
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152125
152125.1 GI:2473326
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Best Local Similarity 87.5%;
Matches 14; Conservative
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Matches 14; Conservative
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1 (bases 1 to 26)

1 (bases 1 to 26)

PARÁINIMA, E., Kakhuuma, S., Takemoto, A., Miyoda, Y. and Fukuyama, S., PROTEASE, ITS PRODUCTION AND USE
PATENT: JP 1993091876-A 13 16-APR-1993;

SHOWA DENKO KK.
OS Artificial gene
OC Artificial sequence; Genes.
OS Bacillus NKS-21
PN JP 1993091876-A/13
PD 16-APR-1993
PF 02-OCT-1991 JP 1991280313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 21)
Lander, E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.Q. and Mccarthy, J.J.
Single nucleotide polymorphisms in genes
Patent: WO 0118250-A 1903 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
Pharmaceuticals, Inc. (US)
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Synthetic DNA for site directed mutagenesis of protease derived
from Bacillus NKS-21.
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                                                                                      Length 18;
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                                                                                 67.0%; Score 13.4; DB 10; 93.3%; Pred. No. 8.4e+03; iive 0; Mismatches 1;
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Sequence 1903 from Patent WO0118250.
AX096725 GI:13512979
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/db_xref="taxon:9606"
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Gaps

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Indels

Length 21;

30-MAR-2001

PAT

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Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 21)

Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and Mccarthy,J.J.

Single nucleotide polymorphisms in genes
Patent: WO 0118250-A 640 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL. RESEARCH (US); Millennium
Pharmaceuticals, Inc. (US)
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
                                                                                                                                              Score 12.4; DB 10;
Pred. No. 3.3e+04;
1; Mismatches 2;
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Pred. No. 3.3e+04;
l; Mismatches 2;
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Juan,S., Lichenstein,H.S. and Wright,S.D.
Anti-inflammatory CD14 polypeptides
Patent: US 5869055-A 24 09-FEB-1999;
Location/Qualifiers
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Sequence 640 from Patent WO0118250.
AX095462
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 6 c 4 g
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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 2 c 6 g
             Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Seguence 24 from patent
AR032341
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81.2%;
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81.2%;
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Best Local Similarity 81.2
Matches 13; Conservative
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Best Local Similarity 81.2
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AX095462/c
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AR032341/C
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C12N9/54,C11D3/386,C12N1/21,C12N15/57,(C12N9/54,C12R1:07), PC
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 21)
Lander, E. S., Gargill, M., Ireland, J. S., Bolk, S., Daley, G. Q. and Mccarthy, J. J.
Single nucleotide polymorphisms in genes
Patent: WO 0118250-A 23 15-MAR-2001;
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 TAKINISHI EIKO, KAKINUMA SHINJI, TAKEMOTO AYANO, PI
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                                                                                                                                                                                                                                                                  Length 26;
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Pred. No. 1.9e+04;
0; Mismatches 2;
                                                                                                                                                                        /organism="synthetic construct"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unclassified.

1 (bases 1 to 32)
Thomas Jnr.K.A. and Linemeyer,D.L.
Mutant acidic fibroblast growth factor
Patent: EP 0319052-A2 27 07-JUN-1989;
Location/Qualifiers
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Sequence 23 from Patent W00118250.
AX094845
                                                                                                 topology: Linear;
hypothetical: No;
anti-sense: No;
Location/Qualifiers
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                                                                    C12R1:07);
strandedness: Single;
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Best Local Similarity 87.5%;
Matches 14; Conservative
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YOSHIAKI,
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29-SEP-1999

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Unclassified.

1 (bases 1 to 25)

1 (bases 1 to 25)

Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H.

Manmallan telomerase

Patent: US 5958680-A 27 28-SEP-1999;

Location/Qualifiers
    AKU75530 25 bp DNA
Sequence 27 from patent US 5958680.
AR075530
                                                                                                                                                                                                                                                                                                                                                                                              Search completed: October 2, 2001, 15:56:45 Job time: 14169 sec
                                                                                                                                                                                             /organism="unknown"
                                                  AR075530.1 GI:10002278
                                                                                                                                                                                                                                                             Query Match 61.0%;
Best Local Similarity 82.4%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                1 ggtaagcagctgccatt 17
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Yazawa,K., Yamada,A., Kato,S. and Kondo,K.
Gene coding for eicosapentaenoic acid synthesizing enzymes and process for production of eicosapentaenoic acid
Patent: US 5798259-A 22 25-AUG-1998;
                                                   Gaps
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                        Score 12.4; DB 9; Length 39;
Pred. No. 3.4e+04;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 25;
                                                                                                                                                                                                                                         Unknown.
Unclassified.
1 (bases 1 to 25)
1 (bases 2 to 25)
Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H. Assays for the DNA component of human telomerase Patent: US 5776679-A 26 07-UUL-1998;
Location/Qualifiers
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Pred. No. 4.4e+04;
); Mismatches 3; Indels
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Sequence 22 from patent US 5798259.
AR025451. GI:3978079
                                                                                                                                                                 AR016058 25 bp DNA
Sequence 26 from patent US 5776679.
AR016058 1 GI:3972335
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82.4%;
                       Query Match 62.0%;
Best Local Similarity 92.9%;
Matches 13; Conservative
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Best Local Similarity 82.4%;
Matches 14; Conservative
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Score 12.2; DB 9; Length 25; Pred. No. 4.4e+04; 0; Mismatches 3; Indels

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Polymorphic fragme Mutagenic oligo fo PCR primer ES. Not! PCR primer ES. Not! PCR primer ES. Not! PCR primer es aingle Human gene single PCR primer O-551 used Oligonucleotide us Primer o-551 used Oligonucleotide us PCR primer For PGB u PCR primer for PGB u PCR primer for PGI Human biallelic po Human biallelic po Human C-myc cDNA P Primer for icosape RNA component of h Primer for S. putr Human telomerase R Nuclease resistant Nuclease resistant Human meg-3 DNA pr PEA toxin gene and Transformed lympho L-selectin truncat ByDy-PAV Illinois L-selectin truncat Human GDP-fucose p Nucleic acid ligan Human GDP-fucose p Nucleotide sequenc 24 gene cap Site, 24 gene cap Site, 25 gen

BP

(first entry)

8 x 5 5 5 5 5 5 5 5 5 8 8

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Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 1163; 2245pp; Japanese.
                                                                                                          AAT22589 standard; cDNA to mRNA; 29
                                                                                                                                                                                                                     Human gene signature HUMGS04205.
                    16 GGTAAGCAGCTGCCAT
       WPI; 1995-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  11-NOV-1994;
                                                                                                                                                                                  01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-1993;
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                                                                                                                                               AAT22589;
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                                   The present invention describes a number of phosphorothicate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR primers AAX36327-28 were used to amplify human FAK cDNA, in the course of the invention. The specification describes a method for altering the tumorigenicity or malignancy of brain cancer cells by changing the activity of glycosyltransferase in the cell so that glycosylation of cellular proteins is modified. The method is applied to glicom or meningioma, for prevention or treatment of brain tumours. Measuring the level of glycosyltransferase expression in brain cells is used to detect or predict their tumorigenicity.
                                                                                        in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the
                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; tumorigenicity; glycosyltransferase;
malignancy; brain cancer cell; protein glycosylation; glioma;
meningioma; brain tumour; FAK; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Altering tumorigenicity and malignancy of brain cancer cells
                                                                                                                                                                                                                                      22; Length 20;
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                                                                                                                                                                                                                                    DB 22
                                                                                                                                                                                Sequence 20 BP; 5 A; 4 C; 5 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sense primer used to amplify human FAK cDNA.
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                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                      Score 20;
Pred. No. (
Example 2; Column 23; 30pp; English.
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100.0%; Pre
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tive 0;
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                                                                                                                             antisense sequences, inclu
treatment of all of these.
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                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-327411/27.
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93JP-0355504. 94WO-JP01916.

Okubo K;

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A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(") as the sole primer. Since the 3'-end of mRNA by using poly(") as the sole primer. Since the 3'-end of mRNA by using poly(") as the sole primer. Since the 3'-entraclated cDNAs hybridise with specific mRNAs Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Mismatches
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Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                            determined (esp. using primers an sequences) as a means of diagnosi recognising different cell types.
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85.0%;
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Matches 17; Conservative
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Length 22; 0; Indels

DB 20; 33;

Score 16; Pred. No.

Mismatches

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fibronoectin collagen-binding domain. The amplified sequence was used to construct a collagen-binding physiologically active polypeptide. This polypeptide comprises a peptide from fibronectin ligated to a physiologically active peptide. The polypeptides are used in an agent for enabling topical retention or sustained release of a physiologically active peptide active peptide active peptide or physiological activity-imparting agent. They may be used in gene therapy and in tissue regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphism; biallelic; paternity testing; forensic; genetic mapping; phenotypic typing; medicament; disease; marker; human; ss.
                                                                                                                                                                                                           Collagen-binding active polypeptide for use in an agent for enabling topical retention or sustained release of a physiologically active peptide or physiological activity-imparting agent comprises a fibronectin peptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid segments containing polymorphic sites - used for, e.g. detecting a disease phenotype, in forensics, paternity testing or genetic mapping of phenotypic traits
                                                                                                                                                                                                                                                                                                                                                   PCR primers AAA64261-62 were used to amplify cDNA encoding a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.0%; Score 14.4; DB 21; Length 49; 93.8%; Pred. No. 2.4e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human biallelic polymorphic DNA fragment SGC30775.
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                                                                                                                                                                                                                                                                                                          Example 1; Page 124; 135pp; English.
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21-FEB-2000; 2000WO-JP00964
                                    99JP-0041913
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Les 15; Conservative
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                                                                                                                                 Ishikawa T, Kitajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-080963/07.
                                                                                                                                                                       WPI; 2000-565375/52.
                                                                                            (TERU ) TERUMO CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                      19-FEB-1999;
                                                      01-NOV-1999;
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Best Local S:
Matches 15,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, anglogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fibrononectin; collagen-binding domain; sustained release; gene therapy; physiologically active polypeptide; topical retention; PCR primer; tissue regeneration; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                               Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer for human fibrononectin collagen-binding domain cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                          Human focal adhesion kinase antisense sequence #28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.0%; Score 15; DB 22; 100.0%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15 BP; 4 A; 4 C; 3 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; Column 25; 30pp; English.
                                                                                                                                                                       antisense; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                            99US-0377310.
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                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaarde WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-006141/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                            19-AUG-1999;
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                                                      12-FEB-2001
                                                                                                                                                                                                                                                US6133031-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Monia BP,
                  AAC65562;
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Gaps

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Sequences AAX06101-X06558 represent human DNA fragments which contain
biallelic polymorphic markers. The base occupying the polymorphic site
is indicated by the appropriate IUPAC-IUB ambiguity code. These
fragments can be used in a method for determining polymorphic forms in
an individual. The invention further provides computer-readable storage
medium for storing data for access by an application programme being
executed on a data processing system. Such a method comprises a data
structure stored in the computer-readable storage medium, the data
structure including information resident in a database used by the
application programme and including records, each record comprising
information identifying a polymorphism shown in the above sequences. The
products and methods can be used for analysing polymorphic sites in
individuals for testing for the presence of a disease phenotype or in
formatics, paternity testing or genetic mapping of phenotypic traits.
They can also be used for the production of transgenic animals. The nucleic
entities are and for the production of transgenic animals. The nucleic
entities are also be used in the manufacture of medicaments for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 14; DB 20; Length 31
Pred. No. 3.7e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 31 BP; 5 A; 7 C; 6 G; 12 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment or prophylaxis of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 87.5%;
Matches 14; Conservative
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Criptin growth factor; CGF; anglogenesis; wound healing; vulnerary; muscle wastrage; osteoporosis; implant fixation; tissue regeneration; panoreas cancer; diagnosis; gene therapy; primer; PCR; polymerase chain reaction; COS; ss. Human criptin growth factor 3' primer for COS expression. AAT51062 standard; cDNA; 30 BP. (first entry) 5 agcagctgccattatt 20 6 agcaggtgccrttatt 21 05-APR-1997 Synthetic. AAT51062; RESULT ద ð

New isolated human Criptin Growth Factor polypeptide - which can be used to stimulate anglogenesis and develop products for use in Example 3; Page 36; 52pp; English. (HUMA-) HUMAN GENOME SCI INC. 95WO-US07087 95WO-US07087 Meissner PS; diagnosis and therapy WPI; 1997-043055/04. 05-JUN-1995; 05-JUN-1995; 12-DEC-1996. Coleman TA,

WO9639420-A1

Sequence 40 BP; 9 A; 12 C; 7 G; 12 T; 0 other;

A 3' PCR primer (AAT51062) contains a PvuII site followed by 15 nucleotides that are the reverse complement of human criptin growth factor (CGF) 3' DNA starting at the translational stop codon (see also AAT51058). It was used with a 5' primer (AAT51061) to

ö Human; MMSC1 protein; MMAC1 interacting protein; tumour suppression; MMAC1 pathway; immunogen; cancer; cell neoplastic growth; PCR primer; ss. function) to a cell, which has lost the gene function due to a MMSC1 gene mutation. The gene suppresses neoplastic growth of the cell. Transgenic animals having an altered MMSC1 can be used as a model for identifying drug candidates useful in treating cancer. Gaps MMSC1, an MMAC1 (tumour suppressor) interacting protein and related amplify the CGF DNA clone deposited as ATCC 97142. The PCR proc was incorporated into plasmid pN346 to allow prodn. of CGF (see also AAW09111) in transfected COS cells. ö PCR primer PDZK5.5C used to amplify DNA encoding MMSC1 protein. Length 30; Indels Score 13.8; DB 18; Pred. No. 4.6e+02; ; Mismatches 2; Sequence 30 BP; 11 A; 7 C; 3 G; 9 T; 0 other; Example 5; Page 51; 107pp; English. BP. 69.0%; 88.2%; (MYRI-) MYRIAD GENETICS INC. 99WO-US00995. AAX86412 standard; DNA; 40 29-SEP-1999 (first entry) Query Match 69.0° Best Local Similarity 88.2 Matches 15; Conservative 4 aagcagctgccattatt 20 4 aaccagctgctattatt 20 Tavtigian SV; WPI; 1999-458472/38. polynucleotides Homo sapiens. WO9936566-A1. 19-JAN-1999; 20-JAN-1998; 22-JUL-1999. Bartel PL, Synthetic. AAX86412; œ AAX86412 88888δ g

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Telomerase; human; immune response; cancer; vaccine; treatment;
                                                                                                                                                                                                     Human clone 28-1 telomerase oligonucleotide oligo-13.
AAZ23630 standard; DNA; 30
                                                                                                                                                                    07-JAN-2000 (first entry)
                                                                                                                                                                                                                                                    disease; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GERO-) GERON CORP.
                                                                                                                                                                                                                                                                                                                           Key
modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Atkinson EM,
Vasserot AP;
                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-APR-1997;
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                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                         AAZ23630;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents an antisense oligonucleotide
directed against the human telomerase RNA component gene sequences.
The oligonucleotide can be used as an affinity agent in the methods of
the invention, which are used to purify human telomerase. The methods
involve the use of several sequential steps, including the use of two
matrixes that bind molecules bearing negative charges, a matrix that
binds molecules bearing positive charges, an affinity purification step
and a size separation. Telomerase is a particular target of anticancer
therapies, and is useful in assays for characterizing (pre)cancerous
cells. Telomerase can also be used to screen for specific modulators,
for biochemical analysis of its activity, and in preparation of
antibodies. Fragments of telomerase, or nucleic acid encoding them,
are used in vaccines, and for treating over expression of telomerase,
particularly in cancer.
                                             0
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.g.
                                                                                                                                                                                                                                                                                                       Human; telomerase RNA component; anticancer therapy; purification; assay; vaccine; cancer; antisense oligonucleotide; ss.
                                                                                                                                                                                                                                                                            Antisense oligonucleotide 13 for human telomerase RNA component.
                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purification of telomerase on affinity material - useful for, diagnosis and treatment of cancer
                Length 40;
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lichtsteiner SP, Pruzan RA;
              Score 13.8; DB 20;
Pred. No. 4.8e+02;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30 BP; 6 A; 6 C; 8 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/note= "biotinylated"
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 24; 76pp; English.
                                           ;
                                                                                                                                                                                   AAV63648 standard; DNA; 30 BP.
            69.0%;
88.2%;
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Weinrich SL;
                                                                                                                                                                                                                                                (first entry)
                                                                        4 aagcagctgccattatt 20
                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
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              Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                       Key
modified_base
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Vasserot AP,
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                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-APR-1997;
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                                                                                                                                                                                                                                             15-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-OCT-1998
                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                  AAV63648;
                                                                                                                                                                      AAV63648
                                                                                                                                                    RESULT
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Kealey JT;

Pruzan RA,

Lichtsteiner SP, Weinrich SL,

97US-0833377. 95US-0510736

/*tag= a
/note= "5'-biotinylated guanosine"

Location/Qualifiers

ВР

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                                                                                                                                                                              This invention describes a novel composition comprising human telomerase having at least 2000-fold (preferably at least 60000-fold) increased relative purity compared with crude extract of cells from adenovirus-transformed kidney cell line. The composition is useful for eliciting an immune response in animals and may therefore be used as a vaccine for treating diseases associated with the overexpression of telomerase e.g. cancer. AAZJ3626-Z3637 represent oligonucleotides used in the isolation of human clone 28-1 which contains a fragment of the human telomerase described in the method of the invention.
                                                   Compositions comprising human telomerase, useful for treating diseases associated with overexpression of telomerase e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13.6; DB 20;
Pred. No. 5.8e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 30 BP; 6 A; 6 C; 8 G; 10 T; 0 other;
                                                                                                                                  Disclosure; Column 45-46; 34pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.0%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
WPI; 1999-590379/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 16; Conserv
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ID AAF971
XX
AC AAF971
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Gaps

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Indels

Query Match 68.0%; Score 13.6; DB 19; Best Local Similarity 80.0%; Pred. No. 5.8e+02; Matches 16; Conservative 0; Mismatches 4;

Length 30;

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Polymorphic fragment of hypertension associated gene AGT.
                                                                                                                                                                                                                       10-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ86352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                  Fan JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a method of diagnosing a vascular disease in an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensics, parently testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of the human gene SNPS shown in the specification.
                                                                          Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
polymorphism; vascular disease; coronary artery disease; forensics;
myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McCarthy JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                      /standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Daley GQ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.0%; Score 13.2; DB 22;
83.3%; Pred. No. 8.9e+02;
ive 0; Mismatches 3;
                                              Human gene single nucleotide polymorphism #1899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ireland JS, Bolk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21 BP; 8 A; 4 C; 4 G; 5 T; 0 other;
                                                                                                                         pulmonary embolism; paternity test; ds
                                                                                                                                                                                                                                                                                                                                                                                                                            (WHED ) WHITEHEAD INST BIOMEDICAL RES. (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                        Location/Qualifiers replace(11,T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Examples; Page 177; 242pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                99US-0153357.
2000US-0220947.
2000US-0225724.
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              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA03899 standard; DNA; 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gargill M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-226749/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                     WO200118250-A2
                                                                                                                                                                                                                                                                                                                                                              10-SEP-1999;
26-JUL-2000;
16-AUG-2000;
                                                                                                                                                         Homo sapiens
              06-JUN-2001
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                                                                                                                                                                                                                                                                                                    15-MAR-2001
                                                                                                                                                                                        Key
Variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA03899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lander
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The invention provides polymorphic fragments of genes associated with hypertension. The nucleic acids including the polymorphic sites can be used as probes or primers for expressing variant proteins. Detection of the polymorphisms is useful in designing prophylactic and therapeutic regimes customized to underlying abnormalities. The polymorphisms can be used for association studies for hypertension, and in hypertension of diagnostic assays. Where the polymorphisms have a crusative role in hypertension, within a gene, they are likely to have a causative role in hypertension. This information can be used to find the precise role of a polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. The polymorphisms can be tested for association with other diseases e.g. agammaglobulinemia, diabetes insiplius, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Pabrys disease, familial hypercholesterolemia, polycystic kidney disease, hereditary sphercotytosis, von Willebrands disease, tuberous sclerosis, hereditary hemorthagica telangiectasia, familial colonic polyposis, Ehhers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus; Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome; Eabrys disease; familial hypercholesterolemia; hereditary spherocytosis; polycystic kidney disease; von Willebrands disease; forensic; human; tuberous sclerosis; hereditary hemorrhagica telangiectasia; familial colonic polyposis; osteogenesis imperfecta; porphyria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acute intermittent porphyria. The polymorphic forms can also be used in forensics to identify individuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids containing polymorphisms used in the diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 9.3e+02;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29 BP; 5 A; 4 C; 12 G; 7 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haluska MK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AFFY-) AFFYMETRIX INC. (UYCA-) UNIV CASE WESTERN RESERVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 19; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.0%;
ilarity 75.0%;
Conservative 1
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99US-0304232.
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AAQ86352 standard; DNA; 30
                                                                                                                                                                                                                        Ehlers-Danlos syndrome; ss
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Les 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-MAY-1998;
03-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypertension
                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAY-1999;
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WO200017342-A2
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                                                                                                                                            21-SEP-1998;
20-SEP-1999;
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                                                                                                 30-MAR-2000
                                                       Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA13302;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                           For preparing a protein S (PS) expression vector, partial cDNAs coding for human protein S were first isolated as described by Ploos van Amstel et al., FEBS Lett., 222:186-190 (1987) from a puCG human liver cDNA library. The cDNA sequence is given in Q86-38. The PS nt sequence is also listed in GenBank having the accession number Y00692. The MRA encodes a preprotein having 676 AAs. After posttranslation processing the corresp. translated mature PS consists of 635 AAs as given in R72350. The AA sequence is also listed in GenBank having the accession no. A26157. PS can be modified without significant loss of anticoagulant activity by introducing one or more mutations in the region between residues 425 and 432 to reduce significantly or eliminate the ability of PS to bind C4BP. A variant protein S is claimed having AA residues substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K429E, 1425A/1426A and K432E (AA residue nos. corresp. to R72350).
Oligos Q86349-Q86350 were used to produce mutations
in the first disulfide loop in the sex hormone binding globulin-like
                                                                                                                                                                                                                                                                                                              New recombinant protein S variants - having reduced C4b binding protein binding activity and anticoagulant activity for treating
                      Protein S; PS; vitamin K-dependent protein; mutagenic oligo; ss.
                                                                                     a
"nts for introducing desired AA substn."
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/note= "nts for introducing desired AA substn."
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Mutagenic oligo for human protein S variant I425A/I426A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13.2; DB 16;
Pred. No. 9.3e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 30 BP; 16 A; 4 C; 7 G; 3 T; 0 other;
                                                              Location/Qualifiers
13..14
                                                                                                                                                                                                                                                                                                                                                         Example; Column 18; 24pp; English.
                                                                                                                                                                                                                                                                   Griffin JH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                92US-0985691.
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Best Local Similarity 83.3%;
Matches 15; Conservative
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                                                                          misc_difference
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                                                                                                                                                                                                                      02-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain of PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUL-2000
                                                                                                                                                     US5405946-A
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                                                                                                                                                                                                                                                                   Bertina R,
                                                                                                                                                                                                                                                                                                                                     thrombosis
                                          Synthetic
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This sequence represents a PCR primer used in the construction of trans-splicing vectors to illustrate the invention. The present invention relates to the in vivo production of recombinant nucleic acid sequences. The method comprises expressing in a cell, two transcripts, one containing a first exon and first intron component, and a second transcript comprising a second intron component and a second exon. Transcript comprising a second intron component and a second exon. Transcript and transcript 2 are allowed to trans-splice, forming a product containing exon 1 and exon 2, but not the intron components. The invention makes use of the ability of intronic sequences derived from group I or group I introns to mediate specific cleavage and ligation of discontinuous nucleic acids, their products, or ribozymes in vivo. The method is preferably used for the preparation of exons are random. The method is preferably used for the assembly, or for the assembly of genes ordered at some exons but randomized at others. New genes can be selected rapidly and efficiently, and a very wide range of exons may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primer E5.Not1 used in the production of vectors for trans-splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                In vivo production of nucleic acid, useful e.g. for producing combinatorial gene libraries or ribozymes, by trans-splicing two RNAs containing exon and intron component .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Recombinant nucleic acid production; combinatorial gene library; ordered gene assembly; trans-splicing; tissue plasminogen activator; vector production; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant nucleic acid production; combinatorial gene library; ordered gene assembly; trans-splicing; tissue plasminogen activator; vector production; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Donahue W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Page 49; 186pp; English.
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nes 15; Conserv
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Synthetic.

WO20001342-A2.

WO20001342-A2.

YE 21-SEP-1999; 99W0-US21929.

YE 21-SEP-1999; 99US-010128.

YE 21-SEP-1996; POUR PROPERTY NEW GRADER MAP PROPERTY NEW GRADER MAP PROPERTY NEW GRADER MAP PROPERTY NEW GRADER MAP PROPERTY NEW GRADER SEPANDERTY NEW
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Ouery Match 66.0%; Score 13.2; DB 21; Length 48; Best Local Similarity 83.3%; Pred. No. 1e+03; Matches 15; Conservative 0; Mismatches 3; Indels COY 2 gtaagcagctgccattat 19

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Gaps

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Search completed: October 2, 2001, 16:18:39 Job time: 15483 sec

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        GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                  em_gss_pln1:*
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em_gss_rot5:*
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mRNAs using full-length enriched and 5'-end enriched CDNA libraries JOURNAL Unpublished (2001) COMMENT Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo	# 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano sorchruction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997). Location/Qualifiers source /cation/Qualifiers forganis="Homo sapiens" /clone="Hep14884"	UGIN Query Match Best Local Similarity 85.0%; Pred. No. Matches 17; Conservative 0; Mismatc 1 ggtaagcagctgccattatt 20	RESULT 2 AZ634745 41 bp DNA GSS 13-DEC-2000 LOCUS AZ634745 41 bp DNA GSS 13-DEC-2000 DEFINITION 1M0490012 R Mouse 10kb plasmid UUGCIM 11brary Mus musculus genomic closes Clone UUGCIM0490012 R, DNA sequence. ACCESSION AZ634745 AZ634745 GI:11756935 VERSION AZ634745 GI:11756935 ACCESSION AZ634745 GI:11756935	NISM NCE ORS	JOURNAL Unpublished (2000) COMMENT Contact: Robert B. Weiss Contact: Robert B. Weiss University of Utah Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606	EAX: 801 585 7177 Email: ddundgenetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0490 row: 0 column: 12 Seq primer: CACACAGGAACAGCATGACC Class: plasmid ends High quality sequence stop: 41. I. organism="Mus musculus" /strain="C57BL/6J" /db_xref="Laxon:10090" /clone="UUGCIM0490012" /strain="C57BL/6J" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
COM	FEA	ORI O M M Qy Oy	RES AZ6 LOC DEF ACC VER KEY	SO SEE O	COM	F
Description	AU103462 AU103462 AZ634745 IM0490012 AA76442 v 105903.r AL497072 T. brucei AL497072 T. brucei AA78928 T. brucei AA79828 AZ58005.s AZ79762 ZM0055C18 AZ311284 IM0026608 AA839551 of09h01.s T17561 mps v160 Th AA665608 nr16a12.s		AA914273 vy99a03.r AU105748 AU105748 D18234 MUSGS00613 AZ785014 2M028D03 BF036586 601460534 AU103473 AU103473 AZ481008 1M0302M15 AZ768476 1M0568D08 AZ768477 1M0518D08	A283466 2M012/200 A2329485 1M0053E17 A1076044 t197b11.x A0107071 A0107071 A0107431 A0107430 A0107431 A0107431 BG077090 H3010F02- D21048 HUMGS02033 A2425719 1M0205R21	ກທດ	EST 05-APR-2001 Consisted Homo sapiens CDNA clone Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. 1., Mizushima-Sugano,J., Sese,J., Hata A.T., Nakamura,Y., Morishita,S., Okubo ranscription start sites of human
SUMMARIES Query Score Match Length DB ID		8 59.0 50 10 10 10 10 10 10 10 10 10 10 10 10 10	6 58.0 49 13 6 58.0 50 10 6 57.0 31 24 6 57.0 34 24 6 57.0 50 10 7 56.0 20 24 7 56.0 20 24 7 56.0 33 25 24 7 60 33 25 25	25 56 56 56 56 56 56 56 56 56 56 56 56 56	55.0 40 24 55.0 41 25 55.0 46 19	AU103462 50 bp mRNA AU103462 Sugano Homo sapiens of HEP14884, mRNA sequence. AU103462 I GI:13552983 EST. human. Homo sapiens Eukaryota; Metazoa; Chordata; Mammalia; Eutherla; Primates; I (bases I to 50) Suzuki, Y., Tsunoda, T., Taira, I, H., Otta, T., Isogal, T., Taira, I, H., Otta, T., Isogal, T., Taira, I, H., Otta, T., Isogal, T., Taira, I, K., Suyama, A. and Sugano, S. Fine Structural analysis of the
Result No.	00000000000000000000000000000000000000	0 113 113 114 115 115 115 115 115 115 115 115 115	2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3		0 4 4 4 4 10	RESULT 1 AU103462/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

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(bases 1 to 28)
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Matches 14; Conservative
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Best Local Similarity
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                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 [gb]ARL29072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli xL10.Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 45)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schallenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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VIOSQA3.rI Knowles Solter mouse blastcoyst B3 Mus musculus cDNA clone IMAGE:1110964 5' similar to 9b:M76124 Mus musculus EGP314 precursor mRNA, complete cds (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Knowles Solter mouse blastocyst B3"
/tissue_rype="blastocyst"
/dev_stage="embryo (pre-implantation)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.0%; Score 13.2; DB 247; Length 41; 83.3%; Pred. No. 1.7e+04; ive 0; Mismatches 3; Indels 0;
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Frace considered overall poor quality
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/strain="B6D2 Fl/J"
/db_xref="taxon:10090"
/clone="IMAGE:1110964"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 1. Location/Qualifiers
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Matches 15; Conserve
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Constructed at the Institute for Genomic Research (71GR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (71GP27/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
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Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G. Direct Submission Submitted (10-DEC 2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CBI0 ISA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                          Gaps
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AL497072.1 GI:11872664
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Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Pred. No. 5.1e+04;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                        Length 45;
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                                                                                                                                                                                                                                                                                     Score 12.4; DB 12;
Pred. No. 4.4e+04;
0; Mismatches 1;
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/clone="355f03"
5 c 4 g
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92.9%;
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82.4%;
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 31)
Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
'M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ798762 31 bp DNA GSS 16-FEB-2001
2M0055C18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0055C18 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 40;
                                                                                                                                       Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1216 Std Error: 0.00
Seg primer: 40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
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Pred. No. 5.5e+04;
0; Mismatches 3;
                                                                                                                                                                                                                                                                               1. .40
/organism="homo sapiens"
/db_xref="taxon:9606"
/clone="1391624"
/clone_lib="Soares_testis_NHT"
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Insert Length: 10000 Std Error: 0.00
Plate: 0055 row: C column: 18
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Seq primer: CACACAGGAAACAGCTATGACC
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
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AZ798762.1 GI:12949191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.0%;
82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
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Best Local Similarity 82.4
Matches 14; Conservative
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.
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                                                                                                                                                                                                                           Trypanosoma.

1 (bases 1 to 30)
Hall, N., Bowman, S.,
Hall, N., Bowman, S.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 LSA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                Constructed at the Institute for Genomic Research (TIGR),
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRED27/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects.
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 40)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
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                            13-DEC-2000
TA272C09Q 30 bp DNA GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 272c09, reverse sequence,
genomic survey sequence.
                                                                                                                                                                                                               Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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/clone="272c09"
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                                                                                                                  AL487818.1 GI:11852489
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AA789284.1 GI:2849404
                                                                                                                                                               Trypanosoma brucei,
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Matches 14; Conserv
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/db_xref="taxon:10090"
/clone="UUGCIM0026G08"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                    (http://www.lax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (qi|4732114 qiplaF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
T=1: 801 585 506
Fax: 801 585 7177
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AZ311284
AZ311284.1 GI:10354094
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Dunn, D., Aoyat, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv: Purified genomic DNA from M.
musculus C57BL/G3 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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0
                                                                                                                                   /db_xref="taxon:10090"
/clone="UUGC2M0055C18"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 11.8; DB 249; Length 31;
Pred. No. 8.4e+04;
0; Mismatches 2; Indels 0;
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Insert Length: 10000 Std Error: 0.00
Plate: 0026 row: G column: 08
                     High quality sequence stop: 31.
Location/Qualifiers
                                                                                                               /strain="C57BL/6J
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86.7%;
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Best Local Similarity 86.7
Matches 13; Conservative
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1 (Dases 1 to 41)

S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
/Jab.host-E. Coli strain XL10-Gold, T1-resistant, F-"
// hote="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/G1 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 8.5e+04;
); Mismatches 2; Indels 0;
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86.7%;
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Best Local Similarity 86.7
Matches 13; Conservative
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sequences that lack an initiation codon; expression of lacz is only provided by in frame fusion to yeast coding sequence. The yeast genomic DNA carrying the transposon was excised from piez6 and transplaced back onto the yeast chromosome. Yeast colonies expressing lacz were screened for in a color assay. A plasmid containing the genomic DNA/lacz fusion junction was recovered from each individual yeast colony that expressed lacz activity. These recovered plasmids comprise 'The blue guys library'. The fusion junction was then sequenced to identify the expressed ORF upstream of the fusion. " a 13 c 8 g 10 t
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/organism="Homo sapiens"
/db_xref="texton:9606"
/clone="InhaGE:1166126"
/clone=lib="NCI_CGAP_EW1"
/tissue_type="Ewing's sarcoma"
/lab_host="DH108"
/note="Vector: pAMP10; mRNA made from Ewing's sarcoma,
cDNA made by oligo-dT priming. Non-directionally cloned.
Size-selected on agarose gel, average insert size 600 bp.
Reference: Krizman et al. (1996) Cancer Research
56:3380-5383."
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP chone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA662608 50 bp mRNA EST 12-NOV-1997 nr16a12.s1 NCI_CGAP_Ew1 Homo sapiens CDNA clone IMAGE:1168126 similar to SW:RL24_HUMAN P38663 60S RIBOSOMAL PROTEIN L24. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.
Ph.D.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 9.1e+04;
0; Mismatches 2; Indels (
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www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
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AA662608.1 GI:2615457
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Best Local Similarity 86.7%;
Matches 13; Conservative C
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Best Local Similarity 86.7
Matches 13; Conservative
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                                                                                                                                                                                                                                                                            /ssue_type="colon tumor"
/issue_type="colon tumor"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: colon; Vector: Bluescript SK-; Site_1: EcoRI
; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Pooled colon tumors. 5' adaptor sequence: 5'
CTCGAGTITTTTTTTTTTTTT 3' Average insert size: 1.2 kb."

6 c 11 g 14 t
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Saccharomyces cerevisiae
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 45)
Burns, N., Grimwade, B., Ross-Macdonald, P.B., Choi, E.-Y., Finberg, K., Roeder, G.S. and Snyder, M.
Large-scale analysis of gene expression, protein localization and gene disruption in Saccharomyces cerevisiae
Genes Dev. 8, 1087-1105 (1994)
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//db_xref="taxon:4932"
//clone_lib="The blue guys library"
/lab_host="E.coli"
//note="Vector: pRECMID: A yeast genomic DNA library was prepared in the vector pHSS6, and subjected to transposon mutagenesis with mIn3. This mini-transposon carries lac2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pattern:
50 cytoplasmic spots; Disruption phenotype: inviable, unbudded
51 cytoplasmic spots; Disruption phenotype: inviable, unbudded
52 cytoplasmic codon12 of ORF next to BRF1. Sequence below near
or adjacent to lac2.
56 primer: Lac2 sequences in transposon.
Location/Qualifiers
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     Trace considered overall poor quality Insert Length: 660 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1.
                                                                                                                                1 .41
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1420657"
/clone=lib="NCI_CGAP_CO12"
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Department of Biology
Yale University
New Haven CT 06520-8103
Tel: 2034326139
Fax: 2034326161
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T17561.1 GI:458583
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Best Local Similarity 86.7
Matches 13; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                            Ontact: Yutaka Suzuki
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukitelia.u-tokyo.ac.jp waruyama,K., Suyama,A. and Sugano
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
'S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mamanila; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogal,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Contact: Yutaka Suzuki
Department of Virology
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AU103485 GI:13553006
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Pred. No. 9.1e+04;
); Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADKA01276"
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AU102666.1 GI:13552187
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86.7%;
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Best Local Similarity 86.7
Matches 13; Conservative
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3 taagcagctgccatt 17
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Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ilms.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched as 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata: Euteleostomi;
Eukaryota: Metazoa: Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 50)
Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries (Dnublished (2001)
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ims.u-tokyo.ac.jb
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).
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COLF4166, mRNA sequence.
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

Mammalla; Euto60,

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1. (bases 1 to 50,

1. Taunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata

1. Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo

1. K., Suyama,A. and Sugano,S.

Fine Structural analysis of transcription start sites of human

MRNAs using full-length enriched and 5'-end enriched cDNA libraries

To published (2001)

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

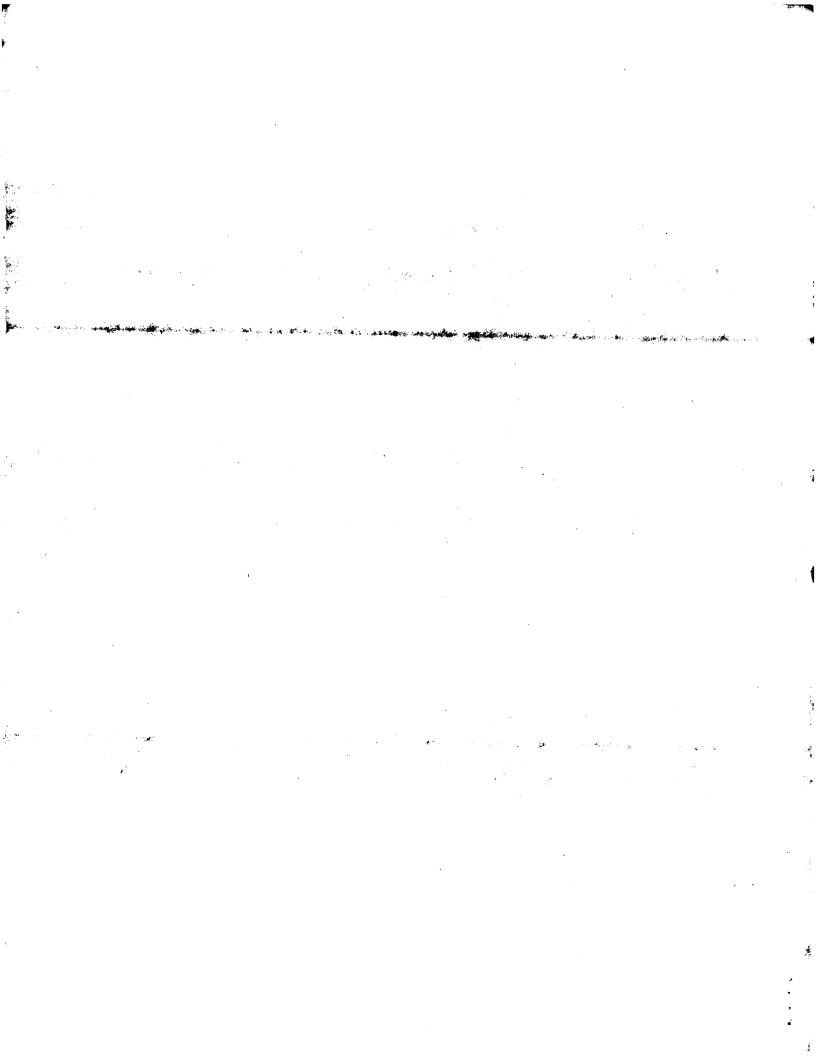
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano

5. Construction and characterization of a full length-enriched and

a S'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Homo sapiens
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Search completed: October 2, 2001, 15:00:56 Job time: 10825 sec

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Sequence:

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130544 Sequence 7
175320 Sequence 69
AR091705 Sequence
AR075823 Sequence
E30456 Method for
A3480 ARV probe.
AR067320 Sequence
AR067320 Sequence
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Perfect score:
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03-APR-1998

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Unclassified.

Unclassified.

(bases 1 to 29)

Brown, S. Marie, Dean, D.Allen, Fromm, M.Ernest and Sanders, P.Rigden.
Synthetic DNA sequences having enhanced expression in
monocotyledonous plants and method for preparation thereof
Patent: US 5689052-A 69 18-NOV-1997;

Location/Qualifiers
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Unclassified.
(I chases 1 to 48)
Nadeau, J.G., Pitner, J.Bruce, Linn, C.Preston and Schram, J.L.
Detection of nucleic acids by fluorescence quenching
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Ting,J.Pan-Yung and Chin,K.
Forms of class II MHC transactivator (CIITA)
Patent: US 5994505-A 15 30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                  Score 12.8; DB 10;
Pred. No. 1.4e+04;
); Mismatches 2;
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Hoke,G.D., Bradley,M.O., Williams,T.J. and Lee,C.
Antisense oligonucleotides directed against human ICAM-I RNA
Patent: US 5580969-A 7 03-DEC-1996;
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Pred. No. 6.4e+03;
); Mismatches 1;
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130544
130544.1 GI:1821335
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AR089975
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AR033826
AR042486
AR042988
AR058366
AR088192
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AR108361
116318
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AR013900
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AR058394
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Renard, A. and Thiry, M. Recombinant polypeptides of the haemorrhagical septicemia virus in
                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 22)
Evans,63. and Smith,M.W.
Method for generation of sequence sampled maps of complex genomes Patent: US 5851760-A 668 22-DEC-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Durkly, L.C., Chisholm, P.L., Thomas, D.W., Rosa, M.D. and Rosa, J.J. anti-CD4 antibody homologs useful in prophylaxis and treatment of AIDS, ARC and HIV infection
Patent: US 5871732-A 36 16-FEB-1999;
Location/Qualifiers
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Pred. No. 2.6e+04;
0; Mismatches 1; Indels
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/organism="synthetic construct"
/db_xref="taxon:32630"
a 4 c 7 g 2 t
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Sequence 668 from patent US 5851760.
AR067320
                                          Fatent: EP 0377349-A 20 11-JUL-1990;
EUROGENTEC S.A
Location/Qualifiers
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12 c 14 a
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AR035220
AR035220.1 GI:5951888
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92.9%;
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Best Local Similarity 92.9
Matches 13; Conservative
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14 CCCAGGTCAGTCTT 1
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AR035220/c
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Solution DICKINSON & CO
OS Unidentified
PN JP 1999056380-A/6
PD 02-MAR-1999
PF 29-MAY-1999 UP 1998166141
PR 30-MAY-1999 US 08/865.675
PI JAMES G NADEAU, J BLUCE PITONA, C PRESTON RIN, JAMES L SHURAMU PC CINIS/09, C1201/68, G01N33/566, C12N15/00 CC Strandedness: Single, FH Key
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Method for detecting target nucleic acid sequence and
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Pred. No. 1.4e+04;
0; Mismatches 2; Indels (
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Pred. No. 1.4e+04;
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/organism="unidentified"
/db_xref="taxon:32644"
a 8 c 10 g 15
Patent: US 5958700-A 6 28-SEP-1999;
Location/Qualifiers
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                                           /organism="unknown"
a 8 c 10 g
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JP 1999056380-A/6.
unidentified.
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Best Local Similarity 87.5%;
Matches 14; Conservative (
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Best Local Similarity 87.5%;
Matches 14; Conservative
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synthetic construct
artificial sequence.
1 (bases 1 to 18)
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ACCESSION VERSION KEYWORDS SOURCE

RESULT E30456/c

ò 셤 AUTHORS TITLE JOURNAL

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BASE COUNT

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RESULT (A34802/c LOCUS

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PROTEINS PREVENTING INTERACTION BETWEEN A FRAGMENT FC OF AN IMMUNOSLOBBLIN AND ITS RECEIVER, AND THERAPEGTIC USE, PARTICULARILY IN TREATING AFFECTIONS LINKED TO THE HIV VIRUS PATENT: WO 9108301-A 6 13-JUN-1991; Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Universitied.

I (bases I to 41)
I (bases I to 41)
Instrup.O., Tullin,S.slashed.ren, Poulsen,L.Kongsbak and Bj.o slashed.rn,S.Petersen.
Method of detecting biologically active substances by using green fluorescent protein
Patent: US 5958713-A 8 28-SEP-1999;
Location/Qualifiers
       12-JUN-1995
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Pred. No. 5.7e+04;
0; Mismatches 2; Indels
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100.0%; Pred. No. 4.3e+04;
ive 0; Mismatches 0;
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/db_xref="taxon:32630"
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Sequence 8 from patent US 5958713.
AR075947
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Oligonucleotide xol23.
                                                                         synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 39)
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86.7%;
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Matches 12; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
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1 (bases 1 to 44)

Burkly,L.C., Chisholm,P.L., Thomas,D.W., Rosa,M.D. and Rosa,J.J.

Burkly,A.C., Chisholm,P.L., Thomas,D.W., Rosa,M.D. and today the state of Albs, ARC and HIV infection
Patent: US 5871732-A 59 16-PEB-1999;
                                                Gaps
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Unclassified.
Unclassified.
I (bases I to 20)
Eriksson, U., Olofsson, B., Alitalo, K. and Pajusola, K. Vascular endothelial growth factor-B Patent: US 5840693-A 53 24-NOV-1998;
Location/Qualifiers
                  Score 12.2; DB 9; Length 44;
Pred. No. 3.2e+04;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 12.2; DB 9; Length 44;
Pred. No. 3.2e+04;
0; Mismatches 3; Indels
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Sequence 59 from patent US 5871732.
AR035241
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Sequence 53 from patent
AR060552
AR060552.1 GI:5987002
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Best Local Similarity 82.4%;
Matches 14; Conservative
                Query Match 61.0%;
Best Local Similarity 82.4%;
Matches 14; Conservative
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hes 12; Conservative
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CE 1 (bases 1 to 26)
RS Gallatin,W.Michael and Vazeux,R.
S Method to identify compounds which modulate ICAM-related protein interactions
INAL Patent: US 5773218-A 87 30-UUN-1998;
Location/Qualifiers
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1 (bases 1 to 23)
Edelman,L., Margaritte,C., Kaczorek,M. and Chaabihi,H.
MONOCLONAL RECOMBINANT ANTI-RHEGUS D (D7C2) ANTIBODY
PATENT: WO 9507740-A 11 14-MAR-1996;
PASTEUR INSTITUT (FR)
Other publication FR 2724182 960308.
                                                                                                                                                                                                 58.0%; Score 11.6; DB 9; Length 23; 77.8%; Pred. No. 7.8e+04; tive 0; Mismatches 4; Indels
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/organism="unidentified"
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Sequence 87 from patent US 5773218.
AR013888 1 GI:3971342
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Sequence 34 from Patent WO9915696.
A97534 GI:6780880
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1 (bases 1 to 26)
Qin,Y.
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Listing first 45 summaries
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Perfect score:
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est48 est498 est50 est51 est51 est50 est50 est50		\$167: \$168: \$170: \$171: \$171: \$171: \$171: \$173: \$174: \$174: \$173: \$174: \$174: \$175: \$176:
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90. gb_es 91. gb_es 92. gb_ht 93. em_gs 94. em_gs 95. em_gs 96. em_gs 97. em_gs 97. em_gs 97. em_gs 97. em_gs 97. em_gs	em_gss_1 em_gss_0 em_gss_0 em_gss_p em_gss_r	226. 99 years 228. 99 years 22	42: 9b gss2 45: 9b gss2 45: 9b gss2 46: 9b gss2 46: 9b gss2 46: 9b gss3 49: 9b gss3 50: 9b gss3 50: em gss 55: em gss 55: em gss 56: 9b gss3 56: 9b gss3 56: 9b gss3 56: 9b gss3 56: 9b gss3

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Unpublished (2000) COMMENT Contact: Robert B. Weiss University of Utah Genome Center	penetical Polymers Research Bldg., 20 S. 2030 E., SLC, 2006. 1777 9enetics.utah.edu 1777 9enetics.utah.edu 1777 10000 Std Error: 0.00 1777 1767AAAAGGACGGCAGT 18 ends 18 ends	cccaggtgagtcttag 20	RESULT 2 AZ666528 LOCUS AZ66528.1 GI:11803674 KEYWORDS SOURCE LOCUS LOCUS LOCUS REYMORDS SOURCE LOCUS
\$ Query The Match Length DB ID SUMMARIES A property to the match Length DB ID B property to the match Length DB ID	2.8 64.0 25 245 AZ506197 AZ506197 IM0347C11 2.6 63.0 37 247 AZ666528 AZ506197 AZ506197 IM0347C11 2.6 63.0 37 241 AZ503920 IM0003F118 1.6 58.0 50 50 10 1000613 1.6 58.0 41 250 AZ822374 AZ0105613 1.7 56.0 34 249 AZ79299 AZ77468 AZ00000017 1.2 56.0 34 249 AZ79299 AZ77468 AZ00000017 1.2 56.0 34 249 AZ79299 AZ77468 AZ700000017 1.2 56.0 34 249 AZ79299 AZ7000000000000000000000000000000000000	ALIGNMENTS	AZ506197 25 bp DNA GSS 05-OCT-2000 1M0347C11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0347C11 F, DNA sequence. AZ506197 AZ506197. GSS. AZ506197. GSS. Mus mouse. Mus musculus Bukaaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaaryota; Mazmalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (Dases 1 to 25) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacres,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly and Wright,D.,Weiss,R., Stokes,R., Tingey,A., von Niederhausern,A.
Result No. Scor	0 00 00 00 00 00 00 00 00 00 00 00 00 0	}	RESULT 1 AZ506197 LOCUS DEFINITION ACCESSION VERSION VERSION VERSION CORGANISM REPERENCE AUTHORS

4

JOURNAL

COMMENT

TITLE

FEATURES

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gil4732114) ipiAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Lee,C..C., Yazdan1,A., Wehnert,M., Bailey,J., Couch,L., Xiong,M.,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
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                                                       Mouse whole genome scaffolding with paired end reads from 10kb
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HUMXP1F11B Human placenta Homo sapiens cDNA clone XP6G6B, mRNA
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/db_xref="taxon:10090"
/clone="Un0003E19"
/clone_lib="Mouse lOkb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0003 row: F column: 19
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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                                                                                plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                           and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
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Matches 13; Conserv
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Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 32)
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                     Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0548 row: A column: 18
Seq primer: CACACAGGAAACAGCTATGACC
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/strain="C57BL/6J"
                                                                                                                                     University of Utah Genome Center
University of Utah
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High quality sequence stop: 37.
Location/Qualifiers
                                                    plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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and Wright, D., Weiss, R.
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Gaps

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Query Match

Matches

BASE COUNT ORIGIN

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ACCESSION VERSION KEYWORDS ORGANISM

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RESULT

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source

FEATURES

COMMENT

JOURNAL MEDLINE

TITLE

BASE COUNT

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(http://www.jax.org/nscources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel. electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114[gblAR129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coli XLLO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 46)

10 (bases 1 to 46)

11 (bases 1 to 46)

12 (bases 1 to 46)

13 (bases 1 to 46)

14 (bases 1 to 46)

15 (bases 1 to 46)

16 (bases 1 to 46)

17 (bases 1 to 46)

18 (bases 1 to 46)
                                                                                                                                                 AZ826374 46 bp DNA GSS 20-FEB-2001
2M0102K06F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0102K06 F, DNA sequence.
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Fax: 801 585 7177
Email: ddunnégenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0102 row: K column: 06
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 46.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 50)
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata
Suzuki,Y., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo
,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human
mRNAs using full-length enriched and 5'-end enriched cDNA libraries
Contact: Yutaka Suzuki
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
5-20 Suzukiélins.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library, Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
Coolbaugh, M.I., Chinault, C.A., Baldini, A., Lindsay, E.A., Zhao, Z.-Y. and Caskey, C.T.H.
Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries
arrayed cDNAs and cosmid libraries
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AU105613 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP22150, mRNA sequence.
AU105613
AU105613.1 GI:13555134
                                                                                                                                                                                                                          1. 27
/organism="Homo sapiens"
/db_xref="taxon:9606"
//db_xref="taxon:9606"
//doc="xq27.3-q28"
/clone="xp6068"
/clone=lib="Human placenta"
/note="Arrayed cDNAs and cosmid libraries from human placental tissue"
a 4 c
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/db_xref="taxon:9606"
/clone="HEP22150"
/clone_lib="Sugano Homo sapiens cDNA library"
/ c 22 9 15 t
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Pred. No. 6.5e+04;
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Pred. No. 4.8e+04;
0; Mismatches 5;
                                                                                                                                                                                                                          Contact: Caskey, C.T.H.
Location/Qualifiers
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75.0%;
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Matches 13; Conserv
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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RESULT SAU105613

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pw042 (gil4732114) gblAR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10.Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 33)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
.M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Welss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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2M0056M03R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0056M03 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="UGCC2M003017"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 11.2; DB 249; Length 31;
Pred. No. 1.3e+05;
0; Mismatches 3; Indels 0;
                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0003 row: O column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource
                                                                                                                                     Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.

    .31
    /organism="Mus musculus"

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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
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81.2%;
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Best Local Similarity 81.2
Matches 13; Conservative
Tel: 801 585 5606
Fax: 801 585 7177
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Win 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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clone UUGC2M0003017 R, DNA séquence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 47)
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                                                                                                                                        D38689 47 bp mRNA EST 31-MAY-1995 HUMCI264 Human chromosome 8 Homo sapiens cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                 Koyama, K., Sudo, K. and Nakamura, Y.
Isolation of 115 human chromosome 8-specific expressed-sequence tags by exon amplification
Genomics 26, 245-253 (1995)
95324915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Tokyo
4-6-1, Shirokanedal, Minato-ku, Tokyo 108, Japan
Tel: 81-3-5449-5372
Fax: 81-3-5449-5433
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/db_xref="taxon:9606"
/map="8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: yusuke@ims.u-tokyo.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yusuke Nakamura
Institute of Medical Science
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77.8%;
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Best Local Similarity 77.8
Matches 14; Conservative
21 AGTTATCAGGTGTGTCTT
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BASE COUNT ORIGIN

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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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Gaps

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 (pblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Bunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb
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/note="Vector: PWD42Nv; Purifled genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/db_xref="taxon:10090"
/clone="uloxon:10059C44"
/clone=lib="Mouse llokb plasmid UUGC1M library"
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                                                                                                                                    Std Error: 0.00
                                                                                                                                                        Plate: 0559 row: C column: 04
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                 High quality sequence stop: 34.
                                  7.11.5 0.25
Fax: 801 585 5606
Eax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 5td Errc
Plate: 0559 row: C column: 04
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Rm. 308, Bi
84112, USA
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/note="Vector: PWADADY; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114gb AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 34)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Menen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Walss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
/db_xreff="taxon:10090"
/clone_Tibe="Mouse 10kb plasmid UUGCIM library"
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              Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0056 row: M column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 33.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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81.2%;
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Matches 13; Conservative
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polywuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qi|4732114|qib|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the innert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-complement. E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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1 (bases 1 to 48)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Hall, N., Bowman, S., Lennard, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                         \rm Rm.~308,~Biomedical~Polymers~Research~Bldg.,~20~S.~2030~E.,~SLC,~84112,~USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="mouse_l0kb plasmid UUGClM library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 11.2; DB 249; Length 43; Pred. No. 1.3e+05; 0; Mismatches 3; Indels 0
                                                                                                             Tel: 801 585 5606
Fax: 801 585 7177
Email: ddundgenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0069 row: O column: 06
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University of Utah Genome Center University of Utah
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/db_xref="taxon:10090"
/clone="UUGC2M0069006"
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81.2%;
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Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/G4 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (qil4732114|qb]APL29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZBO6794 43 bp DNA GSS 20-FEB-2001
2M0069006F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0069006 F, DNA sequence.
                        Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  /db.xref="taxon:10090"
/clone="UUGCIM0302M10"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Pred. No. 1.3e+05;
0; Mismatches 3; Indels 0;
                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0302 row: M column: 10
Seq primer: cGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                          High quality sequence stop: 43. Location/Qualifiers
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Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ806794.1 GI:12970500
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81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male"
University of Utah
                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 81.2
nes 13; Conservative
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Best Local 8
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BASE COUNT ORIGIN

Matches

ð g LOCUS

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

AZ806794/c

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Gaps

COMMENT

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FEATURES

BASE COUNT

Matches

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1 (bases 1 to 34)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kutaba, T., Leh.M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohling, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7 ear: 314 286 1800
Fax: 314 286 1810
Fax: 316 286 1810
Fax
                                                                                                                                                                                                                                                  yo38c05.rl Soares adult brain N2b4HB55Y Homo sapiens cDNA clone
IMAGE:180200 5' similar to gb:M92302 DIHYDROPRYRIDINE-SENSITIVE
L-TYPE, BRAIN CALCIUM CHANNEL (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 11; DB 188; Length 34; Pred. No. 1.7e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="GDB:3826844"
/db_xref="taxon:9606"
/db_xref="IMAGE:180200"
/clone=lib="Soares adult brain N2b4HB55Y"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 1.
Location/Qualifiers
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R84653.1 GI:943059
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   gtacccaggtgagtct 17
                                    11 GTACCGCGCTGAGTCT
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Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: ysuzukielms.u-tokyo.ac.jp
Suzuki.Y: Yoshitomo-Nakagawa,K., Maruyama.K., Suyama,A. and Sugano
'S. Construction and characterization of a full length-enriched and
a S'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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                          Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma bruce; (TREU927/4 GUTAT 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                          Email: nelsayed@tigr.org Details of {\tt T}. brucel sequencing at the Sanger Centre are available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AU106341 50 bp mRNA EST 05-APR-2001
AU106341 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone
COL03664, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.4e+05;
0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 48;
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                                                                                                                                                                                                                                                                                                                                                                           at http://www.sanger.ac.uk/Projects/T_brucei/
Location/Qualifiers
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Pred. No. 1.4e+05;
0; Mismatches 3; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="117f12"
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/db_xref="taxon:9606"
/clone="COL03684"
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81.2%;
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81.2%;
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nh1@sanger.ac.uk
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RESULT 14 AU106341

DEFINITION

ACCESSION

VERSION KEYWORDS

ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

BASE COUNT ORIGIN

FEATURES

6; Indels Matches 14; Conservative 0; Mismatches

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0; Gaps

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Search completed: October 2, 2001, 15:00:58 Job time: 10827 sec

Run on:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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gb_sts3:*
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gb_vi2:*
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Match Length
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Database

153690 Sequence 14 AX095079 Sequence 127043 Sequence 64 AR021414 Sequence AR42976 Sequence 143923 Sequence 12 I62967 Sequence 62

AR046638 Sequence

Description

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 21)
Lander; E.S., Gargill, M., Ireland, J.S., Bolk, S., Daley, G.Q. and
Mccarthy, J.J.
Single nucleotide polymorphisms in genes
Patent: WO 0118250-A 257 15-WAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
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1 (bases 1 to 17)

Stinchcomb.D.T., Draper,K., McSwiggen,J. and Jarvis,T.
C-myb targeted ribozymes
Patent: US 5646642-A 1431 08-JUL-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                               Length 17;
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Pred. No. 9.4e+03;
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  17 bp DNA Sequence 1431 from patent US 5646042.
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Sequence 64 from patent US 5563036.
I27043.
I27043.1 GI:18170-2
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Sequence 257 from Patent W00118250.
AX095079.1 GI:13511282
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/db_xref="taxon:9606"
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Location/Qualifiers
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88.2%;
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Matches 15; Conservative
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AS1561 Sequence 18
AS1561 Sequence 21
ARD4147 Sequence 11
A91147 Sequence 20
12555 Sequence 20
12560 Sequence 20
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ARG4721 Sequence 20
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AR050319 Sequence
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1 (Joses I to 17)
Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
C-myb ribozymes having 2'-5'-linked adenylate residues
Patent: US 5817796-A 1431 06-OCT-1998;
Location/Qualifiers
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Pred. No. 9.4e+03;
0; Mismatches 2; Indels
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AR046638.1 GI:5968103
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KEYWORDS

Unknown.

AR046638

LOCUS

RESULT 1 AR046638/c DEFINITION

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Unknown.
Unclassified.
Unclassified.
I (bases 1 to 42)
Lonberg, N. and Kay, R.M.
Transgenic non-human animals capable of producing heterologous antibodies
Patent: US 5633425-A 12 27-MAY-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unclassified.

1 (bases 1 to 42)
Lonbergy, N. and Kay, R.M.
Transgenic non-human animals capable of producing heterologous antibodies of various isotypes
Patent: US 5661016-A 64 26-AUG-1997;
Location/Qualifiers
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Sequence 64 from patent US 5661016.
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Best Local Similarity 80.0
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Unclassified.
I (bases I to 42)
Lonberg, N. and Ray, R.M.
Transgenic non-human animals for producing heterologous antibodies
Patent: US 5789650-A 64 04-AUG-1998;
Location/Qualifiers
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1 (bases 1 to 42)

Lonberg,N. and Kay,R.M.

Transgenic non-human animals for producing heterologous antibodies

Patent: US 5814318-A 64 29-SEP-1998;

Location/Qualifiers
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        1 (bases 1 to 30)
Peterson, M.G., Baichwal, V.R. and Strulovici, B. Transcription factor-DNA binding assay
Patent: US 5563036-A 64 08-OCT-1996;
Location/Qualifiers
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Sequence 64 from patent US 5814318.
AR042976.1 GI:5963984
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Sequence 64 from patent US 5789650.
AR021414
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Best Local Similarity 80.0
Matches 16; Conservative
                                                                                                                                             Query Match 69.0
Best Local Similarity 88.2
Matches 15; Conservative
Unclassified
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Unclassified.
1 (bases 1 to 30)
Foulkes, J. Gordon, Liechtfried, F.E., Pieler, C., Stephenson, J.R. and
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Foulkes,J.Gordon, Liechtfried,F.E., Pieler,C., Stephenson,J.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methods of determining chemicals that modulate transcriptionally expression of genes associated with cardiovascular disease Patent: US 5580722-A 17 03-DEC-1996;
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Pred. No. 2e+04;
0; Mismatches 3;
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Pred. No. 2e+04;
0; Mismatches 3;
   Pred. No. 1.2e+04;
                                                                                                                                                                                                                                                                                                                          associated with cardiovascular disease
Patent: US 5846720-A 17 08-DEC-1998;
Location/Qualifiers
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Sequence 17 from patent US 5846720.
AR063732 1 GI:5993040
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83.3%;
   Best Local Similarity 80.0%;
Matches 16; Conservative
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83.3%;
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Best Local Similarity 83.3
Matches 15; Conservative
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L06994.1 GI:184940
V-region; antigen binding region; complementarity determining
region; immunoglobulin heavy chain; mu-immunoglobulin; processed
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chihara,Y., Matsuoka,H. and Kurosawa,Y.
rganization of human immunoglobulin heavy chain diversity gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 45)
Raaphorst, F.M., Sanz, I., Vossen, J.M., Schuurman, R.K.B. and van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin heavy chain CDR3 regions in human fetal organs: Evidence for selection of rearrangements on the basis of CDR3
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                                                                                                                                 Melanoma and prostate cancer specific antibodies for immunodetection and immunotherapy Patent: 18 5719032-A 64 17-FEB-1998; Location/Qualifiers
                                                                                                                                                                                                                                                                                  Length 42;
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Homo sapiens
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Pred. No. 1.2e+04;
0; Mismatches 4;
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Sequence 64 from patent US 5719032.
188720
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                                                                                                                                                                                                       /organism="unknown"
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Location/Qualifiers
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/gene="IGHM"
/note="G00-120-086"
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Best Local Similarity 80.0%;
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/gene="IGHM"
                                GI:3408660
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1 (bases 1 to 42)
Vielkind,J.R.
                                188720.1
                                                           Unknown.
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Search completed: October 2, 2001, 15:56:47 Job time: 14171 sec
 A51561.1 GI:2304389
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NCE I (bases 1 to 21)

ORS Audonnet J.F., Bublot,M.J., Darteil,R.J., Duinat,C.V., Laplace,E.L.

LE Live recombinant avian vaccine based on an avianherpes virus,

and Riviere,M.A.

LE Live recombinant avian vaccine based on an avianherpes virus,

against Gumboro disease

FRNAL Patent: EP 0728842-A.18 28-AUG-1996;

RNAL Patent: EP 0728842-A.18 28-AUG-1996;

ENT Other publication FR 2728794 960705

Other publication AU 4063095 960711.

Other publication AU 4063095 960711.
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"In (bass 1 to 23)

RS Fowlkes, D.M., Broach, J., Manfredi, J., Klein, C., Murphy, A.J.,
Paul, J. and Trucheart, J.
"Yeast cells engineered to produce pheromone system protein
surrogates, and uses therefor
surrogates, and uses therefor
NAL Patent: US 578184-A 59 04-AUG-1998;
ES Location/Qualifiers
              05-DEC-1998
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Pred. No. 3.3e+04;
0; Mismatches 2;
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           AR020665 23 bp DNA
Sequence 59 from patent US 5789184.
AR020665.1 GI:3975280
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Sequence 18 from Patent EP0728842.
A51533 GI:2304354
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Sequence 21 from Patent EP0719864.
A51561
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87.5%;
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Best Local Similarity 87.5
Matches 14; Conservative
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1 (bases 1 to 21)
Audonnet,J.F., Bublot,M.J., Darteil,R.J., Duinat,C.V., Laplace,E.L. and Riviere,M.A.
Recombinant live avian vaccin, using an avian herpes virus as
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Pred. No. 3.3e+04;
0; Mismatches 2;
                                                                                          Patent: EP 0719864-A 21 03-JUL-1996; RHONE MERIEUX (FR)
Other publication FR 2728795 960705 Other publication CA 2166367 960701 Other publication AU 4071595 960711.
Location/Qualifiers
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/organism="unidentified"
/db_xref="taxon:32644"
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87.5%;
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9D_est46:*
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em_estro5:
em_estro6:
         \begin{array}{c} \mathbf{4444444} \\ \mathbf{474444} \\ \mathbf{4747} \\ \mathbf{676} \\ \mathbf{676}
                                                                                                                                                                                                October 2, 2001, 15:00:58 ; Search time 10798.2 Seconds (without alignments) 17:508 Million cell updates/sec
                              GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10228115 seqs, 4726426750 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                       US-09-757-100B-12
20
1 cctgacatcagtagcatctc 20
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Unpublished (2000) COMMENT Contact: Robert B. Weiss University of Utah Genome Center	MILEO CORNERS MILEO CORNERS MILEO CORNERS MILEO CORNERS Tell 12 (018) Tell 13 (018) Tell 14 (018) Tell 14 (018) Tell 14 (018) Tell 15 (018) Tell 18 (018) Tell 1	Qy 1 cctgacatcagtagcatc 18 	RESULT 2 A1098615 A1098615 LOCUS LOCUS DEFINITION ue31h01.y1 Sugano mouse liver mlia Mus musculus cDNA clone TMGE:1482001 5' similar to TR:P97298 P97298 STROMAL CELL DERIVED ACCESSION A1098615 alone A1098615 A1098615 alone REYWORDS SSURCE ORGANISM Mus musculus ENATHORS A1098615 Lot 49) A1098615 Alone A109
\$ Query SummARIES Query The Match Length DB ID Summare Match Length DB ID Summare Match Length DB ID	Color 19 250 AZ848554 AR84854 AR84854 ZW0149407	ALIGNMENTS	AZ848554 19 bp DNA GSS 21-FEB-2001 2M0149A07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZM0149A07 R, DNA sequence. AZ848554.1 GI:13031758 GSS. house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Mus. Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Result No. Scor	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		RESULT 1 AZ848554/C LOCUS DEFINITION A ACCESSION VERSION VERSION VERSION COURCE ORGANISM REFERENCE 1 ACTHORS 1

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/crganism="Homo sapiens"
/db_xref="Laxon:9606"
/dlone="IMAGE:1520736"
/clone="IMAGE:1520736"
/clone="Lb="NCI_CGAB_Kid3"
/clone="Lb="NCI_CGAB_Kid3"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT773D-Pac (Pharmacia) with a modified polyllnker; Site_1: Not I; Site_2: Eco RI; Ist strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), dispessed with Not I and cloned into the Not I and Eco RI sites of the modified p7733 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo.
                                                                             CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: NCI-GEP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Gound through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 40)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Itssue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 bp mRNA EST 08-MAR-2000 wq53g05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2475032 3'similar to TR:088247 088247 MSZF52 ;, mRNA sequence. A1962543 EST. EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 12.4; DB 13; Length 31;
Pred. No. 4.5e+04;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                           Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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92.9%;
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Best Local Similarity 92.9
Matches 13; Conservative
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Unpublished (1997)
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TITLE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: liver; Vector: pME185-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTT]; double-stranded cDNA was
[ATGTGGCCTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCTACTGG], digested
and cloned into distinct DraIII sites of the pME185-FL3
vector [5' site CACTGTGTG, 3' site CACTATGTG). Xhol should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTGGAGACA."
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Tel: 314 286 1800
Fax: 314 286 1810
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Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
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/strain="C57BL"
/db_xref="taxon:10090"
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/clone_lib="Sugano mouse liver mlia"
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                                                                                                                                 Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                                                                          The WashU-HHMI Mouse EST Project Unpublished (1996)
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/lab_host="DH10B"
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Matches 15; Conserv
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Query Match 60.0
Best Local Similarity 75.0
Matches 15; Conservative
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                                                                                                                                                                  /tissue_rype="pooled germ cell tumors"
/lab_host="Pooled germ cell tumors"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library
NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 146964-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "subtraction by Bar 13 c 3 g 15 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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/clone="lmAGE:1555308"
/clone=lib="NLIGGAP_Kid3"
/lab_host="DHIOB"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          om99c07.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1555308 3' similar to TR:019048 019048 HNRNP-E1 PROTEIN. ;, mRNA sequence. AA975152.1 GI:3150944 EST.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 7.4e+04;
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High quality sequence stop: 1.
Location/Qualifiers
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                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2475032"
/clone_lib="NCI_CGAP_GC6"
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Seq primer: -40UP from Gibco
High quality sequence stop: 1.
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AI657872 34 bp mRNA EST 06-MAY-1999 fc14f02.yl Zebrafish WashU MPIMG EST Danio rerio CDNA 5' similar to SW:T2D6_HUMAN Q15545 TRANSCRIPTION INITIATION FACTOR TFIID 55 KD
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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo.
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CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
Info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
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Tel: 314 286 1800
Fax: 314 286 1810
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Possible reversed clone: similarity on wrong strand
Seq primer: T3 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/clone_lib="Zebrafish WashU MPIMG EST"
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Pred. No. 7.6e+04;
0; Mismatches 5;
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Other_ESTs: fc14f02.x1
Contact: Stephen L. Johnson
Washington University School
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT ;, mRNA sequence.
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75.0%;
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14 CAACAGGAGCATCTC 28
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double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORTI vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). CDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic sheld stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
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Submitted (17-MAR-1995) Stylianos E. Antonarakis, Division of
Medical Genetics, University and Cantonal Hospital of Geneva, CMU,
1 rue Michel-Servet, 1211 Geneva, SWITZERLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 41)
Chen, H. M., Rossier, C., Chrast, R. and Antonarakis, S.E. Cloning of trapped exons from human chromosome 21
Chases 1 to 41)
Antonarakis, S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen, H., Chrast, R., Rossier, C., Morris, M.A., Lalioti, M.D. and Antonarakis, S.E. Cloning of 559 potential exons of genes of human chromosome 21 by
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H.sapiens DNA for trapped exon (ID RMC04C05), genomic survey
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Pred. No. 9.1e+04;
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Genome Res. 6 (8), 747-760 (1996)
97011340
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86.7%;
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Best Local Similarity 86.7
Matches 13; Conservative
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Chen, H., Chrast. R.
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6 catcagtagcatete 20

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/clone_lib-"Mouse 10kb plasmid UUGCIM library"
/sex-"Male"
/lab_host-"E. Coli strain XLIO-Gold, TI-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/G0 (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XLIO-Gold (Stratagene) cells
and selected for amplicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
WR. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 46)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
AZ758330 46 bp DNA GSS 16-FEB-2001
1M0550115F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0550 row: I column: 15
                                                                         clone UUGC1M0550I15 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: 0550 row: I column: 15
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0550115"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 46. Location/Qualifiers
                                                                                                                                               AZ758330.1 GI:12864016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 801 585 5606
Fax: 801 585 7177
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Mus musculus
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1 (bases 1 to 49)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., La,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMAGE: 2470653 3'
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 49)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Possible reversed clone: similarity on wrong strand
Seq primer: -20ml3 rev1 Er from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A1949145 49 bp mRNA EST wq08b11.x1 NCI_CGAP_K4G12 Homo sapiens CDNA clone similar to TR:060455 060455 POLYADENYLATE BINDING PROTEIN'INTERACTING PROTEIN'1.; , mRNA sequence. A1949145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Stratagene mouse lung 937302"
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Pred. No. 1.2e+05;
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/organism="Mus musculus"
/strain="c57BL/6 x CBA"
/db xref="taxon:10090"
/clone="IMAGE:551996"
mRNA sequence.
AA087870
AA087870.1 GI:1631078
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Best Local Similarity 77.8%;
Matches 14; Conservative
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2 CCTGACATGCATAGCCTC 19
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AI949145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                    wi95g10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401122 3' similar to WP:F55F8.5 CE11196 ; mRNA sequence. A1767413 GI:5233842 Resp.
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                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 49)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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/db_xref="taxon:9606"
/clone="IMAGE:2401122"
/clone_lib="NCI_CGAP_Kid12"
/tisus_type="2 pooled tumors (clear cell type)"
/lab_host="DH108"
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Pred. No. 9.6e+04;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trace considered overall poor quality Insert Length: 969 Std Error: 0.00 Seq primer: -400P from Gibco High quality sequence stop: 1. Location/Qualifiers
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86.7%;
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Unpublished (1997)
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Best Local Similarity 86.7
Matches 13; Conservative
4 gacatcagtagcate 18
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                                         7
                       18 GACATCAGTAGAACC
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Email: buckler@helix.mgh.harvard.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Conservative
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Fax: 801 585 7177
                                                 Seq primer: T3.
    Fax: 6177265736
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A2769505
                                                                     FEATURES
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                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note--organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI: Plasmid DNA from the normalized library NCI CGAP Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs (CloneIDS 1323912-1325831, 1471368-1472903 and R492104-1492285). Subtraction by Bento Soares and M. Fatima Bonaldo.
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1 (bases 1 to 47)

Trofatter, J. A., Long, R. R., Murrell, J. R., Stotler, C. J., Gusella, J. F. and Buckler, A. J.

An expression-independent catalog of genes from human chromosome 22 Genome Res. 5 (3), 214-224 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H55380 47 bp mRNA EST 07-DEC-1995
CHR220319 Chromosome 22 exon Homo sapiens CDNA clone C22_405 5',
mRNA sequence.
H55380.1 GI:1108246
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2470653"
/clone=lib="NCI_CGAP_Kid12"
/tlssue_type="2 pooled tumors (clear cell type)"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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Pred. No. 1.2e+05;
0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular Neurogenetics Unit
Massachusetts General Hospital
Massachusetts General Hospital
Massachusetts General Hospital
Tel: 6177249616
                                                                                                                                                                                                                                                                                                                              Trace considered overall poor quality Insert Length: 779 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 1. Location/Qualifiers
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Best Local Similarity 77.8%;
Matches 14; Conservative
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Contact: Buckler AJ
                                             Tumor Gene Index
Unpublished (1997)
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AUTHORS
TITLE
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MEDLINE
COMMENT
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KEYWORDS
SOURCE
                                                                   JOURNAL
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H55380
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/organism="Homo sapiens"

/db_xref="taxon:9606"

/db="c22.405"

/clone="c22.405"

/clone="c22.405"

/lab_host="E. coli DH5a"
/lab_host="E. coli DH5a"

/note="Vector: pBluescriptIKS+; Site_1: Sal I; Site_2: Bam HI (destroyed); Exons were isolated from human chromosome 22 specific cosmids using a modification of the method of exon amplification (Proc. Natl. Acad. Sci. USA 88:4005-4009, 1991). Amplified exons were digested with Sal I and Bgl II and subsequently cloned into pBluescriptIKS+ at the Sal I and Bam HI sites:"
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1M0570L17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0570L17 F, DNA sequence.
AZ769505 GI:12889709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
Tab host = E. Coli strain XL10-Gold, T1-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.0%; Score 11.4; DB 158; Length 47; 92.3%; Pred. No. 1.5e+05;
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Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 0570 row: L column: 17
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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/clone="UUGC1M0570L17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 27. Location/Qualifiers
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 27)
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Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT RM. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunndgenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0452 row: P column: 14
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                  /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 31)

Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ620204 31 bp DNA GSS 13-DEC-2000 MING42PH1R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0452P14 R, DNA sequence.
AZ620204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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/strain="C57BL/6J"
/db_xr=f="taxon:10090"
/db_xr=urgC1M0452P14"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 11.2; DB 17;
Pred. No. 1.8e+05;
0; Mismatches 3;
                                  /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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High quality sequence stop: 31.
Location/Qualifiers
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Best Local Similarity 81.2%;
Matches 13; Conservative
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
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KEYWORDS
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musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

( Dases 1 to 31)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A1174159 31 bp mRNA EST 07-OCT-1998 vz84e05.rl Soares_mammary_gland_NbMMG Mus musculus cDNA clone IMAGE:1333184 5' similar to SW:NUIM_MOUSE P03888 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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Contact: Marra M/Mouse EST Project
Washlo-HHM House EST Project
Washlngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Far: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 11.2; DB 249; Length 27;
Pred. No. 1.8e+05;
0; Mismatches 3; Indels 0;
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Possible reversed clone: similarity on wrong strand
Seq primer: -20ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1333184"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.0%;
81.2%;
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Best Local Similarity
Matches 13; Conserv
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Gaps

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 [gilARL29072.1], a copy-number induible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptors competent E. coll XL10-Gold (Stratagene) cells and selected for amplcillin resistance."
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ORIGIN
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ó Gaps .; 0 Score 11.2; DB 246; Length 31; Pred. No. 1.8e+05; 0; Mismatches 3; Indels 0 Query Match 56.0%; Best Local Similarity 81.2%; Matches 13; Conservative (

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Search completed: October 2, 2001, 15:01:00 Job time: 10829 sec

b_htg1:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                              October 2, 2001, 15:56:47; Search time 3339.34 Seconds (without alignments) 92.640 Million cell updates/sec
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Sequence:
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Database :

Searched:

Run on:

AR016339 Sequence 18 159963 Sequence 18 186044 Sequence 18 124249 Sequence 36 AX001078 Sequence AR087980 Sequence 180128 Sequence 87 107710 Sequence 15

159963 186044 124249 AX001078 AR087980 180198 107710

100 600

AR016339

Length DB

Description

SUMMARIES

07-0CT-1997

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1 (bases 1 to 24)
Sheiness,D.K., Cangelosi,G.A. and Britschgi,T.B.
Nucleic acid probes useful for detecting microorganisms associated
with vaginal infections
Patent: US 5654418-A 18 05-AUG-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 24)
Sheiness, D.K., Adams, T.H., Stamm, M.R., Cangelosi, G.A.,
Sheiness, D.K., and Dix, C.K.
Britschgi, T.B. and Dix, C.K.
Methods for selectively detecting microorganisms associated with vaginal infections in complex biological samples
Patent: US 5700636-A 18 23-DEC-1997;
Location/Qualifiers
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Pred. No. 1.8e+04;
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Pred. No. 1.8e+04;
0; Mismatches 2;
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Sequence 18 from patent US 5700636.
186044 GI:3205762
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Sequence 36 from patent US 5543293.
124249.
I24249.1 GI:160443.
                Sequence 18 from patent US 5654418. IS9963.
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180138 Sequence 27
180136 Sequence 55
180176 Sequence 65
180176 Sequence 65
180192 Sequence 81
180194 Sequence 81
180195 Sequence 82
124263 Sequence 71
274584 H. saplenns 5
274684 H. saplenns 5
274684 H. saplenns 5
276496 Pseudomonas
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A32693 Synthetic p
AX036277 Sequence
AX038887 Sequence
AR053527 Sequence
AR060812 Sequence
I31591 Sequence
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             T-cell rece
(D3(TM4-del
PCR primer
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Shathess, D.K., Addms,T.H., Stamm,M.R., Cangelosi,G.A.,
Britschgi,T.B. and Dix,C.K.
Diagnostic kits useful for selectively detecting microorganisms in
                               E08846 PCR primer AR087898 Sequence AR087948 Sequence AR087948 Sequence AR087958 Sequence AR087976 Sequence AR087978 Sequence AR087978 Sequence AR087978 Sequence AR087978 Sequence AR087978 Sequence AR087978 Sequence
 A92270 Sequence 7
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AR083193 Sequence
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Pred. No. 1.8e+04;
0; Mismatches 2;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 bp DNA
Sequence 18 from patent US 5776694.
AR016339
AR016339.1 GI:3972616
                                                                 AR087948
AR087958
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AR087976
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                                                                                                                                                                                                                                                                 1 (bases 1 to 26)
Goh, S. Han, Chow, A. W. and Hemmingsen, S.
HSP-60 genomic locus and primers for species identification
Patent: US 5708160-A 87 13-JAN-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 32)
Springer, T.A. and Larson, R.
The Alpha-subunit of the LFA-1 leukocyte adhesion receptor
Patent: EP 0362526-A2 15 11-APR-1990;
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            60.0%; Score 12; DB 9; Length 26; 75.0%; Pred. No. 1.6e+05; Live 0; Mismatches 5; Indels
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Pred: No. 1.6e+05;
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107710
107710.1 GI:589756
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Sequence 87 from patent US 5708160.
1180198
180198.1 GI:3208488
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Matches 15; Conservative
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unclassified.
1 (bases 1 to 34)
Sandigy. and Loeser, P.
CLONING VECTORS FOR PRODUCING ADENOVIRAL MINIMAL VIRUSES
Patent: WO 9902647-A 3 21-JAN-1999;
HEPAVEC AG FUER GENTHERABLE (DE); SANDIG VOLKER (DE)
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Goh,S.Han, Chow,A. and Hemmingsen,S.
Universal targets for species identification
Patent: US 5989821-A 87 23-NOV-1999;
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Pred. No. 1.7e+04;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 12.2; DB 9;
Pred. No. 1.2e+05;
); Mismatches 3;
           1 (bases 1 to 30)
Gold, L. and Tasset, D.
DNA ligands of thrombin
Patent: US 554393-A 36 06-AUG-1996;
Location/Qualifiers
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Sequence 87 from patent US 5989821.
AR087980
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Sequence 3 from Patent WO9902647..
AX001078
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/db_xref="taxon:32644"
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/organism="unknown"
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88.2%;
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18 TAGAGTTGGTACCGTCA 2
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Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity 82.4
Matches 14; Conservative
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(D3(TM4-del))-D3 dopamine receptor (3' region, alternatively spliced) [human, peripheral blood lymphocytes, mRNA Partial Mutant,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 45)
Nagal,Y., Ueno,S., Saeki,Y., Soga,F. and Yanagihara,T.
Expression of the D3 dopamine receptor gene and a novel variant transcript generated by alternative splicing in human peripheral blood lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E08846 20 bp DNA PAT 29-SEP-1997
PCR primer to detect polymorphism of Histamine H1 receptor gene.
E08846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="D3R"
/note="This sequence comes from Fig. 4; conceptual
translation presented here differs from translation in
publication"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenBank staff at the National Library of Medicine created this entry [NCBI glubbsq 135517] from the original journal article. This sequence comes from Fig. 4.
Location/Qualifiers
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Shimizu,S., Shimazu,M., Habano,W. and Hayashi,T. .
HUMAN HISTAMINE H1 RECEPTOR GENE AND ITS UTILIZATION
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/organ="Homo sapiens"
/db_xref="taxon:9666"
/cell_type="peripheral lymphocytes"
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/protein_id="AAB27543.2"
/db_xref="G1:7704924"
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S63845
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Jorgensen, J.L., Esser, U., de St Groth, B.F., Reay, P.A. and Davis, M.M.

Mapping T-cell receptor-peptide contacts by variant peptide immunization of single-chain transgenics

Nature 355 (6357), 224-230 (1992)
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S77075 G1:242711
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/protein_id="AAB20961.2"
/db_xref="GI:9027588".
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                                                                                                                            1 (bases 1 to 39)
Kajava,A. and Crameri,R.
METHOD FOR THE OLICOMERISATION OF PEPTIDES
Patent: WO 9818943-A 7 07-MAY-1998;
CIBA GEIGY AG (CH); KAJAVA ANDREY (CH)
Location/Qualifiers
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13 c 12 g 10 t
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/organism="unidentified"
/db_xref="taxon:32644"
a 14 c 13 g 4
   Sequence 7 from Patent W09818943.
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A92270.1 GI:6741040
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Length 26;

Score 11.8; DB 9; Pred. No. 2.1e+05; 0; Mismatches

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1 (bases 1 to 26)
Goh,S.Han, Chow,A. and Hemmingsen,S.
Universal targets for species identification
Patent: US 5989821-A 27 23-NOV-1999;
Location/Qualifiers
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                                                                    /organism="unknown"
                                                                                                                           59.0%;
86.7%;
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Best Local Similarity 86.7
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                                 Artificial sequences.
JP 1955667654-A/4
14-MAR-1993
03-SEP-1993 JP 1993219544
SHIMIZU SHOICHI, SHIMAZU MITSUNOBU, HABANO WATARU, PI
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                                                                                                                                                                     'organism='Artificial sequences'.
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Pred. No. 2.1e+05;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                    Score 11.8; DB 10; Length
Pred. No. 2.2e+05;
0; Mismatches 2; Indels
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Goh,S.Han, Chow,A. and Hemmingsen,S.
Universal targets for species identification
Patent: US 5989821-A 5 23-NOV-1999;
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Location/Qualifiers
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Sequence 27 from patent US 5989821.
AR087920 GI:10014683
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Sequence 5 from patent US 5989821.
AR087898
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/organism="unidentified"
/db_xref="taxon:32644"
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Goh,S.Han, Chow,A. and Hemmingsen,S.
Universal targets for species identification
Patent: US 5989821-A 55 23-NOV-1999;
Location/Qualifiers
 PAT
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Pred. No. 2.1e+05;
0; Mismatches 2;
AR087948 26 bp DNA
Sequence 55 from patent US 5989821.
AR087948.1 GI:10014711
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86.7%;
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New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
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AAF98242
AAT45957
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(c) 1993 - 2000 Compugen Ltd.
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New flea protease genes and proteins - used in vaccine compositions for the prophylaxis and treatment of flea infestation, especially in cats or dogs
                                                                                                                                                                                                                Flea; Siphonaptera; protease; vaccine; prophylaxis; infestation; immunoglobulin protease; larvae; host animal; PCR primer; ss.
                                                                                                                                                                                       Flea serine protease PCR primer SEQ ID NO:58
                                                                                                                                                                                                                                                                                                                                                                                  97US-0042945.
96US-0639075.
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    3 ttagggatggtgccg 17
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Stiegler GL;
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15-NOV-1996;
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Silver G,
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                          The present invention describes a number of phosphorothioate antisense sequences to the human focal adheaion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer -
                                                                                                                                                                                                                  Gaps
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Claim 15; Column 23; 30pp; English.
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Grieve RB, Hunter SW, Rushlow KE;

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The present sequence represents a PCR primer for flea serine protease. The protease, its mimetopes, antibodies (Ab) and inhibitors of the protease, its mimetopes, antibodies (Ab) and inhibitors of the protease, its mimetopes, antibodies (Ab) and inhibitors of the protease as the DNA encoding the protease activity (especially immunoglobulin protease) and so reduce flea infestation, especially immunoglobulin protease) and so reduce flea infestation, especially incass or dogs: Alternatively, flea larvae may ingest the faeces of adult fleas which comprises anti-protease antibodies produced by a host animal in response to administration of the protein. Therapeutic compositions may further comprise a compound that reduces haematophagous ectoparasite to burden by a method other than by reducing flea immunoglobulin protease activity. The novel flea DNA encoding the protein can also used to produce recombinant protein, and fragments of it are used as probes and primers for identification and isolation of related sequences, also as primers of the protein. Ab are also useful for screening expression libraries, to purify the protein and to target cytotoxins to fleas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14.2; DB 19;
Pred. No. 2.9e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 34 BP; 7 A; 11 C; 8 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
Example 23; Page 217; 318pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.0%;
84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 gttagggatggtgccgtca 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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Gaps

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Indels

0; Mismatches Score 15; Pred. No.

Query Match 75.0%; Best Local Similarity 100.0%; Matches 15; Conservative 0

Length 15;

DB 22; L 1.1e+02; 0 Sheiness DK;

RESULT

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The inventors claim a compsn. of at least one oligo probe for the detection of at least one microorganism found in vaginal samples. The sequence below is one such probe. The methods and compsns. can be used for the detection of microorganisms, partic. in vaginal fluid samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe; hybridise; ribosomal RNA; vaginitis; infection; diagnostic; ribosomal RNA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligo:nucleotide probes for detecting microorganisms in vaginal samples - allows selective detection of vaginitis-causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide probe GV003 specific for Gardnerella vaginalis.
                                                                                                                                                                      Detection of microorganisms, partic. in vaginal fluid samples by lysis of cells to release nucleic acid and hybridisation assays using probes
                                                                                                                                                                                                                                                                                                                                                                                                             Score 13.8; DB 14;
Pred. No. 4.5e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                Sequence 24 BP; 7 A; 7 C; 6 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sheiness DK;
                                                                                            Cangelosi GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Column 32; 40pp; English.
                                                                                                                                                                                                                                     Claim 9; Page 42; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cangelosi GA,
93WO-US05085.
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 69.0%;
Best Local Similarity 88.2%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0460344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BECT ) BECTON DICKINSON CO.
                               92US-0896094
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92US-0896094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
AAT89823/c
ID AAT89823 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 ttagggatggtgccgtc 19
                                                                                          Britschgi TB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 TTTGGGATGGAGCCGTC 2
                                                             (MICR-) MICROPROBE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
Gardnerella vaginalis.
                                                                                                                                        WPI; 1993-405847/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-401906/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Britschgi TB,
28-MAY-1993;
                               29-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUN-1995;
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29-MAY-1992;
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                                                                                          Adams TH,
Stamm MR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This oligonucleotide is one example of a probe suitable for diagnosing the presence of G.vaginalis. The preferred target for such probes is 16S rRNA, present in several thousand copies per cell. Oligonucleotides complementary to sequences in the G.vaginalis genome or in G.vaginalis plasmids may also be used.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe; vaginal fluid microorganism; oligonucleotide; gram positive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of probe GV003 for the detection of Gardnerella vaginalis.
                                                                                                                                                       Dipstick; capture probe; 16S ribosomal RNA; vaginal infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting bacterial vaginitis infections - by contacting formed lysate with hybridisation soln, and dipstick comprising non-porous solid support and determining signal associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13.8; DB 13;
Pred. No. 4.5e+02;
0; Mismatches 2;
                                                                                                                      Probe Gv003 specific for Gardnerella vaginalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24 BP; 7 A; 7 C; 6 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 39; 62pp; English.
                             BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.0%;
88.2%;
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                                                                                                                                                                                                                                                                                                                 90US-0600334
                            AAQ24636 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ52752 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ttagggatggtgccgtc 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 TTTGGGATGGAGCCGTC 2
                                                                                                                                                                                                                                                                                                                                                (MICR-) MICROPROBE CORP
                                                                                                                                                                                                                                                                                                                                                                               Adams TH, Sheiness DK;
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-167174/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                         05-NOV-1992
                                                                                                                                                                                                                                                                                 21-OCT-1991;
                                                                                                                                                                                                                                                                                                                 19-OCT-1990;
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                                                                                                                                                                                                                                                  30-APR-1992.
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                                                                                                                                                                                     Synthetic.
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                                                           AAQ24636;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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             AAQ24636/
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AAQ52752/
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Gaps

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Length 24; Indels Sequence 24 BP; 7 A; 7 C; 6 G; 4 T; 0 other;

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            which allow the detection of microorganisms associated with vaginal disorders e.g. Prevotella bivia, Prevotella melaninogenica, Gardnerella vaginalis, Trichomonas vaginalis, Mycoplasma hominis, Mobiluncus spp., Nelsseria gonorrhoeae, Chlamydia trachomatis, Ureaplasma urealyticus, Candida spp., Streptococcus spp. and Enterobacteriaceae. Such microorganisms associated with vagintis can be selectively detected using oligonuclectide probes specific for the organism and this can be incorporated into the design of diagnostic kits. These probes hybridise to regions of the ribosomal RNA with minimum secondary and tertiary interactions. Such hybridisation reactions do not require the additional step of heat denaturing the sample nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe; Gardnerella vaginalis; Candida albicans; Trichomonas vaginalis; dipstick; non-porous solid support; oligonucleotide-coated bead; vaginal disorder; hybridisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is the nucleotide sequence of the Gardnerella vaginalis probe used in the method of the invention which involves the production of Kits for simultaneously detection of Gardnerella vaginalis, Candida albicans and Trichomonas vaginalis, which comprised a dipstick with a non-porous solid support having at least 3 capture oligonucleotide-coated beads attached to it. The kit can be used for detecting microorganisms associated with vaginal disorders.
                                                                                                                                                                                                                                                                                                           Gaps
Sequences AAT89806-T89877 represent novel oligonucleotide probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Test kit for vaginal disorders - comprises dipstick with capture oligonucleotide-coated beads, specific for Gardnerella vaginalis. Candida albicans and Trichomonas vaginalis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sheiness DK;
                                                                                                                                                                                                                                                                        Length 24;
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of the Gardnerella vaginalis GV003.
                                                                                                                                                                                                                                                                    Score 13.8; DB 18;
Pred. No. 4.5e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dix CK,
                                                                                                                                                                                                                     Sequence 24 BP; 7 A; 7 C; 6 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Britschgi TB, Cangelosi GA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
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                                                                                                                                                                                                                                                                      69.0%;
88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gardnerella vaginalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-398025/34.
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUN-1995;
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29-MAY-1992;
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Stamm MR;
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                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                systematic evolution of ligands by exponential enrichment; SELEX; heparin; selection; region of homology; inhibitor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identification of ligands to basic fibroblast growth factor and thrombin - which can be modified for increased in vivo stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mediated conditions and in studying the structure and binding of
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0
          24;
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           Length
                                      Indels
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Score 13.8; DB 19;
Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.8; DB 16;
Pred. No. 4.6e+02;
O: Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30 BP; 4 A; 1 C; 15 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                   Family 1; family 2; ligand; thrombin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 39; Page 95; 236pp; English.
                                      ;
                                                                                                                                                                                                                                                        Thrombin DNA ligand, clone #14.
                                                                                                                                                                  BP.
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90US-0536428.
91US-0714131.
93US-0061691.
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88.2%;
          69.0%;
88.2%;
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                                                                                                                                                                  AAT00210 standard; DNA; 30
                                                                                                                                                                                                                             (first entry)
                                                                3 ttagggatggtgccgtc 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NEXS-) NEXSTAR PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ggttagggatggtgccg 17
        Query Match 69.0
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                11 TTTGGATGGAGCCGTC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-293073/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-FEB-1994;
11-JUN-1990;
10-JUN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                               AAT00210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thrombin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gold L,
                                                                                                                                                   AAT0021(
ID AAT
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Brooks DG;

Sasmor HM,

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A method has been developed of defining a set of compounds that modulate the expression of a target nucleic acid (tNA) sequence via binding of the compounds with the tNA sequence. The method comprises generating a library of virtual compounds in silico according to defined criteria, and evaluating in silico the binding of the virtual compounds with the tNA according to defined criteria. Also described are: (1) a method of defining a set of oligonuclectides (ONS) that modulate the expression of a tNA sequence via binding of the ONS with the tNA sequence comprising generating a library of virtual compounds in silico according to defined criteria, and evaluating in silico the binding of the virtual ONS with the tNA according to defined criteria; and (2) a method of defining a set of compounds that modulate the expression of a tNA sequence via binding of the compounds with the tNA. The methods can be used for the generation and identification of synthetic compounds having defined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             physical, chemical or bioactive properties. Information gathered from assays of such compounds is used to identify nucleic acid sequences the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     are tractable to a variety of nucleotide sequence-based technologies, e.g. antisense drug discovery and target validation. AAZ40852 to AAZ41220, and AAX52701 to AAX52706, represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying compounds which modulate expression of nucleic acids, us to provide compounds having defined physical, chemical or bioactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human RhoC phosphorothioate antisense oligonucleotide SEQ ID NO:121.
Identification; genetic target; gene modulation; human; probe; antisense oligonucleotide; phosphorothioate; PCR primer; nucleotide sequence-based technology; antisense drug discovery; target validation; sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13.4; DB 20;
Pred. No. 7e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                     Freier SM,
Vickers TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 BP; 5 A; 8 C; 3 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 18; Page 96; 264pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  properties, e.g. antisense activity
                                                                                                                                                                                                                                                                                                                                                                                     ', McNeil J,
Borchers AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ40969 standard; DNA; 18 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.0%;
93.3%;
                                                                                                                                                                                                                                               99WO-US08268
                                                                                                                                                                                                                                                                                     98US-0081483
98US-0067638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 67.0
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 gttagggatggtgcc 16
                                                                                                                                                                                                                                                                                                                                                (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 GTTGGGGATGGTGCC 1
                                                                                                                                                                                                                                                                                                                                                                                          Baker BF,
                                                                                                                                                                                                                                                                                                                                                                                                             Wyatt JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-620446/53
                                                                                                                           Homo sapiens.
                                                                                                                                                               WO9953101-A1.
                                                                                                                                                                                                                                             13-APR-1999;
                                                                                                                                                                                                                                                                                     13-APR-1998;
                                                                                                                                                                                                                                                                                                          28-APR-1998;
                                                                                                                                                                                                       21-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                          Cowsert LM,
                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ40969;
                                                                                                                                                                                                                                                                                                                                                                                                          Ohasi C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ40969/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a purified and isolated non-naturally occurring DNA ligands to basic fibroblast growth factor (bFGF). The ligands are useful as part of gene therapy treatments and for diagnosing pathogenesis of vascular diseases including infitation and progression of atherosclerosis, acute coronary syndromes, vein graft disease and restenosis following coronary angloplasty. The ligands have improved stability in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acid ligands to basic fibroblast growth factor that are useful as inhibitors of basic fibroblast growth factors and 2'-amino modified RNA ligands, exhibit increased in vivo stability
                                                                                                                                                                                                                                                                                   Ligand; basic fibroblast growth factor; bFGF; gene therapy; vascular; atherosclerosis; angloplasty; stability; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human RhoC phosphorothioate antisense oligonucleotide SEQ ID NO:120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13.8; DB 22;
Pred. No. 4.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 19; Column 57-58; 153pp; English.
                                                                                                                                                                                                                                           Thrombin high affinity ligand #9.
                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gold L, Tasset D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90US-0536428.
91US-0714131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.0%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0687421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92US-0973333
94US-0195005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-0219012
                                                                                                                   AAF70762 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ40968 standard; DNA; 18
                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NEXS-) NEXSTAR PHARM INC.
Query Match
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 ggttagggatggtagcg 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-158583/16
                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                   US6177557-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JUN-1991;
06-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-FEB-1994;
28-MAR-1994;
                                                                                                                                                                                                     20-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                           23-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Janjic N,
                                                                                                                                                             AAF70762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ40968;
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Gaps

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Indels

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Length 18;

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18-AUG-2000; 2000WO-US22808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 gttagggatggtgcc 16
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                                                                                                                                                                                                (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 GTTGGGGATGGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                WPI; 2001-191677/19
                                                                                        WO200115739-A1.
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                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                      31-AUG-1999;
                                                                                                                                                                                                                         Roberts ML,
                                                                                                                   08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF94690;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                      A method has been developed of defining a set of compounds that modulate the expression of a target nucleic acid (tMA) sequence via binding of the compounds with the tNA sequence. The method comprises generating a library of virtual compounds in silico according to defined criteria, and evaluating in silico the binding of the virtual compounds with the tNA according to defined criteria. Also described are: (1) a method of defining a set of oligonuclectides (ONS) that modulate the expression of a tNA sequence via binding of the ONS with the tNA sequence comprising generating a library of virtual compounds in silico according to defined criteria, and evaluating in silico the binding of the virtual ONS with the tNA according to defined criteria; and (2) a method of defining set of compounds that modulate the expression of a tNA sequence via binding of the compounds with the tNA. The methods can be used for the generation and identification of synthetic compounds having defined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         physical, chemical or bioactive properties. Information gathered from assays of such compounds is used to identify nucleic acid sequences that
                                                                                                                                                                                                                                                                                                                  nseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 are tractable to a variety of nucleotide sequence-based technologies, e.g. antisense drug discovery and target validation. AAZ40852 to AAZ41220, and AAX52701 to AAX52706, represent sequences used in the
                                                                                                                                                                                                                                                  Sasmor HM, Brooks DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                              Identifying compounds which modulate expression of nucleic acids, us to provide compounds having defined physical, chemical or bioactive properties, e.g. antisense activity
Identification; genetic target; gene modulation; human; probe; antisense oligonucleotide; phosphorothioate; PCR primer; nucleotide sequence based technology; antisense drug discovery; target validation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rho C antisense phosphorothioate oligonucleotide SEQ ID 113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.0%; Score 13.4; DB 20; 93.3%; Pred. No. 7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                Freier SM,
Vickers TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18 BP; 6 A; 8 C; 3 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                Example 18; Page 96; 264pp; English.
                                                                                                                                                                                                                                               4, Baker BF, McNeil J,
Wyatt JR, Borchers AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF94689 standard; DNA; 18 BP
                                                                                                                                                        99WO-US08268
                                                                                                                                                                                98US-0081483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 67.0
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                     (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 gttagggatggtgcc 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 GTTGGGGATGGTGCC
                                                                                                                                                                                                                                                                                      WPI; 1999-620446/53.
                                                               Synthetic.
Homo sapiens.
                                                                                                    WO9953101-A1
                                                                                                                                                        13-APR-1999;
                                                                                                                                                                                13-APR-1998;
28-APR-1998;
                                                                                                                              21-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAY-2001
                                                                                                                                                                                                                                                Cowsert LM,
                                                                                                                                                                                                                                                        Ohasi C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF94689
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This sequence represents oligonucleotide #4 which was annealed to oligonucleotides #1, #2 and #3 (AAZ22836-Z22838) to generate a four-way junction used to assay for any resolvase activity in an extreme thermophilic enzyme composition from Thermotoga maritima. Extreme thermophilic enzymes, such as TM-Endo V (from Thermotoga maritima) cleave at a mismatch formed between two polynucleotides in a duplex. It does not exhibit resolvase activity and does not require a GATC sequence to effect cleavage. TM-Endo V cleaves C/C, G/G, T/C, A/A, and T/T mismatch. The enzyme does not cleave a perfectly complementary oligonucleotide pair (no mismatch), a T/G mismatch or a 3 base bubble. It
                                                                                                                         HMGCoA reductase is the enzyme which defines the rate limiting step in cholesterol biosynthesis. Expression of the gene may be prevented by the formation of a triplex between the duplex target DNA sequence and an anti parallel or parallel synthetic oligonucleotide. A suitable target sequence is the binding site for a repressor protein which appears to mediate end-prod. inhibition of transcription by cholesterol, from base -167 to -135 of HMGCoA reductase gene. Oligonucleotides targetted against this sequence will repress HMGCoA expression, and act as agonists of the cellular repressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated extreme thermophilic enzyme, which cleaves at a mismatch formed between two polynucleotides in a duplex \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermophilic; mismatch; cleavage; PCR; amplification; Taq polymerase; mutation; detection; pathogen; cancer; probe; ss.
Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition - which bind to target sequence in duplex DNA forming colinear triplex by binding to major groove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Extreme thermophilic mismatch cleavage enzyme substrate oligo
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13.2; DB 14;
Pred. No. 9.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33 BP; 3 A; 10 C; 13 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            George AL;
                                                                                          Example 9; Column 28; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Fig 2; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US03274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.0%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ22839 standard; DNA; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ggttagggatggtgccgt 18
||| || || ||||||| ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ggtgagagatggtgcggt 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TREV-) TREVIGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-571571/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9942595-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-AUG-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ22839;
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       ð
                                                                                                                                                                                                                                                                                                                                                                                This invention relates to an antisense compound targeted to a nucleic acid molecule encoding a member of the human Rho family of small GTP binding proteins, where the antisense compound inhibits the expression of the member of the human Rho family. The invention includes antisense oligonucleotides AAF94580 - AAF94637 which target a RhoA nucleotide sequence, AAF94725 which target a RhoC nucleotide sequence, AAF94759 which target a RhoC nucleotide sequence, AAF94769 - AAF94769 which target a Rac 1 nucleotide sequence and AAF94765 - AAF94790 which target a Rac 1 nucleotide sequence and AAF94755 - AAF94809 which target a Rac 1 nucleotide sequence and AAF94755 - AAF94809 which target odds 2 nucleotide sequence. The antisense compound is useful for treating hyperproliferative conditions and ischaemia/reperfusion or recoxygenation injury. The compound may also be used to diagnose the above conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                  An antisense compound targeted to a nucleic acid molecule encoding a member of the human Rho family of small GTP binding proteins useful for treating e.g. cancer and ischaemia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cholesterol; repressor protein; transcription; agonist; cellular;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 13.4; DB 22;
Pred. No. 7e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 BP; 6 A; 8 C; 3 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                            Example 16; Page 73; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HMGCOA reductase target sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.0%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            triplex; target; duplex; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88US-0287359
89US-0453532
                       18-AUG-2000; 2000WO-US22808
                                                                    99US-0387341
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                                                                  31-AUG-1999;
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Gaps

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can be used to detect mutations in a target nucleotide or to detect the presence of a non-mutated sequence. In particular, the enzyme can be used for detecting mutations in HIV, sickle cell anaemia hypoxanthine transferase gene, and in genes associated with cancer e.g., p53 and BKCA1. TW-Endo V can be used to cleave mismatches that are created during polymerase, incorporates approximately one incorrect base per 500 bases, which is unacceptable if DNA greater than 500 bp is to be amplified. TW-Endo V cleaves at the mismatch, either on the template or the durther amplification. A chimera of an extreme thermophilic DNA polymerase and TW-Endo V can accomplish the dual roles of pCR plus correction of erroneous base incorporation.
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Sequence 49 BP; 13 A; 15 C; 12 G; 9 T; 0 other;

ö 0; Gaps Length 49; Indels Score 13.2; DB 20; Pred. No. 9.6e+02; 0; Mismatches 3; Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative

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Search completed: October 2, 2001, 16:18:42 Job time: 15486 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Unpublished (2000) COMMENT Contact: Robert B. Weiss University of Utah Genome Center University of Utah Genome Center University of Utah Genome Center Tel: 801 S8, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 506 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0429 row: K column: 17 Seg primer: CACACAGGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 27.	FEATURES Location/Qualifiers 1. 27 /organism="Mus musculus" /strain="657BL/6J" /db_raref="taxon:10090" /clone="taxon:10090" /clone="taxon:10090"	adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance." BASE COUNT 5 a 9 c 6 g 7 t CRIGIN Ouery Match 71.0%; Score 14.2; DB 246; Length 27; Best Local Similarity 84.2%; Pred. No. 6.7e+03; Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy 1 ggttagggatggtcogtc 19 Db 26 GGCTAGGGATGGCGCCATC 8	RESULT 2 AZ592004 LOCUS AZ592004 VERSION VERSION VERSION VERSION KEYWORDS SOURCE Nouse mouse. ORGANISM MS musculus Consolus Corrected to the corrected to th
Score Match Length DB ID Description 12.2 Match Length DB ID Description 12.2 Match Length DB ID Description 12.2 Match Length DB ID Description 12.3 Match Length DB ID Description 12.4 Match Length DB ID Description 12.5 Match Length DB ID Description 13.6 Match Length DB ID Description 13.6 Match Length DB ID Description 13.8 Match Length DB ID Description 14.8 Match Length DB ID Description 15.6 Match Length DB ID Description 16.0 Match Length DB ID Description 17.8 Match Length DB ID Description 18.8 Match Length DB ID Description 19.8 Match Length DB ID Match Ma	A1188838 H188838 H188338 A2399400 A2822907 A2611815 A1721161 H198138 A172159 A1010368 A0103460 A0105469	11 55.0	AZEO7381, C AZEO7381 27 bp DNA GSS 13-DEC-2000 LOCUS DEFINITION 100429K17R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0429K17 R, DNA sequence. AZCESSION AZEO7381.1 GI:11729571 AZEO7381.1 GI:11729571 GSS. SOURCE ORGANISM Mus musculus ELETAROCASION Mus musculus BURATYOLA: Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. AUTHORS Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M.; Rose, M., Rose, M., Rose, M., Rose, M., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

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// ACCE="Vector: pr773D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Ist strand cDNA was primed with a Not I: - oligo(dT) primer [5] rgrand charmacia with a Not I: - oligo(dT) primer [5] rgrand charmacia with a Not I: - oligo(dT) primer [7] rgrand charmacia with a Not I: - oligo(dT) primer [7] rgrand charmacia with a Not I: - oligo(dT) rgrand rgran
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Malsna, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse whole genome scaffolding with paired end reads from 10kb
   Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                    Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="IMAGE:440512"
/clone=lib="Soares mouse embryo NDMEl3.5 14.5"
/sex="unknown"
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
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Pred. No. 3.4e+04;
0; Mismatches 2;
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Trace considered overall poor quality
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                                                                                                                                        The WashU-HHMI Mouse EST Project
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High quality sequence stop: 1.
Location/Qualifiers
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Best Local Similarity 87.5%;
Matches 14; Conservative
                                                                                                                                                                           Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qil4732114 (pplAF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-GOld (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                             Rm.\ 308 , Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112 , USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA009110 45 bp mRNA EST 26-JUL-1996 mg92g09.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone IMAGE:440512 5' similar to gb:X05021 Murine mRNA with homology to yeast L29 ribosomal protein (MOUSE);, mRNA sequence.AA009110
                               Mouse whole genome scaffolding with paired end reads from 10kb
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/clone=lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 29;
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ilarity 100.0%; Pred. No. 2.6e+04;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0402 row: H column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
                                                                                              Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
                                                                  plasmid inserts
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Gaps

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Unpublished (2000)
Contact: Robert B. Weiss
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 506
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HMI Mouse EST Project
WashU-HMI Mouse EST Project
Fast 14 286 1800
Fax: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:520583
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ434508 23 bp DNA GSS 03-OCT-2000 IM0220K22R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0220K22 R, DNA sequence. AZ434508 GI:10558521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Knowles Solter mouse inner cell mass"
/dev_stage="embryo (post-implantation)"
/lab_host="DH10B"
   Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="B6D2 F1/J"
/db_xref="taxon:10090"
/clone="IMAGE:892623"
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82.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pWMA2 (gil4722114|gb]AR129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                    L Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5406
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0429 row: K column: 17
Seq primer: CACAGGAAACAGCTATGACC
Class: plasmid ends
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Mus musculus musculus substance in the substa
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/organism="Mus musculus"
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0429K17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Matches 14; Conservative
plasmid inserts
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(http://www.lax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gild/32114 gblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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84112, USA
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1M0553C23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0553C23 F, DNA sequence.
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Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
/lab.host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="(57BL/64"
/db_xref="taxon:10090"
/clone="UGCIMO571A14"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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100.0%; Pred. No. 8.3e+04;
ive 0; Mismatches 0;
   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                  Plate: 0571 row: A column: 14
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
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University of Utah
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Unpublished (2000)
Contact: Robert B. Weiss
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Eukaryota; Metazoa; C
Mammalia; Eutheria; R
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 47)
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1M0571A14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0571A14 F, DNA sequence.
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                                                                                                                                                                                                                                                              /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0220K22"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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75.0%; Pred. No. 8e+04;
Live 0; Mismatches
                                  Plate: 0220 row: K column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/organism="Mus musculus"
                                                                                                                                    High quality sequence stop: 23.
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Fax: 801 585 7177
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Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Contact: Yutaka Suzuki
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukiéins.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
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AU103569 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS00968, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Pred. No. 1e+05;
0; Mismatches 2; Indels 0
                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0553 row: C column: 23
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 37.
Location/Qualifiers
                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0553C23"
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86.7%;
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Fax: 801 585 7177
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,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997). Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1M0080J04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080J04 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Slam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                        sapiens cDNA library"
10 t
                                                                                                                                                                                                                                                                                                                                                                          Score 11.8; DB 107; Length 50; Pred. No. 1e+05; 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
andl: ddunn@qentics.utah.edu
Insert Length: 10000 Std Brror: 0.00
                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CAS00968"
/clone=lib="Sugano Homo sala 14 c 22 9 10 0
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Seg primer: CGTTGTAAAACGACGCCCAGT
Class: plasmid ends
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/db_xref="taxon:10090"
/clone="UUGC1M0080J04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 20.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                             Query Match 59.0%;
Best Local Similarity 86.7%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
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1 (bases 1 to 41)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston ,R., Williamson,A., Wohldmann,P. and Wilson,R.
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality
Seq primer: Promega -21ml3
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                      H84363 41 bp mRNA EST 13-NOV-1995 yv85c09.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:249520 3' similar to gb:L06505 60S RIBOSOMAL PROTEIN L12 m0.050; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.0%; Score 11.6; DB 158; Length 41; 77.8%; Pred. No. 1.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_InAGE:249520"
/clone_lib="Soares melanocyte 2NbHM"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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/db_xref="GDB:3867226"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
                                                                                                                                                                                                                               H84363
H84363.1 GI:1063034
    2 gttagggatggtgccgtc 19
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Matches 14; Conserv
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                                                                                                          RESULT 12
H84363/c
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JOURNAL
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electrophoresis. Vector DNA was prepared from a derivative electrophoresis. Vector DNA was prepared from a derivative of pMDA (gil4732114[gb]AF129072.1), a coopy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptoretent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A1188838 40 bp mRNA EST 13-OCT-1998 401112.x. Soarse_placenta_Bto9weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:1774399 3' similar to SW:EXTN_TOBAC P13983 EXTENSIN PRECURSOR; ", mRNA sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 40)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
Email: Gapbs-rémail nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                               Score 11.6; DB 242; Length 20; Pred. No. 1.2e+05;
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                                                                                                                                                                                                                                                                                                            4; Indels
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                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                  58.0%;
77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                           18 GGTTAGGGAAGGGGAGGT 1
                                                                                                                                                                                                                                                                                       Best Local Similarity 77.8
Matches 14; Conservative
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AI188838/c
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AUTHORS
TITLE
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COMMENT
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Gaps

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

AZ399400/c

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/Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/Jab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 Kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
TTO: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                 AZ/86429 21 bp DNA GSS 16-FEB-2001
20003LL33R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0031L23 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/61"
/db_xref="taxon:10090"
/db_aref="taxon:10090"
/clone="UGGC2M0031L23"
/clone=lib="Mouse 10kb plasmid UGGCIM library"
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Pred. No. 1.6e+05;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: 0031 row: L column: 23
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Location/Qualifiers
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llarity 92.3%;
Conservative
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                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                             house mouse.
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Best Local Similarity
Matches 12; Conserv
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                                                                                                   DEFINITION
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AUTHORS
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                         RESULT 1
AZ786429
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KEYWORDS
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gil4732114)[pJsAF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. B. (bases 1 to 21)

E. (bases 1 to 21)

E. (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stoke, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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AZ399400 21 bp DNA GSS 03-OCT-2000 1M0165C13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0165C13 F, DNA sequence.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCIM0165C13"
/clone=lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
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Pred. No. 1.6e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0165 row: c column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
                                                                                                                                                        AZ399400.1 GI:10514474
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92.3%;
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Fax: 801 585 7177
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Best Local Similarity
Matches 12; Conserv
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FEATURES

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Gaps

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BASE COUNT ORIGIN

ò q Search completed: October 2, 2001, 15:01:02 Job time: 10831 sec

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerase and T4 polymerase and T4 polymerase are the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (qil4732114 qib lax123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606

Fax: 801 585 5606

Fax: 801 585 7177

Email: dunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0096 row: M column: 03

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

Location/Qualifiers

1. 38

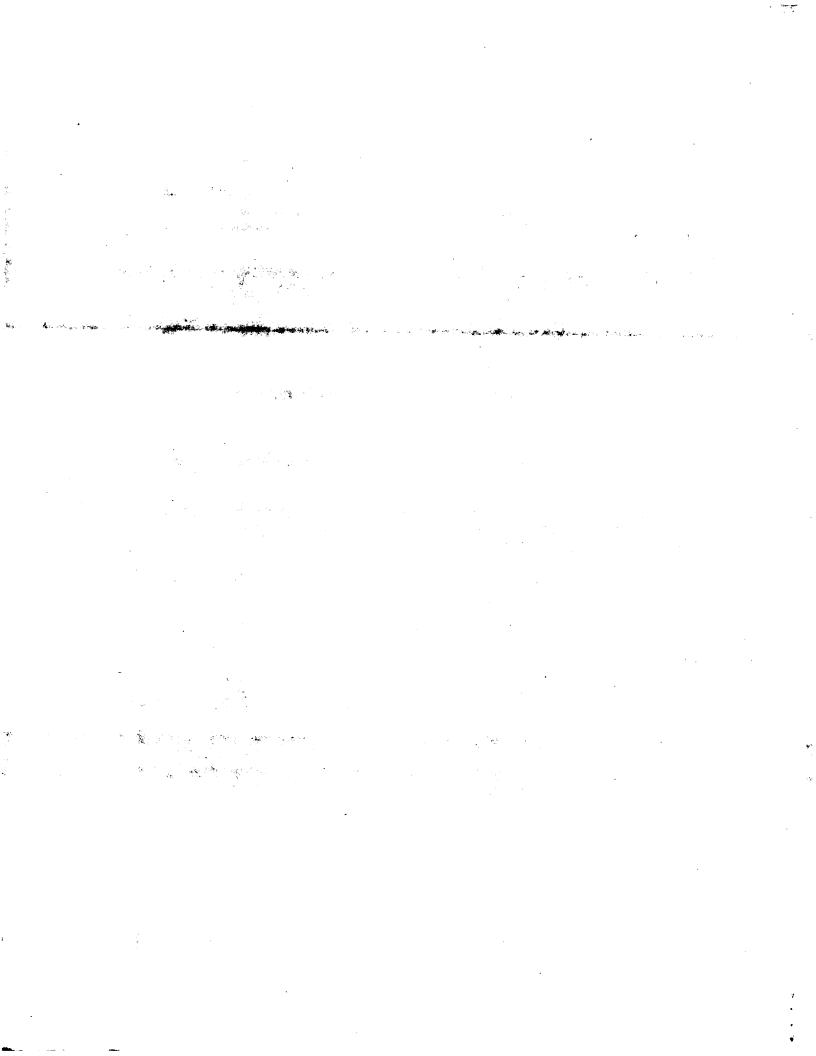
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/clone="UGGC2M0096M03"
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/lab_nost="E. Coli strain XL10-Gold, T1-resistant, F-"
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musculus C57BL/6J (male) was obtained from the Jackson
Labratory Mouse DNA Resource
/http://mrefiles/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dougle/dou
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University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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                                                                         AZ822907 38 bp DNA GSS 20-FEB-2001
2M0096M03R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0096M03 R, DNA sequence.
AZ822907.1 GI:12992815
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. L (base; 1 to 38)

Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly, M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb Unpublished (2000)

Contact: Robert B. Weiss
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Matches 12; Conservative
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
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KEYWORDS
SOURCE
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34, Appl
58, Appl
18, Appl
18, Appl
18, Appl
118, Appl
11, Appl
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12, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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4.5
Compugen Ltd.
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US-09-377-310-34

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US-08-749-699-58

US-08-146-344-18

US-08-166-999-18

US-08-166-999-18

US-08-156-807-11

US-09-156-807-11

US-09-156-807-12

US-09-156-807-12

US-09-156-807-12

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US-09-156-807-12

US-09-156-807-12

US-08-429-1218-87

US-08-429-1218-5

US-08-429-1218-5

US-08-429-1218-5

US-08-429-1218-5

US-08-429-1218-67

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                                                                                                                                                                                                                                                                                                                  hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                      324599 segs, 94655562 residues
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GenCore version (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 50
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Patent No. 6133031
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT APPLICATION NUMBER: US/09/377,310B
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                       Sequence
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APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
           Sequence
                     Sequence
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Pred. No. 0.072;
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                           US-09-003-067-81
US-09-003-067-83
US-08-003-067-85
US-08-859-998-933
US-08-219-012-50
US-08-687-421-238
US-08-793-937-8
                                                                                                          US-08-859-998-709

US-08-859-998-496

US-08-811-492-124

US-08-234-613-43

US-08-418-115

US-08-418-541-76
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          08-09-003-0
08-09-003-0
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                                                                                                                                                                                                                                                    Sequence 14, Application US/09377310B Patent No. 6133031
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Best Local Similarity
Matches 20; Conserv
RESULT 2
US-09-377-310-34
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LENGTH: 20
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LENGTH: 15
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TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 58:
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84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: DNA (primer)
US-08-749-699-58
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          California
                                                                                                                                                                                                            Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94105-1493
                     GENERAL INFORMATION:
                                                                                                                                                                                             Denver
   Patent No. 6210920
                                                                                                                                                                                                                          COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-08-460-344-18/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                            STATE:
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                                                                                                                                                                                                                                                                                                                                                                                      NUCLEIC ACID
                                                                                    DB 3; Length 15;
25;
                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                            APPLICANT: WHENTER, SHIRLEY
APPLICANT: Stiegler, Gary
APPLICANT: Stiegler, Gary
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLE
TITLE OF INVENTION: MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/004,731 FILING DATE: CLASSIFICATION:
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                                                                                    Score 15; DB 3; Pred. No. 25; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
RESISTENCE/DOCKET NUMBER: 2618-25-C3
TELECOMUNICATION:
TELEPHONE: (303)-863-9700
                ; OTHER INFORMATION: antisense sequence US-09-377-310-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: 08/08/749,699 PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NG-DOS
                                                                                                                                                                                                                                                                             Sequence 58, Application US/09004731 Patent No. 6177258 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-749-699-58 ; Sequence 58, Application US/08749699
                                                                                    75.0%;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 34 base pairs
                                                                                 Query Match 75.0
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 84.2
Matches 16; Conservative
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STRANDEDNESS: single
                                                                                                                                                           3 ttagggatggtgccg 17
                                                                                                                                                                                          1 ttagggatggtgccg 15
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: USA
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; MOLECULE TYPE:
US-09-004-731-58
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COUNTRY:
                                                                                                                                                                                                                                                              .09-004-731-58
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FEATURE:
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Sequence 18, Application US/08460344

Patent No. 56544

GENERAL INFORMATION:
APPLICANT: SHEINESS, Diana K.
APPLICANT: STAMM, Michael R.
APPLICANT: CANGELOSI, Gerard A.
APPLICANT: CANGELOSI, Theresa B.
APPLICANT: DIX, Connie K.
TITLE OF INVENTION: METHODS AND DIAGNOSTIC KITS USEFUL FOR
TITLE OF INVENTION: INFECTING MICRORGANISMS ASSOCIATED WITH VAGINAL.
TITLE OF INVENTION: INPECTIONS

NUMBER OF SEQUENCES: 72
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                                                                                  FLEA PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/749,699
APPLICANT: Wu Hunter, Shirley
APPLICANT: Stiegler, Gary
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick
TITLE OF INVENTION: FLEA PROTESE PROTEINS,
TITLE OF INVENTION: MOLECULES AND USES THERE
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CONDIJ, GATY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: ADAMS, Trevor H.
APPLICANT: STAMM, Michael R.
APPLICANT: STAMM, Michael R.
APPLICANT: GANGELOSI, Gerard A.
APPLICANT: CANDING F.
TITLE OF INVENTION: METHODS AND DIAGNOSTIC KITS USEFUL FOR TITLE OF INVENTION: DETECTING MICROORGANISMS ASSOCIATED WITH VAGINAL TITLE OF INVENTION: INPECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Pred. No. 1.1e+02;
0; Mismatches 2; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
| LOCATION: 1.24
| TOTHER INFORMATION: /standard_name= "GV003"
US-08-133-598A-18
                                APPLICATION NUMBER: US/08/133,598A
FILING DATE: 08-0CT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,094
FILING DATE: 29-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/600,334
FILING DATE: 19-0CT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 11652-73-2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: SINGle
                     имыек: US/08/133,598A
08-ОСТ-1993
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/458,319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application US/08886999
Patent No. 5776694
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: SHEINESS, Diana K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.0%;
88.2%;
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       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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US-08-886-999-18/C
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APPLICANT: STAM, Michael R.
APPLICANT: STAM, Michael R.
APPLICANT: STAM, Michael R.
APPLICANT: STAM, Michael R.
APPLICANT: CANGELOSI, Gerard A.
APPLICANT: BRITSCHGI, Theresa B.
APPLICANT: DIX, Connie K.
TITLE OF INVENTION: DEFECTING MICROORGANISMS ASSOCIATED WITH VAGINAL TITLE OF INVENTION: INFECTING MICROORGANISMS ASSOCIATED WITH VAGINAL TITLE OF INVENTION: INFECTING MICROORGANISMS ASSOCIATED WITH VAGINAL TITLE OF INVENTION: INFECTING MICROORGANISMS ASSOCIATED WITH VAGINAL TITLE OF INVENTION: INFECTIONS
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                          SOFTWALES PATENTING SILEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
CLASSIFICATION NUMBER:
CLASSIFICATION DATE:
PRIOR APPLICATION DATE:
APPLICATION NUMBER:
CLASSIFICATION DATE:
APPLICATION NUMBER:
CLASSIFICATION NUMBER:
APPLICATION NUMBER:
CSTANDARE:
APPLICATION NUMBER:
CSTANDARE:
APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
CSTANDARE:
APPLICATION NUMBER:
APPLICATIO
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Pred. No. 1.1e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
; LOCATION: 1.24
; COTERT INFORMATION: /standard_name= "GV003"
US-08-460-344-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 11652-73-2
TELECOMMUNICATION INFORMATION:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-133-598A-18/c
; Sequence 18, Application US/08133598A
Patent No. 5700636
; GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 543-9600
TELERAX: (415) 543-5643
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.0%;
88.2%;
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Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA
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Patent No. 5543293

GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Diane Tasset

TITLE OF INVENTION: Ligands of Thrombin
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beaton & Swanson, P.C.
STREET: 4882 South Ulster Street Parkway, Suite #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage COMPUTER: IBM compatible
                                                                                                                                                                Score 13.8; DB 5;
Pred. No. 1.1e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 13.8; DB 1;
Pred. No. 1.1e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 224, Application US/08687421 Patent No. 6177557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA: none
ATTORNEY/AGENT INFORMATION:
NAME: BALTY J. SWANSON
REGISTRATION NUMBER: 33,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                        linear
E: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (303) 850-9900
TELEFAX: (303) 850-9401
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                69.0%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.08;
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                                                                                                                                                                  Query Match 69.0
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ggttagggatggtgccg 17
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Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                     18 TTTGGGATGGAGCCGTC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 30 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Denver
: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                     STRANDEDNESS:
                                                           MOLECULE TYPE:
HYPOTHETICAL:
PCT-US93-05085-18
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US-08-687-421-224
                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                   RESULT 9
US-08-219-012-36
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STATE: CC
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY:
US-08-219-012-36
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TITLE OF INVENTION: METHODS AND PHARMACEUTICAL KITS USEFUL

TITLE OF INVENTION: FOR DETECTING MICROORGANISMS ASSOCIATED WITH VAGINAL

TITLE OF INVENTION: INFECTIONS
NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 13.8; DB 1;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 1..24
OTHER INFORMATION: /standard_name= "GV003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                  FILING DATE: 08-007-1993
APPLICATION NUMBER: US 07/896,094
FILING DATE: 29-MAY-1992
PRIOR APPLICATION NUMBER: US 07/896,094
FILING DATE: 19-007-1990
ATTORNEY AGENT INFORMATION:
NAME: GALTECT-1990
ATTORNEY AGENT INFORMATION:
NAME: GALTECT-1990
REFERENCE FOOTER: 37,330
REFERENCE FOOTER: 37,330
REFERENCE FOOTER: 11652-73-2
TELECHONE: (415) 543-9600
TELEPATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDENRESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US93/05085 FILING DATE: 28-MAY-1993 CLASSIFICATION:
                   JMBER: US 08/133,598
08-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application PC/TUS9305085
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION UNDABER: 32,762
REFERENCE/DOCKET NUMBER: 1165;
RELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.0%;
02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 ttagggatggtgccgtc 19
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Best Local Similarity 88.2
Matches 15; Conservative
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                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94105-1493
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Gaps

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Sequence 339, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                  Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Cowsert, Lex M.
TITLE OF INVENTION: ARTISENSE MODULATION OF RhoC EXPRESSION
FILE REFERENCE: RTS-0014
CURRENT APPLICATION NUMBER: US/09/156,807
CURRENT FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 47
  TITLE OF INVENTION: ANTISENSE MODULATION OF RhoC EXPRESSION
                                                                                                                                                                                                                                                                                                                                       Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                             Score 13.4; DB 3;
Pred. No. 1.7e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 13.4; DB 3;
Pred. No. 1.7e+02;
0; Mismatches 1;
                                                                                                                                                                                           ; FEATURE:
... OTHER INFORMATION: Antisense Oligonucleotide
US-09-1156-807-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Antisense Oligonucleotide US-09-156-807-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                              CURRENT APPLICATION NUMBER: US/09/156,807
CURRENT FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 11
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/09156807 Patent No. 6030786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.0%;
93.3%;
                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                             Query Match 67.0%;
Best Local Similarity 93.3%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        115 GTTGGGGATGGTGCC 1
                        FILE REFERENCE: RTS-0014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-961-083-339/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-09-156-807-12/c
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LENGTH: 18
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        APPLICANT: Gold, Larry
APPLICANT: Janjic, Nebojsa
APPLICANT: Janjic, Nebojsa
APPLICANT: Tasset, Diane
TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC
TITLE OF INVENTION: THROMBIN
MUMBER OF SEQUENCES: 445
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 6.0 CURRENT APPLICATION DATA:
FILING DATE: 08-MX-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 13.8; DB 4;
Pred. No. 1.1e+02;
0; Mismatches 2;
                                                                                                                                                                                ADDRESSEE: Swanson & Bratschun, L.L.C. STREET: 8400 E. Prentice Avenue, Suite 200 CITY: Englewood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEX07/PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/973,333
FILING DATE: 11-NOVEMBER-1992
PRIOR APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: BATY J. SWANSON
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEXO7/PC
TELECOMMUNICATION:
MEST PRIVAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-156-807-11/c
Sequence 11, Application US/09156807
Patent No. 6030786
SERERAL INFORMATION:
APPLICANT: COWSert, Lex M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,005
FILING DATE: 10-FEBRUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 22-APRIL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/219,012
FILING DATE: 28-MARCH-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (303) 799-3333
TELERA: (303) 793-3433
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.0%;
88.2%;
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Best Local Similarity
Matches 15; Conserv
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             80111
                                                                                                                                                                                                                                                                          COUNTRY:
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US-09-418-641-75
Sequence 75. Application US/09418641A
Sequence 75. Application US/09418641A
Sequence 75. Application US/09418641A
SETEMBRAL INFORMATION:
APPLICANT: Jen N. Cowsert
TILLE OF INVENTION: ANTISENSE MODULATION OF FRA-1 EXPRESSION
FILE REPERBREE: FRS-0105
CURRENT FILING DATE: 1999-10-15
CURRENT FILING DATE: 1999-10-15
SEQ ID NO 75
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5240845-45/c
;Patent No. 5240845
; APPLICANT: FUJII, SETSURO;TAKADA, KAORUKO;. KATANO, TAMIKI;
;MAJIMA, EIJI;OGINO, KOICHI;ONO, KENJI;SAKATA, YASUYO;UENOYAMA,
;TSUTOMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
63.0%; Score 12.6; DB 3; Length 37;
Best Local Similarity 78.9%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 12.6; DB 6; Length 50;
Pred. No. 4.9e+02;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: MUTATED STREPTOKINASE PROTEINS
                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, A. Anders:
REEISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 339:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TERGTH: 37 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 65
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/07/549,049
FILING DATE: 06-JUL-1990
APPLICATION NUMBER: US/08/961,083 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.0%;
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 gttagggatggtgccgtca 20
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Best Local Similarity 78.9
Matches 15; Conservative
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5240845-45
                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY:
US-08-961-083-339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; SEQ ID NO:45:
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Gaps
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                                                                Length 20;
                                                                                                   Indels
                                                                Score 12.2; DB 3;
Pred. No. 6.9e+02;
0; Mismatches 3;
; OTHER INFORMATION: Antisense Oligonucleotide US-09-418-641-75
                                                               Ouery Match 61.0%;
Best Local Similarity 82.4%;
Matches 14; Conservative
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Search completed: October 2, 2001, 16:03:50 Job time: 14594 sec

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Run on:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match Length DB
                                                                         em_vi:*

gb_sts1:*

gb_sts3:*

gb_sts3:*

gb_vi:*

gb_vi:*

gb_vi:*

gb_htg1:*

gb_htg2:*

gb_htg2:*

gb_htg2:*

gb_htg3:*

gb_htg6:*

gb_htg9:*

gb_htg9:*
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em_sts:*
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gb_pr5:*
gb_pr6:*
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gb_pr9:*
gb_ro1:*
gb_ro2:*
gb_in4:*
gb_pr10:*
       em_pat:*
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                                                            2, 2001, 15:56:48 ; Search time 3339.34 Seconds (without alignments) 92.640 Million cell updates/sec
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                    1344157 seqs, 7733874588 residues
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Maximum Match 100%
Listing first 45 summaries
                                            OM nucleic - nucleic search, using sw model
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em_htgo_inv:*
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em_htg_hum6:*
em_htg_hum7:*
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Maximum DB seq length: 50
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Sequence:
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109246 Sequence 12 109244 Sequence 10 109247 Sequence 13 AR109705 Sequence A56687 Sequence 6 E03267 Primer for AX023416 Sequence AX052544 Sequence

109246 109244 109247 AR109705 A56687 E05267 AX023416

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Description

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SUMMARIES

a. 5	AUTHORS Fisher, R.A., Gilbert, W., Sato, V.L., Flavell, R.A., Maraganore, J.I. AUTHORS Fisher, R.A., Gilbert, W., Sato, V.L., Flavell, R.A., Maraganore, J.I. TITLE and Liu, T.R. TITLE DNA SEQUENCES, RECOMBINANT DNA MOLECULES AND PROCESSES FOR JOURNAL PAtent: WO 8901940 **A 10 09-MAR-1989; FEATURES Location/Qualifiers Source 137 /organism="unknown" BASE COUNT 11 a 9 c 10 g 7 t ORIGIN	Ouery Match Best Local Similarity 80.0%; Score 13.6; DB 10; Length 37; Best Local Similarity 80.0%; Pred. No. 8.1e+03; Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps Qy 1 tgttggtttccaatcggacc 20	RESULT 3 109247 38 bp PAT 02-DEC-1994 LOCUS 109247 38 bp DEFINITION Sequence 13 from Patent WO 8901940. ACCESSION 109247 1 GI:588031 KEYWORDS UNKNOWN.	ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 38) AUTHORS Fisher, R.A., Gilbert, W., Sato, V.L., Flavell, R.A., Maraganore, J.B. TITLE and Liu, T.R. TITLE DNA SEQUENCES, RECOMBINANT DNA MOLECULES AND PROCESSES FOR SOURNAL PATENT: WO 8901940-A 13 09-MAR-1989; FRATURES Location/Qualifiers source /organism="unknown" BASE COUNT 8 a 9 c 12 9 t	Ouery Match 68.0%; Score 13.6; DB 10; Length 38; Best Local Similarity 80.0%; Pred. No. 8.1e+03; Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps Qy 1 tgttggtttccaatcggacc 20	RESULT 4 AR109705 AR109705 LOCUS LOCUS AR109705 Sequence 129 from patent US 6114139. ACCESSION AR109705 VERSION AR109705.1 GI:12825981 KEYWORDS SOURCE Unknown.
E32827 Novel compo 169336 Sequence 8 AX019232 Sequence 108124 Sequence 6 A43528 Sequence 8 AR052465 Sequence AR011952 Sequence AR011952 Sequence AX023890 Sequence AX023890 Sequence AX1431 Oliyonucleo	AR011842 Sequence AR109138 Sequence E25881 Blastcoyst AZ0514 PT-261 muta AX097321 Sequence AX090859 Sequence AX09561 Sequence AX082611 Sequence AX082615 Sequence AX082615 Sequence AX082616 Sequence AX082616 Sequence AX082618 Sequence AX082618 Sequence	AR094119 Sequence AR038156 Sequence AR14501 Group 8 Hyb A14502 Group 8 ter A14504 Group 8 ter A14504 Group 9 ter A1459 Hybridizati A21427 Oligonucleo AX085274 Sequence	AXO06548 Sequence AXO06548 Sequence AXO30256 Sequence AXO49934 Sequence	PAT 02-DEC-1994	LES AND PROCESSES FOR	10; Length 36; 33; 4; Indels 0; Gaps 0;
12 60.0 26 10 E32827 12 60.0 30 10 169336 12 60.0 42 9 AX019232 11.8 59.0 24 9 AR052465 11.8 59.0 24 9 AR052465 11.8 59.0 35 9 AR011952 11.6 58.0 27 9 AX023890 11.6 58.0 27 9 S59402 11.6 58.0 30 9 A21431 11.6 58.0 30 9 A21431	58.0 58.0 58.0 57.0 57.0 57.0 57.0 56.0 56.0 56.0 56.0 56.0 56.0 56.0 56	2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2	.2 56.0 .2 56.0 .2 56.0 .2 56.0 .34 .5 .0 34		and Liu.T.R. DAN SEQUENCES, RECOMBINANT DNA MOLECULES PRODUCING SOLUBLE T4 PROTEINS PATENT: WO 8901940-A 12 09-MAR-1989; Location/Qualifiers 136 /organism="unknown" 9 a 9 c 10 9 8 t	ttch al Similarity 80.0%; Score 13.6; DB 10; al Similarity 80.0%; Pred. No. 8.1e+03; 16; Conservative 0; Mismatches 4; tgttggtttccaatcggacc 20
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Maraganore, J.M.

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Maraganore, J.M.

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synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 21)
Lipford,G.B., Heeg,K. and Wagner,H.
G-motif oligonucleotides and uses thereof
Patent. WO 0014217-A 31 16-MAR-2000;
LIPFORD GRAYSON B (DE); HEEG KLAUS (DE); WAGNER HERMANN (DE)
CPG IMMUNOPHARMACEUTICALS GMBH (DE)
OS Artificial gene
OC Artificial sequence; Genes.
PN JP 1993192200-A/37
PD 07-AUG-1993
PF 19-AUG-1990 JP 90P 217067
PI OKAZAWA KAZUHIDE, SHIMADA MASAMITSU, KATOU IKUNOSHIN, PI FUKUSHIMA MICHIO,
PI FUTINAGA KEI
PC C1201/70, C1201/68;
CC strandedness: Single;
CC strandedness: Single;
CC typothetical: No;
CC anti-sense: No;
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/db_xref="taxon:32630"
/note="synthetic, no natural origin"
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Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 0;
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/db_xref="taxon:32630"
4 c 5 9 3 t
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Sequence 31 from Patent WO0014217.
AX023416
AX023416.1 GI:10183816
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Sequence 6 from Patent WO0071668.
AX052544 AX052544.1 GI:12226774
                                                                                                                           FUJINAGA KEI
C1201/70, C1201/68;
strandedness: Single;
topology: Linear;
hypothetical: No;
anti-sense: No;
Location/Qualifiers
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           Unclassified.

1 (bases 1 to 30)
Hinuma, S., Hosoya, M., Fujli, R., Ohtaki, T., Fukusumi, S. and Ohgi, K.
Hinuma, S., Hosoya, M., Fujli, R., Ohtaki, T., Fukusumi, S. and Ohgi, K.
G-protein coupled receptor protein and a DNA encoding the receptor Patent: US 611413-A 129 05-SEP-2000;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Daban, M., Espuna, E., Medrano, A., Querol and Enrique.
Daban, M., Espuna, E., Medrano, A., Querol and Enrique.
Transferrin-binding protein 1 (Tbp1) gene of Actinobacillus pleuropneumoniae, its use in vaccines for pleuropneumonia and as diagnostic reagents

Parent: Ep 0733708-A 6 25-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer for amplifying Human papillomavirus Sapporo gene.
E05267.1 GI:2173457
JP 1993192200-A/37.
synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 19)
DETECTION OF HUMAN PAPILLOMA VIRUS
PARENT: JP 1993192200-A 37 03-AUG-1993;
TAKARA SHUZO CO LTD
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Pred. No. 1.1e+04;
); Mismatches 1;
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83.3%; Pred. No. 1.4e+04;
ative 0; Mismatches 3;
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Other publication ES 2092960 961201
Other publication CA 2172443 960925.
Location/Qualifiers
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a 6 c 9 9
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Sequence 6 from Patent EP0733708.
A56687.1 GI:3712729
                                                                                                                           /organism="unknown"
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93.3%;
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Gaps

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Gaps

04-FEB-1998

PAT

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synthetic construct.
synthetic construct
artificial sequence.

1 (bases 1 to 42)
Huels,C., Muellner,S., Boehnisch,B. and Gallert,K.C.
Expression vector for the production of dead proteins
Patent: WO 9941390-A 1219-AuG-1999;
HUELS CHRISTOPH (DE); WILLIAER STEFAN (DE); AVENTIS RES & TECH GMBH
& CO (DE); BOEHNISCH BRITTA (DE); GALLERT KARL CHRISTIAN (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12; DB 10; Length 30 Pred. No. 6.9e+04; 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                             1 (bases 1 to 30)
Makarow,M.
Method for production of proteins in yeast
Patent: US 5677172-A 8 14-0CT-1997;
Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="pl35-NT5C"
a 13 c 6 g 11 t
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Sequence 6 from Patent EP 0334004.
108124
                                                                  169336 30 bp DNA
Sequence 8 from patent US 5677172.
169336 IC:2831458
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Sequence 12 from Patent W09941390.
AX019232
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Best Local Similarity 75.0
Matches 15; Conservative
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Unclassified.
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                                                                                     Method for identifying components involved in signal transduction pathways in higher plants
Patent: WO 0071668-A 30-NOV-2000;
The Board of Regents of the University of Nebraska (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L Patent: JP 1999137263-A 3 25-MAY-1999;

SMITHKLINE BEECHAM CORP, SMITHKLINE BEECHAM CORP PUBLIC LTD CO
OS Unidentified
PN 1999137263-A/3
PN 1999137263-A/3
PN 1999137263-A/3
PN 1999137263-A/3
PN 1999137263-A/3
PR 20-JUN-1999
PF 18-JUN-1999
PF 18-JUN-1999
PF 18-JUN-1999
PF 20-JUN-1999
PF 20-JUN-199
PF 20-JUN-1
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Pred. No. 4.1e+04;
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/organism - Unidentified'.
Location/Qualifiers
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/organism="synthetic construct"
//b_xref="taxon:32630"
/note="NCO1 Primer"
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/organism="unidentified"
/db_xref="taxon:32644"
a 7 c 1 g 1/
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E32827
E32827. G:13026860
JP 199137263-A/3.
unidentified.
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92.9%;
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synthetic construct
artificial sequence.
1 (bases 1 to 24)
Rhoades, D.M.
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Nicola, G.W.
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Best Local Similarity 92.9
Matches 13; Conservative
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11 TGGTTTCAAATCGG 24
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07-SEP-2000

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02-DEC-1994

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Score 11.8; DB 9; Length 24; Pred. No. 9e+04; 0; Mismatches 2; Indels

59.0%; 86.7%;

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Schweighoffer, F. and Tocque , B. Grb3-3 cDNA and polypeptides
Patent: US 5831048-A 9 03-NOV-1998;
Location/Qualifiers
                                                                     /organism="unknown"
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Matches 13; Conserv
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     Unknown.
Unclassified.
1 (bases 1 to 48)
Smith,J.A. and Lee,F-J.S.
Isolation, purification. characterization, cloning and sequencing of N alpha-acetyltransferase
Patent: EP 0334604.Al 6 27-SEP-1989;
Patent: EP 033400.Al filers
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Pred. No. 9e+04;
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**Synthetic construct
artificial sequence.
1 (bases 1 to 24)
Schweighoffer, F. and Tocque, B.
Schweighoffer, F. and Tocque, B.
GRB3-3 GENE, VARIANTS AND USES THEREOF
PATCH: WO 9507981-A 8 23-WAR-1995;
RHONE POULENC RORER SA (FR)
Other publication PL 313445 960708
Other publication FI 961202 960314
Other publication RA 2169938 950318
Other publication A 9407059 950318
Other publication A 9407059 950318
Other publication RY 950333
Other publication FI 961202 950318
Other publication RY 950333
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/organism="synthetic construct"
/db_xref="taxon:32630"
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Sequence 9 from patent US 5831048.
AR052465 GI:5975829
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Sequence 8 from Patent W09507981.
A43528 43528.1 GI:2298716
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86.7%;
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60d/b., Willis,M., Koch,T., Ringquist,S., Jensen,K. and Atkinson,B.
Systematic evolution of ligands by exponential enrichment: photoselection of nucleic acid ligands and solution selex. Patent: US 5763177-A 29 09-JUN-1998;
Location/Qualifiers
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Sequence 29 from patent US 5763177.
AR011952.1 GI:3969942
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Matches 13; Conservative
18 TGTTTGTTTCCACTC 32
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gb_est26;*
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17.508 Million cell updates/sec
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              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                               OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 50
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b_est4 b_est5 b_est5 b_est5 b_est5 b_est5 b_est5 b_est5 b_est5 b_est6 b_	9D_est62:* 9D_est63:* 9D_est66:* 9D_est66:* 9D_est75:* 9D_est77:* 9D_est77:* 9D_est81:* 9D_est81:*	est105 -est106 -est68:est68:est70:est71:est71:est73:est91:est108:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Anterston, R.
Waterston, R.
The WashU-HHMI Mouse EST Project
L Unpublished (1996)
Contact: Marra M/Mouse EST Project
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLML; contact the IMAGE.Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                   T 3']; double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                            /note="Organ: mammary gland; Vector: pr7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5, primer [5, primer]]
                                                                                                                                                                                                                                                                                                                                                                       Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 29)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZB38877 29 bp DNA GSS 20-FEB-2001
20134E10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0134E10 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000)
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Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                      Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/clone_lib="Soares_mammary_gland_NbWMG"
/sex="male"
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/dev_stage="4 weeks"
/lab_host="DH10B"
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    46
    /organism="Mus musculus"
    /strain="C57BL/6J"

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AZ768472 1M0568C10
AZ380625 1M0136G10
AL97861 T. brucei
AZ537263 AST-2P031
AZ537263 ANT-2P031
AZ537263 ANT-2P031
AZ537263 ANT-2P031
AZ537263 ANT-2P031
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Az77905 2M014121
A1446151 tj07e11.x
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AZ822425 2M0095M09
AI663836 uj06e03.x
AW537238 G0114A01-
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AZ803825 ZM0064124
AA079070 zm95a02.s
BE377955 601230133
AZ479665 1M0300D01
AZ791420 ZM0041014
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AZ819815 2M0091108
AA480235 T. brucei
AA115149 z1070409.r
AU108011 AU108011
AZ794281 2M0048C04
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AZ427281 1M0209H10
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AZ838877 2M0134E10
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AZ822833 2M0096J23
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Martra M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ350054 1M0087L18
AZ324675 1M0046A14
                                                                                                                                                                                                                                                                     AI783759 tu45d08.x
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IMAGE:1244230 5' similar to TR:002668 002668 INTER-ALPHA-INHIBITOR
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-FEB-1998
                                          Description
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         SUMMARIES
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AZ461904
AZ819815
TAZ20G01P
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TA379B06Q
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AA790759
AA790759.1 GI:2850879
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3 AZ427281
9 AZ762518
AI783759
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AZ803825
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AZ779056
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AU103004
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AZ350054
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249 AZ791420
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5 C02388
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/organism="Misculus"
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//db_xref="taxon:10090"
//clone_inbost="le"
//db_xref="taxon:10090"
//clone_inbost="le"
//db_bost="le"
//done_inbost="le"
//done_inbost="le"
//done_inbost="le"
//done_inbost="le"
//dote="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Labostaretry Wouse DNA Resource
//dote="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Labostaretry Wouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114[pilAth29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E.
2 coll XL10-Gold (Stratagene) cells
and selected for amplcillin resistance."
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Dunn,D., Aoyaqi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ380625 28 bp DNA GSS 02-OCT-2000 MINI 3601R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0136G10 R, DNA sequence. AZ380625
                        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 2.4e+04;
0; Mismatches 3; Indels 0
                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                          Insert Length: 10000 Std Error: (
Plate: 0568 row: C column: 10
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                             1. .30 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                            High quality sequence stop: 30.
Location/Qualifiers
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Unpublished (2000)
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Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (bases 1 to 30)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rosse,M., Rosse,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A2768472 30 bp DNA GSS 16-FEB-2001
1M0568C10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0568C10 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                         /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="lub-"Mouse lOkb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 12.2; DB 250; Length 29; Pred. No. 2.4e+04; 0; Mismatches 3; Indels 0.
                                                                                                                                                                                       Std Error: 0.00
                                                                                                                                                                                  Insert Length: 10000 Std Error: (
Plate: 0134 row: E column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                   University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                 High quality sequence stop: 29. Location/Qualifiers
                                                                                                                                                              Email: ddunn@genetics.utah.edu
Contact: Robert B. Weiss
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AZ768472.1 GI:12887815
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82.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 61.0
Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              house mouse.
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Aurora Biosciences Corp.

11010 Torreyana Road, San Diego, CA 92121, USA

Fax: 8584046719

Email: henkelg@aurorabio.com

pools of cells were isolated from a GenomeScreen(TM) library. The library of cells was generated by retroviral integration of a gene tagging element consisting of: 1) A promoterless beta-lactamase proceeded by a splice acceptor as a reporter for gene expression;
2) A promoter driving neomycin resistance followed by a splice donor to trap downstream exons. 3' RACE from neomycin gene was performed using total RNA from isolated pools. Output was shotun bacteria. 5' ends of reported sequences were immediately preceded by a splice donor from the trapping construct.
                                                                              Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Rockville, MD. Genomic DNA isolated from a cloned population of
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Osford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Henkel, G., Liyanage, M., Pratt, E., Huang, D., Riley, M., Bernardino, A., Durick, K. and Pollok, B.
Exon-trap tags from a PC-3 GenomeScreen(TM) Library Unpublished (2000)
Contact: Greg Henkel
Gene Expression
                                                                                                                                                                                                                                                                                                                                                    Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
  Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 40)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ537263 40 bp DNA GSS 06-NOV-2000 AZ57-2203160 Genetrap PC-3 Human Prostatic Carcinoma Library Homo sapiens genomic 5', DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.0%; Score 12; DB 258; Length 37; 75.0%; Pred. No. 3.2e+04; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Trypanosoma brucei"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:5691"
/clone="379b06"
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Best Local Similarity 75.0
Matches 15; Conservative
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerase and T4 polymerase and T4 polymerase to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 k range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qil4732114) plant29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampleillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                            1. 28
//organism=Mus musculus"
//strain="C57BL/6J"
//db_xref="caxon:10090"
//clone="UUGC1M0136G10"
//clone=lib="Mouse 10kb plasmid UUGC1M library"
//sex="Wale"
//lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
//note="Vector: PWIQ42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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T. brucei sheared genomic DNA clone 379bóf, reverse sequence,
genomic survey sequence.
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1 (bases 1 to 37)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S. E., Rajandream, M.A. and Barrell, B.G.

Direct Submission
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Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                     s. 2030
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Pred. No. 3e+04;
0; Mismatches 5; Indels
                                                                                                                             Rm. 308, Biomedical Polymers Research Bldg., 20 84112, USA
Tel: 801 585 5606
Exai: 801 587 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                            Plate: 0136 row: G column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Best Local Similarity 75.0%;
Matches 15; Conservative 0
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TA379B06Q/c
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AUTHORS
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                            g
                                                                                        /cell_type="Epithelial"
/cell_line="PC-3"
/note="Organ: Prostate; Vector: pAmp-1; 3' RACE of total
RNA from genetrap pools; shotgun clone in pAmp-1 and used
to transform DH5-alpha competent bacteria."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 43)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="lung"
/dev_stage="6-8 month old"
/lab_host="6-8 month old"
/lab_host="5OLR (kanamycin resistant)"
/note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI ; Site_2: Xhoi; Cloned unidirectionally. Primer: Oligo dr. 6-8 month old female lung and 1.5 year old male lung were source of mRNA. Average insert size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA895268 43 bp mRNA EST 06-APR-1998 vx49c02.rl Stratagene mouse lung 937302 Mus musculus cDNA clone lung 1278530 5' similar to TR:002754 002754 C/EBP ALPHA PROTEIN.; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:670330
                                                                                                                                                                                                                                                                                                                                                          Gaps
/db_xref="taxon:9606" /clone_lib="Genetrap PC-3 Human Prostatic Carcinoma
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0
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Contact: Marra M/Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fat: 314 286 1810
                                                                                                                                                                                                                                                                                                      60.0%; Score 12; DB 245; Length 40; 75.0%; Pred. No. 3.3e+04; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 revl ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:1278530"
/clone_lib="Stratagene mouse lung 937302"
                                                                       /tissue_type="Adenocarcinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="C57BL/6 x CBA"/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA895268.1 GI:3031687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                      1 tgttggtttccaatcggacc 20
                                                                                                                                                                                                                                                                                                                                                                                                                            5 TGTTGATTTCCACTGAAACC 24
                                                                                                                                                                                                                                                                                                      Query Match 60.0 Best Local Similarity 75.0 Matches 15; Conservative
                                              Library
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ORIGIN
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AA895268/C
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KEYWORDS
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JOURNAL
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SOURCE

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//noce="Vector: PWD42TUF, ALTIFIED GROWN TOOM From M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource of the from the Jackson Laboratory Mouse DNA Resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114) gblazh129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 43)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A2319753 43 bp DNA GSS 29-SEP-2000 HIM0039B02R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0039B02 R, DNA sequence. A2319753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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                                                                                                                                                                                                                            Gaps
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adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 12\ c 14\ g 5\ t
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/db_xref="taxon:10090"
/clone="UGGIM0039B02"
/scone_lib="Mouse 10kb plasmid UGGIM library"
/sex="Male"
                                                                                                                                                           Length 43;
                                                                                                                                                                                                                            Indels
                                                                                                                                                           Score 12; DB 13; L
Pred. No. 3.3e+04;
O; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0039 Tow: B column: 02
Seg primer: CAOACAGGAAACAGCTATGACC
Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                           60.0%;
75.0%;
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                                                                                                                                                           Query Match 60.0
Best Local Similarity 75.0
Matches 15; Conservative
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Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                house mouse.
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// Arcte="Vector: PWAZIVY; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (q1473211419blAR129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
1 (bases 1 to 19)

Unun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.0%; Score 11.8; DB 241; Length 19; 86.7%; Pred. No. 3.6e+04;
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0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                         Std Error: 0.00
                                                                                                                                                                                                                                                                                                               Email: ddunn@enetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0050 row: L column: 09
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="C57BL/6J"
/db_xref="taxon:10090"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                        Class: plasmid ends
                                                                                                                                                Unpublished (2000)
                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
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Matches 13; Conserv
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AZ822425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan 4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan Suzukieli ysuzukielims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance." 11\ c 13\ g \ t \ t
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AU107355 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CASO7628, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                            Length 43;
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                                                                                                                          Score 12; DB 241;
Pred. No. 3.3e+04;
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/db_xref="taxon:9606"
/clone="CAS07628"
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AU107355.1 GI:13556876
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                                                                                                                          60.0%;
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                                                                                                                                           Best Local Similarity 75.0
Matches 15; Conservative
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Matches 15; Conservative
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                                       BASE COUNT
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KEYWORDS
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Gaps

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/note="Organ: liver; vector: pME18S-FL3; Site_1: DraIII (CACCATGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). Also should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAAGCTGCG and 3' end
                                                                               Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Moderwood, K., Steptoe, M., Thelsing, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Other_ESTs: uj06e03.yl
                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: custon primer used
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Washu-NCI Mouse EST Project 1999
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="IMAGE:1891132"
/clone_lib="Sugano mouse liver mlia"
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/organism="Mus musculus"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="female"
/dev_stage="adult"
/lab_host="DH10B"
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92.3%;
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Matches 12; Conservative
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           Mus musculus
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AW537238/c
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AUTHORS
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114[gb]AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 27)
Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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/clone="UUGC2M0095M09"
/clone_llb="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 11.6; DB 250; Length 27;
Pred. No. 5e+04;
0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                      Rm. 308, Biomedical Polymers Research Bldg., 20
84112, USA
                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Emall: ddunnegenetics.utah.edu
lnsert Length: 10000 Std Error: 0.00
Plate: 0095 row: M column: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: 0095 row: M column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                   Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 27. Location/Qualifiers
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AI663836.1 GI:4767419
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77.8%;
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Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                                plasmid inserts
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Indels

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/dev_stage="45 years old"
/dev_stage="45 yea
                                                                                                                                                                                                           Email: cgapDs-remail.nin.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
Michael Brumert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 43)
Dunn,D., Aoyaqı,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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AMO056J23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCZM0096J23 F, DNA sequence.
AZ822833
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 40)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP https://www.ncbi.nlm.nih.gov/ncicgap.
Tunional Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tunior Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.0%; Score 11.2; DB 10; Length 40; 81.2%; Pred. No. 8.9e+04; ive 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trace considered overall poor quality Insert Length: 1233 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1188909"
                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ822833.1 GI:12992741
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III, Becker,K.G. and Ko,M.S. H. Genome-wide expression profilling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="7".5dpc Embryo"
/lab_host="DH10B"
/note="Vector: pSPORT1 (Gibco/BRL Life Technology);
Site_1: Shl; Site_2: Not1; Total RRAs were extracted from 6 Embryo. The double-stranded cDNA was synthesized by Gibco's kit with an Oligo(dT) primer [Not1 primer-adapter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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similar to TR:G1712 G1712 RETROVIRUS RELATED REVERSE TRANSCRIPTASE
confidants L1.tl L1 repetitive element ;, mRNA sequence.
AA652673.1 G1:2584325
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/sex="unknown"
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                                                                                                                                                                                                                                                              Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdnad[gsun.grc.nia.nih.gov
Plate: G0114 row: A column: 01
Seq primer: -21M13 Forward
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Pred. No. 7.3e+04;
0; Mismatches 1; Indels 0
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="G0114A01"
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                                                                                                                                                                                                                                              Contact: George J. Kargul
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92.3%;
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Gaps

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plasmid inserts
Unpublished (2000)
Context: Roberts B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0096 row: J column: 23
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male" rouse two presents continues;
//sex="Male" rouse two presents continues;
//lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
//note="Vector: PWD42Nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 luch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated for a 9.5 to
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 Nb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .43
/organism="Mus musculus"
/strain="C57BL/6J"
/db.xref="taxon:10090"
/clone="UUGC2M0096J23"
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completed: October 2, 2001, 15:01:04 Search comp Job time: 1

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AR100356 Sequence
AR012663 Sequence
129403 Sequence 27
191077 Sequence 27
119158 Sequence 21
AR022673 Sequence
129413 Sequence 28
191087 Sequence 28
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AR032663
I29403
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                                                       Search time 3339.34 Seconds (without alignments) 92.640 Million cell updates/sec
                                                                                                                                                                                     423528
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                  1344157 seqs, 7733874588 residues
                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                        October 2, 2001, 15:56:49;
                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                     OM nucleic - nucleic search, using sw model
                                                                                                               1 ctaggggaggctcagtgtgg 20
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 50
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Perfect score:
                                                                                                                                     Scoring table:
                                                                                                                   Sequence:
                                                                                                                                                                  Searched:
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29-SEP-1999

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1 (bases 1 to 47)
Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E. Sequence-directed DNA-blnding molecules compositions and methods Patent: US 5578444- 275 26-NOV-1996;
Location/Qualifiers
                                                                                     I (bases i to 47)
Edwards, C.A., Cantor, C.R., Andrews, B.M., Turin, L.M. and Fry, K.E. Method of determining DNA sequence preference of a DNA-binding molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unknown.
Unclassified.
1 (bases 1 to 47)
Edwards, C.A., Cantor, C.R., Andrews, B.M. and Turin, L.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 47;
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Pred. No. 4.8e+04;
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Pred. No. 4.8e+04;
0; Mismatches 3;
                                                                                                                                 Patent: US 5869241-A 275 09-FEB-1999;
Location/Qualiflers
                                                                                                                                                                                                                                                                                                    Sequence 275 from patent US 5578444.
122403
122403.1 GI:Jaɔハュɔ׳
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             AR032663 47 bp DNA
Sequence 275 from patent US 5869241.
AR032663
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Sequence 275 from patent US 5726014.
191077
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15 c 13 g
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                                                AR032663.1 GI:5948268
                                                                                                                                                                                                             66.0%;
83.3%;
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Best Local Similarity 83.3°
Matches 15; Conservative
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                  106858 Sequence 2
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X60852 M.musculus
AR050776 Sequence
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143986 Sequence 77
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AR036267 Sequence
AX037078 Sequence
AR101978 Sequence
                                                                                                                                                                                                                                                                                      AX001457 Sequence
AR063468 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 20)
Baker, B. F., Bennett, C. Frank, Butler, M. M. and Shanahan, W. R. Jr., Antisense oligonucleotide modulation of tumor necrosis factor. alpha. (TWF. alpha.) expression Patent: US 6080580-A 87 27-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                        14-FEB-2001
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143985
S80775
AX096203
AR100568
119159
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AR050776
AR050777
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AX023341
AX061521
A23243
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AR040876
AR068407
AR068408
AR075847
AS1622
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E08692
AR021123
AR036267
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AR101978
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I43986
AX001457
AR063468
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3 c 9 g
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AR100356
AR100356.1 GI:12810804
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83.3%;
 Query Match 66.0
Best Local Similarity 83.3
Matches 15; Conservative
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AR100356
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BASE COUNT ORIGIN

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KEYWORDS

AR100356

AUTHORS TITLE

JOURNAL

FEATURES

REFERENCE

TITLE JOURNAL

FEATURES

BASE COUNT

ORIGIN

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Unclassince.

I (bases 1 to 47)

Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E. Sequence-directed DNA-binding molecules compositions and methods Patent: US 5578444-A 285 26-NOV-1996;

Location/Qualifiers
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Edwards,C.A., Cantor,C.R., Andrews,B.M. and Turin,L.M.
Screening assay for the detection of DNA-binding molecules
Patent: US 5726014-A 285 10-MAR-1998;
Location/Qualifiers
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Best Local Similarity 87.5%; Pred. No. 7.6e+04;
Matches 14; Conservative 0; Mismatches 2;
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Sequence 285 from patent US 5726014.
191087 191087.1 GI:3935557
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Sequence 285 from patent US 5578444.
129413
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Sequence 2 from patent US 5851529.
AR066591 GI:5997813
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87.5%;
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8 AGGGAAGGCTCAGTAT 23
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AR066591/c
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Edwards.C.A., Cantor.C.R., Andrews.B.M., Turin.L.M. and Fry.K.E. Bedwards.C.A., Cantor.C.R., Andrews.B.M., Turin.L.M. and Fry.K.E. Method of determining DNA sequence preference of a DNA-binding molecule
molecule
Patent: US 5869241-A 285 09-FEB-1999;
Location/Qualifiers
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Screening assay for the detection of DNA-binding molecules Patent: US 5726014-A 275 10-MAR-1998; Location/Qualifiers
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64.0%; Score 12.8; DB 9; Length 47;
Best Local Similarity 87.5%; Pred. No. 7.6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels
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Pred. No. 4.8e+04;
0; Mismatches 3;
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64.0%; Score 12.8; DB 10;
Best Local Similarity 87.5%; Pred. No. 8.4e+04;
Matches 14; Conservative 0; Mismatches 2;
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Tenen, D.G., Pahl, H.L. and Burn, T.C.
Myeloid cell specific promoter
Patent: US 5502176-A 21 26 MAR-1996;
Location/Qualifiers
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119158
119158.1 GI:1599513
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13 c 5 g
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15 c 12 g
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15 c 13 g
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Best Local Similarity 83.3%;
Matches 15; Conservative
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1 ctaggggaggctcagtgtg 19
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29 CTAGGTGAGACTCATTGAG 11
 I06858
I06858.1 GI:589980
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Best Local Similarity 78.9
Matches 15; Conservative
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AR080756/c
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LOCUS
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21-MAK-1988 U70.515
HALLEY E GRABAR, DOUGLAS J JOLY, JAMES G RESPESU, PAUL K REIKAIND
C12N15/09, A01K67/027, A61K31/00, A61K31/00, A61K35/12, A61K35/76,
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C12N5/10,C12N7/00,C12P21/00//(C12P21/00,C12R1:91),C12N15/00,
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     Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 28)
Guber.H.E., Johly, D.J., Respess, J.G. and Laikind, P.K.
Recombinant retroviruses
Patent: US 5851529-A 2 22-DEC-1998;
Locaton/Qualifiers
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Pred. No. 1.1e+05;
0; Mismatches 4; Indels (
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    .28
    /organism='Artificial Sequence'

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Sequence 2 from Patent EP 0334301.
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/organism="unidentified"
/db_xref="taxon:32644"
                                                                                                  /organism="unknown"
13 c 3 g
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E37410.1 GI:13023106
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78.9%;
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22 TGGGGAGGCTAACTGAGG 4
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Best Local Similarity 78.9
Matches 15; Conservative
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Virus resistant transgenic plants comprising cells transformed with a polynucleotide encoding a potyviridae Pl protein or Pl protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 32) Pehu,E., Pehu,T., Maki-Valkama,T., Valkonen,J., Koivu,K. and
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Pehu, E., Pehu, T., Maki-Valkama, T., Valkonen, J., Koivu, K. and Lehto, K.
Virus-resistant transgenic plants
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1 (bases 1 to 28)
Gruber, H. E., Jolly, D.J., Respess, J.G. and Laikind, P.K.
Recombinant retroviruses
Patent: Bp 0334301-A1 2 27-SEP-1989;
Location/Qualifiers
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Pred. No. 1e+05;
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Sequence 2 from patent US 5968828.
AR080756 GI:10007486
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Sequence 2 from patent US 5576202.
I28948.
I28948.1 GI:181077
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B. (bases 1 to 42)

S. (bases 1 to 42)

G. (bases 1 to 42)

F. (bases 1 to 42)

Noffman, W.L. and Modlin, R.L.

Microanatomic clonality of gamma delta T cells in human leishmaniasis lesions

L. J. Immunol. 148 (4), 1205-1211 (1992)

E. 92148143

E. 92148143

F. (From the National Library of Medicine created this entry [NCBI gibbsq 80775] from the original journal article.

This sequence comes from Figure 4.
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S80775.1 GI:244965
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Lonberg, N. and Kay, R.M.
Transgenic non-human animals capable of producing heterologous antibodies
Patent: US 5633425-A 76 27-MAY-1997;
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Patent: US 5576202-A 2 19-NOV-1996;
Location/Qualifiers
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Sequence 76 from patent US 5633425.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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mRNAS using full-length enriched and 5'-end enriched cDNA libraries JOURNAL Unpublished (2001) COMMENT Contact: Yutaka Suzuki Department of Virology Institute of Madical Science, University of Tokyo 4-6-1. Shirokanedai Minatcku. Tokyo 108-8639. Janan	Email: Suzuki ,S.Co a 5'-e	7 t. DB 107; Length 50 .7e+04; es 3; Indels	RESULT 2 AU107336 LOCUS LOCUS LOCUS DEFINITION AU107336 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone LNG11142, mRNA sequence. ACCESSION AU107336 VERSION AU107336.1 GI:13556857 KEYWORDS EST. SOURCE Numan. ORGANISM Homo sapiens Craniata: Vertebrata: Euteleostom1:	REFERENCE (Dases 1 to 50) AUTHORS Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tainaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S. TITLE Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA librarles JOURNAL Contact: Yutaka Suzuki Conmact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo	4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuukifains.u-Cokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano ,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).  FEATURES Location/Qualifiers Source //organism="Homo sapiens" //db_xref="taxon:9606"	/clone_lib="Sugano Homo sapiens cDNA library"  /clone_lib="Sugano Homo sapiens cDNA library"  ORIGIN  Query Match  Best Local Similarity 83.3%; Pred. No. 3.7e+04;  Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  Qy 1 ctaggggaggctcagtgt 18
SUMMARIES Query Match Length DB ID	1 13.2 66.0 50 107 AU107335 3 12.2 66.0 50 107 AU107336 4 12.6 63.0 46 102 AI809473 5 12 60.0 42 245 AA498822 6 12 60.0 42 245 AA498822 7 11.8 59.0 21 247 AZ660221 9 11.8 59.0 50 107 AU105603	11.8 59.0 50 107 AUT05605 11.8 59.0 50 107 AUT05606 11.6 58.0 20 243 AZ47155 11.6 58.0 26 258 TA91B03P 11.6 58.0 42 167 BE386700 11.6 58.0 43 13 AA933260 11.6 58.0 47 139 BE738401 11.6 58.0 48 139 BE738401 11.6 58.0 48 139 BE738424 11.6 58.0 50 107 AUT06034	23 11.4 57.0 31 24 11.4 57.0 36 25 11.4 57.0 36 27 11.2 56.0 24 28 11.2 56.0 24 30 11.2 56.0 41 31 11.2 56.0 41 31 11.2 56.0 41 32 11.2 56.0 43 33 11.2 56.0 43 34 11.2 56.0 43	35 11 55.0 35 258 TALT7A10Q 36 11 55.0 37 13 AA033928 37 11 55.0 41 244 AA470576 39 11 55.0 42 243 AA470576 40 11 55.0 42 243 AA440678 41 11 55.0 44 128 H22874 42 11 55.0 49 251 AA313961 43 11 55.0 49 251 AA313961 44 11 55.0 50 107 AU106627 45 10.8 54.0 19 249 AZ775541	ALIGNMENTS 50 bp mRNA EST Sugano Homo sapiens cDNA library Homo	156  Chordata; Craniata; Vertebr Primates; Catarrhini; Homin; Homin; Taira,H., Mizushima-Suga Pr., Tanaka,T., Nakamura,Y., yano,S.

DEFINITION

AZ826713

RESULT

ACCESSION

VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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M.D., Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Greg Lennon, Ph.D. DNA Sequencing Warhington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n2498822 42 bp DNA GSS 05-OCT-2000 IM036117F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0336117 F, DNA sequence. AZ498822 G:10677034 GSS.
                                                                                                 wh76cl0.xl NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2386674 3' similar to TR:Q40402 Q40402 EXTENSIN; mRNA sequence.
                                                                                                                                                                                                                                                                                              Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 46)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Emall: cgapbs rfemall.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 46
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 33)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, M., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A.
                                                                                     A2826713 33 bp DNA GSS 20-FBB-2001
2M0102H12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0102H12 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Male"
/lab.host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dmail: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0102 row: H column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
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/clone="UUGC2M0102H12"
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High quality sequence stop: 33.
Location/Qualifiers
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Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                             house mouse.
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Gaps

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BASE COUNT ORIGIN

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JOURNAL COMMENT

TITLE

FEATURES

REFERENCE

SOURCE

AUTHORS

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (qi|q'32114|qb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I base; I to 48)

Dunn, D., Aoyai, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 084112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ660221 21 bp DNA GSS 14-DEC-2000 MD538M09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0538M09 F, DNA sequence.
AZ66021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/G3 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
Email: ddun@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0113 row: P column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/organism="Mus musculus"
/strain="C57BL/6J"
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/clone="UUGC2M0113P15"
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Location/Qualifiers
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                            house mouse.
                                                               Mus musculus
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Best Local Similarity
Matches 15; Conserv
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COMMENT
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                                                                                                                                                  REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerase at T4 polymerase and T4 polymerase at T4 polymerase and T4 polymerase to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114 gblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (asses 1 to 42)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                                                                                                            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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2M0113P15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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/db xref="taxon:10090"
/clone="UGGCIM0336I17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@enetics.utah.edu
Commert Length: 10000 Std Error: 0.00
Plate: 0336 row: I column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends

    .42
    /organism="Mus musculus"

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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 42.
Location/Qualifiers
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Best Local Similarity 75.08
Matches 15; Conservative
                               Mus musculus
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SOURCE

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COMMENT

TITLE

VERSION KEYWORDS

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Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S. See, J., Hata, K., Suyama, A. and Sugano, S. Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).
                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Cta,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S. Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                                                                                                      AU105603 50 bp mRNA EST 05-APR-2001
AU105603 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HSIO0510, mRNA sequence.
AU105603. GI:13555124
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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11 c 20 g 11 t
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Pred. No. 1.7e+05;
0; Mismatches 2; Indels 0
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/clone="HSI00510"
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AU104075.1 GI:13553596
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86.7%;
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with TH DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pm/2 (gil4722114 gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. Coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                          plasmid inserts
Unpublished (2000)
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (21)
Dunn,D., Aoyal,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="MugC1M053BM09"
/clone=lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/sex="Male"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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Pred. No. 1.6e+05;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0538 row: M column: 09
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 21. Location/Qualifiers
AZ660221.1 GI:11797367
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Fax: 801 585 7177
Email: ddunn@qenet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 59.0
Best Local Similarity 86.7
Matches 13; Conservative
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Source

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Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata, H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo, K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
Contact: Yutaka Suzuki
Department of Virology Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y. Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 50)

Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata

H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo

K., Suyama, A. and Sugano, S.
Fine Structural analysis of transcription start sites of human

mRNAs using full-length enriched and 5'-end enriched cDNA libraries

IL Unpublished (2001)

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Makagawa, K., Maruyama, K., Suyama, A. and Sugano

Suzuki, Y., Yoshitomo-Makagawa, K., Maruyama, K., Suyama, A. and Sugano

Suzuki, Y., Yoshitomo-Makagawa, K., Maruyama, K., Suyama, A. and Sugano

Suzuki, Y., Yoshitomo-Makagawa, K., Maruyama, K., Suyama, A. and Sugano

Suzuki, Y., Yoshitomo-Makagawa, K., Maruyama, K., Suyama, A. and Sugano

Suzuki, Y., Yoshitomo-Makagawa, K., Maruyama, K., Suyama, A. and Sugano

Socandariched cDNA library, Gene 200 (1-2), 149-156 (1997).
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AU105606 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
AU105606 AU20612, mRNA sequence.
AU105606 GI:13555127
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Pred. No. 1.7e+05;
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/clone="HSI06872"
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Suzukitute of Medical Science, University of Tokyo
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
'S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Suzuki,Y., Tsunoda,T., Talra,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
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AU105605 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HSI05558, mRNA sequence.
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AU105604 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HSI01710, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.7e+05;
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/db_xref="taxon:9606"
/clone="HSI01710"
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13-DEC-2000

SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

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DEFINITION A2417155/c

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VERSION KEYWORDS

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Constructed at the Institute for Genomic Research (TIGR), Constructed at the Institute for Genomic Research (TIGR), Constructed at the Institute for Isolated from a cloned population of Trypanosoma brucei (TRE927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trypanosoma.

1 (bases 1 to 26)

Hall, N. Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucel genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 LSA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T95881 40 bp mRNA EST 27-MAR-1995
Ye47b02.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:120843 3' similar to gb|M87923|HUMALCE12 Human carcinoma
cell-derived Alu NRA transcript, (rRNA); gb:M57627 INTERLEUKIN-10
PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                 A91B03P 26 bp DNA GSS 13-DEC-200 . brucei sheared genomic DNA clone 91b03, forward sequence,
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Pred. No. 2e+05;
); Mismatches 4; Indels 0;
Indels
  4
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Mismatches
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Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114 qiplaF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
                                                                                                                                                                                                                    AZ417155 20 bp DNA GSS 03-OCT-2000
1M0192P07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0192P07 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus G57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0192 row: P column: 07
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0192P07"
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Location/Qualifiers
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77.8%;
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Fax: 801 585 7177
                       5 gggaggctcagtgtg 19
                                                       40 GGGAGCCTCATTGTG 26
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                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
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Best Local Similarity
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FEATURES

BASE COUNT

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                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: st@watson.wustl.edu
Insert Size: 2754
Source: IMAGE Consortium, LLNL This clone is available royalty-free
through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov)
Insert information: Trace considered overall poor quality
Insert Length: 2754 Std Error: 0.00
1 (bases 1 to 40)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hullman,M., Kucaba,T., Leh.M., Lennon,G., Marra,M., Parsons,J., R. Ifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The Washu-Warck EST Project
Conpublished (1995)
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/organism="Homo sapiens"
/db_xref="GDB:47338"
/clone="IMAGE:120843"
/clone_lib="Soares fetal liver spleen lNFLS"
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High quality sequence stop: 1.
Location/Qualifiers
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|| || || || || || || 21 CTTNNGGAGGCTGAGGGGGG 2
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Matches 14; Conserv
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Search completed: October 2, 2001, 15:01:06 Job time: 10835 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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gb_in4:*
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                                                                                   October 2, 2001, 15:56:49; search time 3339.34 Seconds (without alignments) 92.640 Million cell updates/sec
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                     1344157 segs, 7733874588 residues
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Maximum Match 100%
Listing first 45 summaries
                                                             OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 50
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Perfect score:
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AR012105 Sequence AR014544 Sequence AR059098 Sequence M96133 Human hybri A73580 Sequence 4 AR0770795 Sequence Z50819 H.saplens m

AR012105 AR014544 AR059098 HUMTCIGC1A A73580

AR067419 AR070795 HSCD85706

Description

SUMMARIES

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HUMTCIGCIA 46 bp DNA PRI 13-JAN-1995 Human hybrid T cell receptor/immunoglobulin protein, clone 1 V-D-J segment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                         1 (bases 1 to 40)
Sukhatme, V.P.
Methods and materials relating to the functional domains of DNA binding proteins
Patent: US 5773583-A 52 30-JUN-1998;
Location/Qualifiers
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                   05-DEC-1998
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Location/Qualifiers
                                                                                                                                                                                                   76.0%; Score 15.2; DB 9; Length 40; 85.0%; Pred. No. 4.6e+04; ive 0; Mismatches 3; Indels
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                    PAT
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M96133.1 GI:339188
Trcell receptor/immunoglobulin protein.
Homo sapiens DNA.
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US 5837854.
                            US 5773583
                                                                                                                                                       /organism="unknown"
14 c 13 g
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7 c 4 g
                  AR014544 40 bp
Sequence 52 from patent
AR014544
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Sequence 16 from patent
AR059098
AR059098.1 GI:5984675
                                              AR014544.1 GI:3971998
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84.2%;
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Mulder, C.
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Matches 16; Conservative
                                                                                 Unclassified.
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Matches 17; Conserv
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AR059098/c
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E0474 Synthetic D
AR090975 Sequence
AR050042 Sequence
AR064551 Sequence
AR013956 Sequence
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AR108637 Sequence
AR058955 Sequence
AR105229 Sequence
AX098901 Sequence
AX099321 Sequence
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AR103323 Sequence
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AR078900 Sequence
AR106304 Sequence
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AR051920 Sequence
AR049382 Sequence
AR095543 Sequence
A83263 Sequence
                                               I25076 Sequence 3
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125985 Sequence 2
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AX044085 Sequence
AX044138 Sequence
AX044178 Sequence
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AR068600 Sequence
AR095952 Sequence
                                                                A82991 Sequence 1
A82993 Sequence 3
                                                                                 AX027268 Sequence
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Sukhatme, V.P.
Methods and materials relating to the functional domains of DNA
binding proteins
Patent: US 5763209-A 52 09-JUN-1998;
Location/Qualifiers
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Pred. No. 4.6e+04;
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85.0%; Pred
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Sequence 52 from patent
AR012105
AR012105.1 GI:3970095
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Best Local Similarity 85.0
Matches 17; Conservative
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DEFINITION ACCESSION VERSION

KEYWORDS

ORGANISM

AUTHORS TITLE JOURNAL

REFERENCE

RESULT 1 AR012105/c

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BASE COUNT ORIGIN

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1 (bases 1 to 26)
Brunker, P., Minas, W., Kallio, P. and Bailey, J.E.
Methods and compositions for increasing production of erythromycin
Patent: US 5908764-A 2 01-JUN-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                  1 (bases 1 to 18)
Heym, B., Cole, S., Young, D., Zhang, Y., Honore, N., Telenti, A. and
                                                                   Gaps
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Rapid detection of antibiotic resistance in mycobacterium
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                                       Length 32;
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Pred. No. 3.5e+05;
0; Mismatches 1; Indels
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                                    68.0%; Score 13.6; DB 9; 70.0%; Pred. No. 2.4e+05; Live 2; Mismatches 4;
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د
                                                                                                                                                                                                                                                                                                                               Tuberculosis
Patent: US 5851763-A 16 22-DEC-1998;
Location/Qualifiers
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Sequence 16 from patent US 5851763.
AR067419.1 GI:5998641
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AR070795
AR070795.1 GI:7221683
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/organism="unknown"
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Best Local Similarity 70.0
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Best Local Similarity 93.3
Matches 14; Conservative
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1 (bases 1 to 46)
Kobayashi,Y., Tycko,B., Soreng,A.L. and Sklar,J.
Transrearrangements between antigen receptor genes in normal human
Transrearrangements and in ataxia telangiectasia
J. Immunol. 147 (9), 3201-3209 (1991)
92013154
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unclassified.

E 1 (bases 1 to 32)

S Nemeth.E.F. and Brown.E.M.

CALCIUM RECEPTOR ACTIVE MOLECULES

AAL PATENT: WO 9418959-A 4 01-SEP-1994;

BRIGHAM & WOMENS HOSPITAL (US); NPS PHARMA INC (US)

Location/Qualifiers

.""nidentified"

7 others
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Pred. No. 1.8e+05;
0; Mismatches 2;
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/organism="Homo sapiens"
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Sequence 4 from Patent W09418959.
A73580 GI:6064168
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'note="G00-118-731"
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/note="G00-120-406"
                                                                           Location/Qualifiers
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/note="G00-120-406"
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/map="14q11.2"
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/gene="TCRD"
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88.2%;
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Best Local Similarity 88.2
Matches 15; Conservative
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artificial sequence.
1 (bases 1 to 23)
Hawkes, T.R., Warner, S.A., Andrews, C.J., Bachoo, S. and
Pickerill, A.P.
Herbicide resistant plants
Patent: WO 0066746-A 30 09-NOV-2000;
ZENECA LIMITED (GB)
                                                                                                                                                                                                                                                                                                                                                                                                synthetic construct
artificial sequence.
1 (bases 1 to 23)
Hawkes,T.K., Marner,S.A., Andrews,C.J., Bachoo,S. and Pickerill,A.P.
                                                                                                            65.0%; Score 13; DB 9; Length 23; 100.0%; Pred. No. 4.8e+05; tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 4.8e+05;
iive 0; Mismatches 0;
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer"
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/db_xref="taxon:32630"
/note="Primer"
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/Organiam="synthetic construct"
//Organiam="synthetic construct"
//Note="primer" / C 5 g 6 t
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Patent: WO 0066747-A 38 09-NOV-2000;
ZENECA LIMITED (GB)
LOCATION/QUALIFIERS
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Sequence 38 from Patent WO0066747.
AX044138 GI:11343016
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Sequence 30 from Patent WO0066746.
AX044178 GI:11343056
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Matches 13; Conserv
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AX044178/c
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo.
Wang, E. C., Moss, P. A., Frodsham, P., Lehner, P.J., Bell, J.I. and
Borysiewicz, L.K.
Oligoclonal CD8+, CD57+ T cells in normal, healthy individuals and
Unpublished
                                                                                         250819.1 GI:1004241
constant region; joining region; T cell receptor; variable region.
                                                                                                                                                                                                                                                                                                           Wang, E.C.

Submission

Submitted (17-AUG-1995) Eddie CY Wang, Medicine, University of Wales of College of, Medicine, Heath Park, Cardiff, South Glamorgan, CF4 4XN, Wales UK

3 (bases 1 to 39)

Wang, E.C., Moss, P.A., Frodsham, P., Lehner, P.J., Bell, J.I. and Borystewicz, L.K.

CD8highCD57+ T lymphocytes in normal, healthy individuals are oligocional and respond to human cytomegalovirus

J. Immunol. 155 (10), 5046-5056 (1995)
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artificial sequence.
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Hawkes, T.R., Warner, S.A., Andrews, C.J., Bachoo, S. and Pickerill, A.P.
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                                HSCD85706 39 bp mRNA PRI
H.sapiens mRNA for T cell receptor (ID CD85706).
Z50819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism-"Homo sapiens"
/isolate-"FW"
/db_xref-"taxon:9606"
1. 12
/note-"end T cell receptor V beta 24"
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Pred. No. 2.7e+05;
0; Mismatches 1;
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/note="beginning J beta 2.5"
9 a 11 c 15 g 4 t
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Patent: WO 0066748-A 40 09-NOV-2000;
ZENECA LIMITED (GB)
Location/Qualifiers
1. .23
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Sequence 40 from Patent WO0066748.
AX044085.1 GI:11342963
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93.3%;
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Matches 14; Conservative
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/note="Cl
25. .39
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19 CCTCTCTGCTGGTGG 5
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HSCD85706/c
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Kawasaki, H., Tsuchiya, M., Miwa, K. and Kawahara, Y.
Coryneform bacteria deficient in a cell surface protein
Patent: US 5547864-A 3 20-AUG-1996;
Location/Qualifiers
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                                                                                                       63.0%; Score 12.6; DB 9; Length 20; 78.9%; Pred. No. 7.5e+05; ive 0; Mismatches 4; Indels
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Kawasaki, H., Tsuchiya, M., Miwa, K. and Kawahara, Y.

DNA encoding novel cell surface protein

Patent: US 5681717-A 3 28-0cT-1997;

Location/Qualifiers
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Sequence 3 from patent US 5681717.
171129
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Sequence 3 from patent US 5547864.
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/organism="unknown"
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/organism="unknown"
a 9 c 7 g
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Location/Qualifiers
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|1 TTCATCGCTGTCGGCA 19
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125076.1 GI:1604946
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Matches 15; Conservative
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125076
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                                                                                                                                                                                                                                                                                                                                                                                   A functional link for major TCR expansions in healthy adults caused by persistent Epstein-Barr virus infection J. Cilin. Invest. 102 (8), 1551-1558 (1998)
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1 (bases 1 to 20)
Bennett,C.Frank, Ackermann,E.J. and Cowsert,L.M.
Antisense modulation of X-linked inhibitor of apoptosis expression
Patent: US 6087173-A 43 11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (12-PEB-1998) Silins S.L., Queensland Institute of
Medical Research, The Bancroft Centre, 300 Herston Road, Brisbane,
                                                                                                                                                                    HSA224214 48 bp mRNA PRI 23-FEB-2001 HOMO Sapiens mRNA for T cell receptor beta chain V-D-J junctional region (TCRBV6BJ1S5).
                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 48)
Silins,S.L., Cross,S.M., Krauer,K.G., Moss,D.J., Schmidt,C.W. and
                                                           Gaps
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T cell receptor; T cell receptor beta chain; variable region
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                           Length 23;
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/organism="Homo sapiens"
/dbalotype="A1, A3, B8, B35"
/cell_line="JS11"
/cell_type="cytotoxic T lymphocyte"
/issue_type="blood"
/rearranged
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                        Query Match 65.0%; Score 13; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 4.8e+05;
Matches 13; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 13; Conservative 0; Mismatches 0;
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Sequence 43 from patent US 6087173.
AR103323
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Silins, S.L.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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gb_gss20: gb_gss21: gb_gss22:

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R. TITLE The Wash U-HHMI Mouse EST Project JOURNAL Unpublished (1996)	COMMENT CONTECT: Marra M/Mouse EST Project Washington University School of MedicineP Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.	MGI:636622  Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1. FEATURES Location/Qualifiers 1 .37 /organism="Mus musculus" /strain="C57BL/6J" //organism="Mus musculus" //clone="Tamare: 10090"	/clone_lib="Soares_mammary_gland_NbMMG" /sex="male" /tissue_type="mammary gland" /dev_stage="4 weeks" /lab_host="DH10B" /note="Organ: mammary gland; Vector: pT773D-Pac (Pharmacia ) with a modified polylinker; Site_l: Not I; Site_2: Eco RI; lst strand cDNA was primed with a Not I - oligo(dT) primer [5'	T3'j; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima BASE COUNT 10 a 14 c 7 g 6 t	Query Match 76.0%; Score 15.2; DB 11; Length 37; Best Local Similarity 85.0%; Pred. No. 4.6e+03; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy 1 attcctcgctgctggggaa 20 Qy 1 attcctcgctgctggggaa 20 Lilili	RESULT 2	S E S	and Wright, D., Weiss, R.  TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Unpublished (2000)
SUMMARIES	Length DB ID Description  37 11 AA734467 AA73496  50 107 AU107726 AU107726  50 107 AU107729 AU107729  50 107 AU107739 AU107730  50 107 AU107730 AU107730  50 107 AU107730 AU107730  50 107 AU107730 AU107730  50 107 AU107730 AU107730	50 107 AU107733 AU10773 50 107 AU107734 AU10773 50 107 AU107735 AU10773 50 107 AU107738 AU10773 50 107 AU107739 AU10773 45 246 AZ599531 AZ599531 42 249 AZ771500 AU10590 50 107 AU102691 AU10269 50 107 AU102691 AU10269 50 107 AU102691 AU10269	49 11 AA780186 30 250 AA2821583 50 107 AU106715 50 107 AU106716 50 107 AU106718 50 107 AU106718 50 107 AU106722 50 107 AU106722 50 107 AU106723 50 107 AU106723	50 107 AU106725 AU10672 50 107 AU106725 AU10672 50 107 AU106733 AU10673 50 107 AU106733 AU10673 50 107 AU106733 AU10673 50 107 AU106735 AU10673 50 107 AU106735 AU10673 50 249 AZ802269 AZ80226 34 23 AGGS 252	44 187 R3534 50 107 AU103987 AU103987 50 107 AU10394 AU103987 23 244 AZ45557 AZ45554 34 141 BE914450 AZ455057 40 9 AA61822 AA61822 AA618222 ng	ALIGNMENTS  AA734467 37 bp mRNA EST 07-JAN-1998  Vt94a08.rl Soares_mammary_gland_NbAMG Mus musculus cDNA clone  IMAGE:1178774 5' similar to TR:009472 Q09472 ElA-ASSOCIATED PROTEIN	mRNA sequence.  1 GI:2756134 ise. i.hus Lus Eutharia; Craniata; Vertebrata; Eutele Euthberia; Rodentia; Sciurognathi; Muridae; Murin	<pre>1 (bases 1 to 37) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,</pre>
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Gaps

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Indels

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Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki@ims.u-tokyo.ac.jp
Suzuki@ims.u-tokyo.ac.jp
Suzukifyr. Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
'S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: ysuzukieins.u-tokyo.ac.jp
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Suzukl, Y., Taunda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata
Suzukl, Y., Tsunoda, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo
, K., Suyama, A. and Sugano, S.
Fine Structural analysis of transcription start sites of human
mRNAs using full-length enriched and 5'-end enriched cDNA libraries
Unpublished (2001)
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AU107726 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
COL02114, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerase are the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (qil4732114) qblasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptores and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 50)
2 (bases I to 50)
3 (bases I to 50)
4 (bases I to 50)
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AU107725 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
BX3A0030, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
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/clone_lib="Mouse 10kb plasmid UUGCIM library"
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Pred. No. 3.9e+04;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                 Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
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Watches 15; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 50)

2 Suzuki, Y., Tsunoda, T., Tanaka, T., Makamura, Y., Morishita, S., Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Suyano, S.

Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries on Upublished (2001)

Contact: Yutaka Suzuki
Department of Virology Institute of Medical Science, University of Tokyo
1 Opartment of Virology Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp Suzuki, Y., Yoshitomo-Makagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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AU107732 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP13686, mRNA sequence.
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AU107733 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP13813, mRNA sequence.
AU107733. GI:13557254
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22 c 14 g 6 t
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Pred. No. 4.9e+04;
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/db_xref="taxon:9606"
/clone="HEP13686"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP01701"
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Cranrini; Hominidae; Homo.

1 (bases 1 to 50)
Suzukl,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: Suzuki@ins.u-tokyo.ac.jp
Suzuki@ins.u-tokyo.ac.jp
Suzukij.r. Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and 5'-end-enriched cDNa library. Gene 200 (1-2), 149-156 (1997).
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AU107730 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone
HEP01701, mRNA sequence.
                                    AU107729 50 bp mRNA EST 05-APR-2001
AU107729 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP01448, mRNA sequence.
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/db_xref="taxon:9606"
/clone="HEP01448"
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Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata, H., Offa,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries of Unpublished (2001)

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Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
5. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50)
Suzukl, Y., Tsunda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S.
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AU107736 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT09254, mRNA sequence.
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AU107737 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
REC00765, mRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="KAT09254"
/clone=lib="Sugano Homo sapa 20 c 14 q 9 p
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Matches 13; Conservative
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I (Dases 1 to 50)

Suzuki,Y., Tsunoda,T., Talra,H., Mizushima-Sugano,J., Sese,J., Hata, H., Otar,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.

Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries on upublished (2001)

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Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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AU107734 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP14963, mRNA sequence.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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FEATURES

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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Bukaryota, Metazoa, Chordata; Catarrhini, Hominidae, Homo.

(bases 1 to 50)
Suzukli,Y. Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isoqai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mnNAs using full-length enriched and 5'-end enriched cDNA libraries
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                          AU107739 50 bp mRNA EST 05-APR-2001
AU107739 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
2RV61978, mRNA sequence.
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Contact: Robert B. Weiss
University of Utah Genome Center:
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2RV61978"
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Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries of npublished (2001)
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1 Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)

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Sistitute of Medical Science, University of Tokyo
Bmail: ysuzuki@ims.u-cbkyo.ac.jp
Suzuki,Y., Yoshitcmo-Nakagawa,K., Maruyama.K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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AU107738 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ZRV61429, mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/db_xref="taxon:9606"
/clone="REC00765"
/clone_lib="Sugano Homo sapiens cDNA library"
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/db_xref="taxon:9606"
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AU107738.1 GI:13557259
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

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Search completed: October 2, 2001, 15:01:07 Job time: 10836 sec
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

El (bases 1 to 50)

Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.

Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries on the full beat suzuki

Opublished (2001)

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                            /Jab host-"E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/G1 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (qi|4732114 qib|AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (stratagene) cells
and selected for ampicillin resistance."
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AU105903 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT08022, mRNA sequence.
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                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0414 row: M column: 23
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Seg primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 45.
Location/Qualifiers
                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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Tel: 801 585 5606
Fax: 801 585 7177
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Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
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Pred. No. 6.1e+04;
0; Mismatches 2; Indels 0
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/db_xref="taxon:9606"
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                             OM nucleic - nucleic search, using sw model
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AR038139 Sequence 179867 Sequence 7 A87694 Sequence 2 AR075944 Sequence E10759 PCR primer E10798 PCR primer A97414 Sequence 4 AR022050 Sequence

Description

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NON-COVALENT COMPLEX COMPRISING AT LEAST AN ANTIBODY AND ELEMENT BINDING WITH IMMUNOGLOBULINS ASSOCIATED WITH AN ACTIVE SUBSTANCE, BETHOD OF PREPARING AND APPLICATIONS PATENT: WO 9834956-A 2 13-AUG-1998; COMMISSARIAT ENERGIE ATOMIQUE (FR); DREVET PASCAL (FR)
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                                                                                                        Martens, G. JulianusMaria, Chaudhuri, B. and Stephan, C. Production of proteins using 7B2 protein Patent: 18, 5708140-A 7 13-JAN-1998; Location/Qualifiers
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Pred. No. 2.1e+04;
0; Mismatches 4; Indels
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Pred. No. 1.6e+04;
0; Mismatches 2;
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/db_xref="taxon:32644"
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   1/9867 29 bp DNA
Sequence 7 from patent US 5708140.
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A21585 MDH3 oligon
ARO84169 Sequence
A36486 Sequence
                                   159435 Sequence 10
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AR028960 Sequence
A23344 Artificial
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AR079838 Sequence
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117561 Sequence 24
 I92840 Sequence 14
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AR036134 Sequence
AR069509 Sequence
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Unclassified.
1 (bases 1 to 29)
Martens, G. JulianusMaria, Chaudhuri, B. and Stephan, C. Recombinant production of proteins using 7B2 protein Patent: US 5804417-A 9 08-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69.0%; Score 13.8; DB 9; Length 29; 88.2%; Pred. No. 1.6e+04; 1ve 0; Mismatches 2; Indels
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Sequence 9 from patent US
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Query Match

Unknown.

ORGANISM

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VERSION KEYWORDS SOURCE

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Higashida H., Murakami K., Hama Y., Tsukamoto Y., Isoai A., Kumagai H.; "FUSED PROTEIN AND GENE CODING SAID PROTEIN"; Patent number JP1996053500-A/8, 27-FEB-1996. ASAHI GLASS CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                   11-AUG-1994 JP 1994209368
HIGASHIDA HIDEKI, MURAKAMI KIMIKO, HAMA YUKO, TSUKAMOTO YOKO, ISOAI ATSUSHI, KUMAGAI HIROMICHI
COTALPJOOO,CL2N1/19,Cl2N15/09,Cl2P21/02,(Cl2N1/19,Cl2R1:645),
CL2P21/02,
                           Length 20;
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                         66.0%; Score 13.2; DB 45;
83.3%; Pred. No. 3.2e+04;
iive 0; Mismatches 3;
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02-SEP-2000 (Rel. 65, Last updated, Version 2)
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/db_xref="taxon:32644"
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JP 1996053500-A/8
27-FEB-1996
                                                                  2 atgatgcttaaaagctta 19
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1 (bases 1 to 44)
Thastrup,O., Tullin,S.slashed.ren, Poulsen,L.Kongsbak and Bj.o slashed.rn,S.Petersen.
Method of detecting biologically active substances by using green fluorescent protein
Fluorescent protein
Patent: US 5558713-A 5 28-SEP-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         Higashida H., Murakami K., Hama Y., Tsukamoto Y., Isoai A., Kumagai H., "MoDIFIED GENE CODING HUMAN SERUM ALBUMEN";
Patent number JP1996051982-A/11, 27-FEB-1996.
ASAHI GLASS CO LID.
                                                                                                                                                             Gaps
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HIGASHIDA HIDEKI, MURAKAMI KIMIKO, HAMA YUKO, TSUKAMOTO YOKO, ISOAI ATSUSHI, KUMAGAI HIROMICHI
C12N15/09,C07K19/00//C12N1/19,C12P21/02,(C12N1/19,C12R1:645),
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                                                                                                                                   Score 13.4; DB 9; Length 44;
Pred. No. 2.6e+04;
0; Mismatches 1; Indels
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/organism="Artificial sequences"
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02-SEP-2000 (Rel. 65, Last updated, Version 2)
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93.3%;
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Artificial sequences.
JP 1996051982-A/11
27 FEB-1996
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Best Local Similarity 93.3
Matches 14; Conservative
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hypothetical: No;
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Length 33;

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Unclassified.
1 (bases 1 to 25)
Sasaki,K., Mori,T. and Makino,S.
Attenuated measles virus vaccine containing specific nucleotide sequence and a method for its absolute identification
Patent: US 5824777-A 10 20-OCT-1998;
Location/Qualifiers
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Pred. No. 3.3e+04;
0; Mismatches 3;
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Pred. No. 6.4e+04;
0; Mismatches 4;
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Other publication DE 19534763 970515.
Location/Qualifiers
        Patent: US 5728821-A 14 17-MAR-1998;
Location/Qualifiers
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AR049871
AR049871.1 GI:5971863
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/organism="unidentified"
/db_xref="taxon:32644"
a 7 c 7 g 1:
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Sequence 3 from Patent W09712969.
A61915
A61915.1 G1:3716021
                                                 /organism="unknown"
7 c 7 g
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78.9%;
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83.3%;
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1 (bases 1 to 35)
Poustka, A. and Coy, J.
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Best Local Similarity 78.9°
Matches 15; Conservative
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Matches 15; Conservative
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                                                                                                                1 (bases 1 to 33)
Waldmann, H. and Zelenika, D.
TRANSGENIC MOBEL COMPRISING TCR ALPHA AND BETA CHAINS
PATENT: WO 9916867-A 4 08-APR-1999;
COBBOLD STEPHEN P (GB); ISIS INNOVATION (GB)
Location/Qualifiers
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Yelton, D., Glaser, S., Huse, W. and Rosok, M. Joanne.
Mutant BR96 antibodies reactive with human carcinomas
Patent: US 5792456-A 14 11-AUG-1998;
Location/Qualifiers
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Mutant BR96 antibodies reactive with human carcinomas
                                                                                                                                                                                                                                                                                         66.0%; Score 13.2; DB 9; Length 33; 83.3%; Pred. No. 3.3e+04; Live 0; Mismatches 3; Indels
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Sequence 14 from patent US 5728821.
192840
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/organism="unidentified"
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a 5 c 9 9 9
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AR022050
AR022050.1 GI:3976112
A97414 33 bp DNA
Sequence 4 from Patent WO9916867.
A97414
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Gaps

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Length 35;

29-SEP-1999

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1 (bases 1 to 29)
Jepson, I., Greenland, A.J., Thomas, D.R. and Philippe.
CYSTEINE PROTEASE PROMOTER FROM OIL SEED RAPE AND A METHOD FOR THE CONTAINMENT OF PLANT GERMPLASM
Patent: WO 9735983-A 24 02-0CT-1997;
ZENECA LTD (GB)
Other publication AU 2033797 19971017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 29)
Elrod, S.L. and Cherry, J.R.
Aspergillus oryzae 5-aminolevulinic acid synthases and nucleic acids encoding same
Patent: US 5871991-A 4 16-FEB-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                        61.0%; Score 12.2; DB 9; Length 29; 82.4%; Pred. No. 1e+05; ive 0; Mismatches 3; Indels
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Pred. No. 1e+05;
0; Mismatches
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/organism="unidentified"
/ob_xref="taxon:32644"
/clone="CYSG12CR"
7 a 4 c 8 9 10
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Sequence 4 from patent US 5871991.
AR035134 GI:5952802
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82.4%;
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Matches 14; Conservative
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Unclassified.
Unclassified.
1 (bases 1 to 25)
Sasaki,K., Mori,T. and Makino,S.
Attenuated measles virus vaccine, containing specific nucleotide sequence and a method for its absolute identification
Patent: US 5654136-A 10 05.AUG-1997;
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1 (bases 1 to 27)

1 (bases 1 to 27)

Hun'Y., Ruben,S.M., Sancar,A., Hsu,S.D. and Kazantsev,A.G.

Human blue-light photoreceptor hCRY2

Patent: US 6114503-A 13 05-SEP-2000;

Location/Qualifiers
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Pred. No. 1e+05;
0; Mismatches 3;
Pred. No. 1e+05;
0; Mismatches
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159435
159435.1 GI:2478067
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Sequence 13 from patent US 6114503.
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ilarity 82.4%;
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gb_est25:*
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        Gencore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                 10228115 segs, 4726426750 residues
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mouse who plasmid in the plasmid is contact: Contact: Universit Universit Rm. 308, 84112, US Tel: 801 Fax: 801	Corganism="Mus musculus"	Query Match  Query	RESULT 2 AZ785639 LOCUS LOCUS DEFINITION LOCUS DEFINITION LOCUS DEFINITION LOCUS DEFINITION LOCUS DEFINITION LOCUS AZ785639 AZ785639.1 GI:12922599 KEYWORDS SOURCE MARMALIA MA
\$ COMMARIES \$ COMMARIES \$ COMMARIES \$ COMMARIES \$ COURTY	TA213B010 TA3552 TA3552 TA3552 AZ487125 AZ487125 AZ34501 AZ4800965 AZ378007 AZ800965 AZ378007 TA154F100 AZ819685 AZ37800 AZ819685 AZ378007 AZ66447 AZ66447 AZ66447 AZ66447 AZ66447 AZ6544033 AZ45154 AZ45154 AZ45150 AZ45120 AZ45120 AZ45120 AZ45120 AZ45120 AZ45120 AZ45120 AZ45120 AZ45120	11 55.0 46 249 11 55.0 46 249 11 55.0 50 105 11 55.0 50 105 10.8 54.0 35 249 10.8 54.0 36 250 10.8 54.0 36 250 10.8 54.0 43 241 10.8 54.0 43 241 10.8 54.0 69 200 10.6 53.0 28 249 10.6 53.0 28 249	RESULT 1 AZ403428 LOCUS AZ403428 AZ403428 AZ403428 AZ403428 CIONE UUGCIMU17117F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0171117 F, DNA sequence. AZ403428 AZ403428 AZ403428 AZ403428 AZ403428 AZ403428 AZ403428 AZ403428 AZA103428 AZA103428 AZA103428 AZA103428 AZA103428 AZZIONE AZA103428 AZZIONE AZZION

us-09-757-100b-20.szlim50.rst

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also expressed in brain, cerebellum, eye, lung, kidney and liver as determined by RT-PCR.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRE0927/4 GUTAT 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
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Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hall, M., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 18A, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Rebillard,G., Vago,P., Pujol,R. and Hamel,C.P.
Identification of preferentially expressed cochlear genes by
systematic sequencing of a rat cochlea cDNA library
Brain Res. Mol. Brain Res. 47 (1-2), 1-10 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TA37H11P 37 bp DNA GSS 13-DEC-200
T. brucei sheared genomic DNA clone 37h11, forward sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="pco83"
/clone_lib="rat lambda ZAPII library (C.P.Hamel)"
/dev_stage="postnatal day 24"
/lab_host="Escherichia col1"
/lab_host="Escherichia col1"
                                                                                                                     Contact: Hamel, CP
Laboratoire de Neurobiologie de l'Audition - INSERW U254
Institut National de la Sante et de la Recherche Medicale
C.H.R. St-Charles, 34295 Montpellier cedex, France
Tel: (33) 04 67 33 69 75
Fax: (33) 04 67 52 56 01
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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100.0%; Pred. No. 2.1e+04;
ive 0; Mismatches 0;
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/organism="Rattus norvegicus"
/strain="Wistar"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                  Email: biomol@mnet.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwayot (gill47321141gbla712972.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/67 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                       Mouse whole genome scaffolding with paired end reads from 10kb
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Soto-Prior,A., Lavigne-Rebillard,M., Lenoir,M., Ripoll,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="UUGC2M0029012"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0029 row: 0 column: 12
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
                                                                      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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U74031
                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 27.
Location/Qualifiers
Wright, D., Weiss, R.
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                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@qenet
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                                               plasmid inserts
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Length 30;

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Liber, Sanger Centre. The Wellcome Trust Genome sequencing project, Sanger Centre. The Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk and nhl@sanger.ac.uk and nhl@sanger.ac.uk and constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TRED9274 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of T. burcel sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
  with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLI0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TA52H11Q 31 bp DNA GSS 13-DEC-2000 T. brucei sheared genomic DNA clone 52h11, reverse sequence, genomic survey sequence.
AL456059 AL456059.1 GI:11856930
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1 (bases 1 to 31)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                            61.0%; Score 12.2; DB 250;
82.4%; Pred. No. 5.2e+04;
ive 0; Mismatches 3; I
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Pred. No. 5.2e+04;
0; Mismatches 3;
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/db_xref="taxon:5691"
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6 TGAGGGTTAATAGCTTA 22
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Best Local Similarity 82.4
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonocleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarcse gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil47321H4glb/H2129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly, and Wright,D.,Weiss,R., Stokes,R., Tingey,A., von Niederhausern,A. Pouse Whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ833603 30 bp DNA GSS 20-FEB-2001
2M0115J16R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0115J16 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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/db_xref="taxon:10090"
/db_caref="taxon:10090"
/clone="UGGC2M0115J16"
/clone=lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                    Score 12.8; DB 258; Length 37;
Pred. No. 2.7e+04;
); Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rm. 308, Biomedical Polymers Research Bldg., 20
/organism="Trypanosoma brucei"
/strain="TRD1927"
//db_xref="taxon:5691"
/clone="37h11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0115 row: J. column: 16
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/organism="Mus musculus"
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Location/Qualifiers
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ilarity 87.5%;
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Fax: 801 585 7177
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Gaps

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Length 31; Indels 27-AUG-1998

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 48)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Upublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapps-remail.nih.gov

Tissue Procurement: ATCC/CTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 48.
                                                                                 Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMS259 row: g column: 01
High quality sequence stop: 38.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies.

Investigator providing samples: Gilbert Smith, NIH"
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BE896146
  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strafn="CSECH II"
/db_xraf="taxon.10090"
/clone="IMAGE:4014744"
/clone_lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
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0; Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:3923841"
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82.4%;
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Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing Center
information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF144195 38 bp mRNA EST 24-OCT-2000 601786804F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4014744 5', mRNA sequence.
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ov73a08.sl Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1642934
3' similar to gb:Dl3748 EUKARYOTIC INITIATION FACTOR 4A-I (HUMAN);,
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 37)

1. (CGAP http://www.ncbl.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 38)
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Pred. No. 5.3e+04;
); Mismatches 3;
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Insert Length: 669 Std Error: 0.00
Seq primer: -40m13 fwd. Erf from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/clone_lib="Soares_testis_NHT"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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AI024143.1 GI:3239187
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82.4%;
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                                             mRNA sequence.
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Mus musculus
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Gaps

Gaps

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(Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M.Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRE0927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
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Details of T. brucel sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-DEC-2000
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1 (bases 1 to 48)
Hall.N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TA78C03Q 48 bp DNA GSS 13-DEC-200 T. brucei sheared genomic DNA clone 78c03, reverse sequence,
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Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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/strain="TREU927"
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S. Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hullman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R., Waterston, The Washu-Merck EST Project

L. Onpublished (1995)

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Fax: 14 286 1800

Fax: 14 286 1800

Fax: 1280
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                       /tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/tab_host="DH10B (phage-resistant)"
/note="Organ: Skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Syverage insert size 2 kb. Library constructed by Life
Technologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1280 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H40544 31-JUL-1995
yn87h08.rl Soares adult brain N2b5HB55Y Homo sapiens cDNA clone
IMAGE:175455 5' similar to gb:X63526 ELONGATION FACTOR 1-GAMMA
HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                           Score 12.2; DB 141; Length 48;
Pred. No. 5.5e+04;
0; Mismatches 3; Indels 0;
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/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="GDB:3837490"
/db_xref="taxon:9606"
/clone="IMAGE:175455"
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High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                           61.0%;
82.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                     19 CATGATCCTCACAAGCT 35
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                           1 catgatgcttaaaagct 17
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AUTHORS
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Gaps

8

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High qality sequence starts: 1 High qality sequence stops: 1 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 873 Std Error: 0.00
  Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Generation ex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRE0927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INSIBDOSP 32 bp DNA GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 318d05, forward sequence,
genomic survey sequence.
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1 (bases 1 to 32)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M.A. and Barrell, B.G.
                                                                                         97044478
Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Pred. No. 8.7e+04;
0; Mismatches 5; I
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/organism="Homo sapie
/db_xref="GDB:499780'
                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
Insert Size: 873
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72.2%;
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Matches 13; Conserv
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TA318D05P/c
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 50)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins

'M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, M., Mortis, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T73552 50 bp mRNA EST 02-MAR-1995 yc35h10.rl Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:82723 5' similar to gb:J04449 CYTOCHROME P450 IIIA4 (HUMAN);,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Constructed at the Institute for Genomic Research (TIGR),
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRE0327/4 GuTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
lnsert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: nelsayed@tigr.org
Details of T. brucel sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                               l (bases I to 49)
Hall, M. Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitsed (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
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                                                                                                                 TA213B01Q 49 bp DNA GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 213b01, reverse sequence,
genomic survey sequence.
                                                                                                                                                                                                                                                                              Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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0; Mismatches
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/clone="213b01"
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AL478475.1 GI:11844434
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Best Local Similarity 86.7
Matches 13; Conservative
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20 GATGCTTAACAGCCT 34
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T73552
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                                                                                                                                    DEFINITION
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Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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                                                                                                               Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Joses 1 to 38)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ487122 38 bp DNA GSS 05-OCT-2000
1M0316P22F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0316P22 F, DNA sequence.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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/db_xref="taxon:10090"
/clone="UGGC1M0316P22"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 258; Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Pred. No. 1e+05;
0; Mismatches 4;

    .32
    /organism="Trypanosoma brucei"

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Insert Length: 10000 Std Error: 0.00
Plate: 0316 row: P column: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 38.
Location/Qualifiers
                                                                                                                                                                                                                                                           /strain="TREU927"
/db_xref="taxon:5691"
/clone="318d05"
6 c 5 g
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77.8%;
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Best Local Similarity 77.8
Matches 14; Conservative
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Fax: 801 585 7177
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotides where ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance. and selected for a selected
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176917 Sequence 25
E26933 Vascular en
AR090736 Sequence
111623 Sequence
854330 V alpha J a
AR080704 Sequence
AR019663 Sequence
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95_htg16: **
95_htg10: **
95_htg10: **
95_htg21: **
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95_htg22: **
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                                                              October 2, 2001, 15:56:52 ; Search time 3339.34 Seconds (without alignments) 69.480 Million cell updates/sec
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                            1344157 seqs, 7733874588 residues
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Maximum Match 100%
Listing first 45 summaries
                                            OM nucleic - nucleic search, using sw model
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C12N1/21,C12N5/10,C12P21/02//(C12N1/21,C12R1:19),(C12N5/10, PC
                                                                                           1 (bases 1 to 22)
Roblin,R.O. III, Hu,M., Tang,J.S. and Lee,S.
Mycoplasma polymerase chain reaction testing system using a set of mixed and single sequence primers
Patent: US 5693467-A 25 02-DEC-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (C12P21/02,C12R1:19), (C12P21/02,C12R1:91),C12N15/00,A61K37/24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIROSHI MITSUI, SUNIL C KAURU, TAKASHI SUGIHARA, RENU WADAWA, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A61K37/24, A61K37/24, A61K37/24, C12N5/00, (C12N5/00, C12R1:91) CC
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PC C12N15/09, A61K38/22, A61K38/22, A61K38/22, A61K38/22, A61K38/22,
            03-APR-1998
                                                                                                                                                                                                                                                                                                                                        07-FEB-2001
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Hiroshi, M.S.C.C., Takashi, S.R.W.W. and Suzuki.
Vascular endothelial cell growth factor
Patent: JP 199169183-A 13 29-JUN-1999;
AGENCY OF IND SCIENCE & TECHNOL, TOAGOSEI CHEM IND CO LTD
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                                                                                                                                                                                                                        Length 22;
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Location/Qualifiers
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                                                                                                                                                                                                                      Score 11.4; DB 10;
Pred. No. 4.3e+04;
0; Mismatches 1;
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Vascular endothelial cell growth factor.
E26933
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    1/6917 22 bp DNA
Sequence 25 from patent US 5693467.
176917

    .21
    /organism="unidentified"
    /db_xref="taxon:32644"

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JP 1999169183-A/13
29-JUN-1999
11-DEC-1997 JP 1997362118
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8 c 4 g
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CC Topology: Linear;
FH Key Loc
FT source 1.
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92.3%;
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                                         I76917.1 GI:3013071
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JP 1999169183-A/13.
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Matches 12; Conservative
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186209 Sequence 6
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A58772 Sequence 18
AX019995 Sequence
AX020004 Sequence
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AX007130 Sequence
E51076 Novel Esche
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X70713 M.musculus
I46492 Sequence 47
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AR095615 Sequence
AR049682 Sequence
AR098915 Sequence
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A69911 Sequence 6
AX041988 Sequence
AR017555 Sequence
AR084745 Sequence
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I21731 Sequence 6
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Sequence 18
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AR017553 Sequence
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Cowsert,L.M.
Antisense modulation of RhoG expression
Patent: US 5965370-A 17 12-Ocr-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17 from patent US 5965370.
AR078873
AR078873.1 GI:10005619
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AR090849
I06514
MMTCRAIC7
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AX007130
E51076
AR095613
AR095615
AR098915
179755
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Score 11; DB 10; Length 21;

73.3%;

Query Match

RESULT

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Gaps

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bass 1 to 3)
Roth, M.E., Holman, P.O. and Kranz, D.M.
                                                                                                                                                                                                            General Staff at the National Library of Medicine created this entry [NCBI gibbsq 45430] from the original journal article. This sequence comes from Figure 2 B. On Nov 21, 1996 this sequence version replaced gi:1619731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Bennett, C.Frank, Condon, T.P. and Cowsert, L.M.
Antisense inhibition of integrin alpha.4 expression
Patent: 18 596826-A 9 19-0CT-1999;
Location/Qualifiers
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/note="T-cell receptor alpha chain"
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J. Immunol. 147 (3), 1075-1081 (1991)
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                                                           Mus sp. BALB C adult day-37 thymus.
Mus sp.
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Sequence 9 from patent US 5968826.
AR080704
AR080704.1 GI:10007434
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DEFINITION Sequence 2 from patent US 5783683.
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/organism="Mus sp."
/db_xref="taxon:10095"
 day-37 thymus, Genomic, 37 nt].
S45430
S45430.1 GI:1679985
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1 c 5 g
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/partial
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Smith, R.S., Curtiss, L.K., Koduri, K.R., Witztum, J.L. and Young, S.G.
Monnatural apolipoprotein B-100 peptides and apolipoprotein
B-100-apolipoprotein A-I fusion peptides
Patent: US 5408038-A 8 18-APR-1995;
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Unclassified.

Unclassified.

E. (bases 1 to 25)

S. Chenchik, A., Jokhadze, G. and Bibilashvilli, R. Methods of assaying differential expression

AL Patent: US 5994076-A 856 30-NOV-1999;

Location/Qualifiers
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 Pred. No. 7.8e+04;
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Sequence 856 from patent US 5994076.
AR090736
               Mismatches
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Sequence 8 from Patent US 5408038.
111623
111623.1 GI:909141
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9 c 6 a
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Best Local Similarity 100.
Matches 11; Conservative
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Unclassified.

Unclassified.

(bases 1 to 29)

Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and Thompson,J.D.

Thy nef targeted ribozymes
Patent: US 5972704-A 50 26-OCT-1999;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                     Unknown.
Unclassified.
In (bases 1 to 24)
I (bases 1 to 24)
Garner J., Dalrymple, M.L., Prunkard, D.E. and Foster, D.C.
Production of fibrinogen in transgenic animals
Patent: US 5639940-A 10 17-JUN-1997;
Location/Qualifiers
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                                                                                     Score 10.8; DB 9; Length 24;
Pred. No. 1e+05;
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85.7%; Pred. No. 9.9e+04;
tive 0; Mismatches 2;
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Sequence 50 from patent US 5972704.
AR082206
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Sequence 10 from patent US 5639940.
1147711 GI:2471676
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85.7%;
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Garner,I., Cottingham,I.R., Temperley,S.M., Foster,D.C.,
Sprecher,C.A. and Prunkard,D.E.
Protein C production in non-human transgenic mammals
Patent: US 5905185-A 9 18 MAY-1999;
Location/Qualifiers
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Pred. No. 1e+05;
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Leung, W., Darrow, A. and Andrade-Gordon, P.
PAR2 modified transgenic mice
Patent: US 6077990-A 9 20-JUN-2000;
Location/Qualifiers
                                                                                                                                 gene
Patent: US 5783683-A 2 21-JUL-1998;
Location/Qualifiers
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Sequence 9 from patent US 5905185.
AR070473
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Sequence 9 from patent US 6077990.
AR099765.1 GI:12809531
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/organism="unknown"
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AR019663.1 GI:3974777
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85.7%;
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Morrison, R.S.
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Best Local Similarity 85.7
Matches 12; Conservative
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Matches 12; Conservative
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synthetic construct.
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a (bases 1 to 36)
Schantz,C. and Kopetzki,E.
Escheritchia coli host/vector system based on antibiotic-free selection by complementation of an auxotrophy Patent: EP 0972838-A 16 19-JAN-2000;
ROCHE DIAGNOSTICS GMBH (DE)
                                                                                                                                                                                                                                                                           Score 10.8; DB 9; Length 3
Pred. No. 9.5e+04;
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1 (bases 1 to 30)
Tandon, N., Sun, B., Nakamura, T. and Yamamoto, N.
Platelet membrane glycoprotein vi (gpvi) dna and protein sequences, and uses thereof
Patent: WO 0116321-A 8 08-MAR-2001;
OTSUKA PHARMACEUTICAL CO., LTD. (JP)
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Unclassified.
1 (bases 1 to 29)
1 (bases 1. Chowrira, B., McSwiggen, J., Stinchcomb, D.T. and Thompson, J.D.
Thompson, J.D.
HIV targeted ribozymes
Patent: US 5693535-A 50 02-DEC-1997;
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    /organism="synthetic construct"
/db_xref="taxon:32630"

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                                                                  178252 29 bp DNA
Sequence 50 from patent US 5693535.
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AX007130
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Sequence 8 from Patent WO0116321.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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DOURNL Context: Robert B. Weiss  COMMENT (Context: Robert B. Weiss  COMMENT (Context: Robert B. Weiss  CONTEXT: To 10 (Tab) Genome Center  University of Utah  FM. 108, Sincedical Polymers Research Bldg., 20 S. 2030 E., SiC, UT 8412, USA  FM. 208, Manual Context Column: 13  FEATURES  Column: Corporation Column: 13  Seq primer: Colone. Lib. Nation Colone. Lib. Nation Colone. Lib. Nation: N	Qy         1 gcgggctcacagtgg 15           i                                 Db         25 GGGCCTCACAGTGG 11	RESULT 2 AZ834614 50 bp DNA GSS 20-FEB-2001 LOCUS LOCUS DEFINITION 2M0117121F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZM0117121 F, DNA sequence. ACCESSION AZ834614.1 GI:13004522 KEYWORDS GSS. SOURCE ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. I (bases 1 to 50) AUTHORS Dunh, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly ,M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Description  A245304 1M0254A13  A283464 2M0105328  AU102352 AU102352  AU102355 AU102355  AU202356 AU102356  A2455866 1M0258K21  A2591206 1M0401K03  AA822940 vp30903.r  AA822940 vp30903.r  AA822940 vp30903.r  AU4017932 AU107932  AU406405 T. brucei  A277048 1M0572G03  A2786210 2M0031P01  A2786210 2M0031E20  A281261 LM03706.x  A1735009 as44e04.x  A281261 LM03706.x  A1735009 as44e04.x  A281261 LM03706.x  A1735009 as44e04.x  A2812781 2M005512  A2812781 LM03706.x  H99190 VRYSGOT.s  A2812781 LM0379817  A173641 LC36806.x  A278621 LM02590  AU102590 AU105590  AU10550 AU105505  AU105512 AU106912  A2812038 AU106559  AU106512 AU106512  A2812038 AU106532  A2396435 IM0161C03  A236445 IM0161C03  A2364461 IM0161C03  A236446		GSS 04-OCT-2000 juence.  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus. Beacorn,T., Duval,B., Hamil,C., J.M., Meenen,E., Pedersen,T., Reilly R., Tingey,A., von Niederhausern,A.
Score Match Length DB ID  11.8 78.7 40 244 AZ453043 11.8 78.7 50 250 AZ844614 11.4 76.0 50 107 AU105352 11.8 72.0 27 244 AZ45866 10.8 72.0 27 244 AZ45866 10.8 72.0 44 258 AZ45866 10.8 72.0 44 258 AZ45866 10.8 72.0 44 258 AZ45866 10.4 69.3 22 258 AZ470438 10.4 69.3 37 249 AZ345803 10.4 69.3 37 249 AZ34586 10.4 69.3 37 249 AZ34586 10.4 69.3 37 249 AZ34586 10.4 69.3 37 249 AZ345803 10.2 68.0 34 250 AZ48818 10.2 68.0 34 250 AZ48818 10.2 68.0 37 249 AZ36290 10.2 68.0 37 250 AZ820369 10.2 68.0 40 20 AI17561 10.2 68.0 40 24 AZ36283 10.2 68.0 50 107 AU105588 10.2 68.0 50 107 AU105562 10.2 68.0 50 107 AU105562 10.2 68.0 50 107 AU105659 10.2 68.0 50 107 AU105659 10.2 68.0 50 107 AU105629 10.3 66.7 52 249 AZ36435 10 66.7 44 166 BE311212	ALIGNMENTS	A2453043 40 bp DNA LM0254A13F Mouse 10kb plasmid clone UUGCIM0254A13 F, DNA sec A2453043 G1:10610442 GSS.  Mus musculus Eukaryota; Metazoa; Chordata; Musmulalia; Eutheria; Rodentia; 1 (bases 1 to 40) Dunn,D., Aoyagi,A., Barber,M., Longaore,S., Mahmout,M., Longaore,S., Mahmout,M., Rose,M., Rose,R., Stokes, and Wright,D.,Weiss,R.
No. 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		RESULT 1 AZ453043/C LOCUS DEFINITION ACCESSION VERYWORDS SOURCE ORGANISM REFERENCE AUTHORS

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Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries (10published (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
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4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
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HRC01304, mRNA sequence.
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/db_xref="taxon:9606"
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Department of Virology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab host-"E. Coli strain XL10-Gold, T1-resistant, F-"
/note-"Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/G1 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pwD42 (qi|4732114 qb) hR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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AU106328 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT00883, mRNA sequence.
                                                                                                                                                                           Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
                            Mouse whole genome scaffolding with paired end reads from 10kb
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/clone="UUGC2M0117121"
/clone_11b="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0117 row: I column: 21
                                                                                                                                                                                                                                                                                                                                                 Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                          University of Utah Genome Center
University of Utah
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Location/Qualifiers
                                                   plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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       and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                             Class: plasmid ends
                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@qenet
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Matches 13; Conserv
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/ctone_library load strain XIIO Gold, T1-resistant, F-"
/lab_host="E. Coli strain XIIO Gold, T1-resistant, F-"
/lab_host="E. Coli strain XIIO Gold, T1-resistant, F-"
/note="Wector: PWD420; Purified genomic DNA from M.
musculus C57BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was bludt end repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
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of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
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chemically-competent E. coli XIIO-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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1M0401K03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0401K03 F, DNA sequence.
           S. 2030 E., SLC,
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        308, Biomedical Polymers Research Bldg., 20
  Rm. 308, Biomedical Polymers Research Bld 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0.258 row: K column: 21
Seq primer: CGTYGTAAAACGACGCCAGT
                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0258K21"
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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Location/Qualifiers
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AZ591206.1 GI:11713312
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Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Otar, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S.
Fine Structural analysis of transcription start sites of human manka, susing full-length enriched and 5'-end enriched cDNA libraries Unpublished (2001)

Contact: Yutaka Suzuki
Department of Yurology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: Ysuzukiélms.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
A., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Musch Wolse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                             AU102356 50 bp mRNA EST 05-APR-2001
AU102356 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ADSH00944, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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19 GCGGGCTCACA 9
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                                                                                                                                                                                                                                                                                                                                 human.
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ORGANISM
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AU102356/c
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Contact: Marra M/Mouse EST Project
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwb42 (qilq/32114 qib]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and Materston, R. The Washu-HHMI Mouse EST Project
Unpublished (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/G3 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                     Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
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                                                                                                                                   Std Error: 0.00
                                                                                                                                   Plate: 0401 row. K column: 03
Seg primer: CGTYGTAAAACGACGCCAGT
Class: plasmid and
                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGC1M0401K03"
                                                                                                                                                                                                                         High quality sequence stop: 38.
Location/Qualifiers
                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
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85.7%;
University of Utah
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Best Local Similarity 85.7
Matches 12; Conservative
                                                            Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genet
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KEYWORDS
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3/); double-stranded CDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. "
12 c 12 g 6 t
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Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTAt 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
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1 (bases 1 to 44)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Chillingworth, C., Sanondream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucel genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:592524

Trace considered overall poor quality
Seq primer: -28ml3 revz ET from Amersham
High quality, sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:1078228"
/clone_lib="Barstead mouse proximal colon MPLRB6"
/dev_stage="7 day juvenile"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trypanosoma brucei.
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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Pred. No. 7.2e+04;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="FVB/N"
/db_xref="taxon:10090"
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85.7%;
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Gaps

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 50)

Suzuki, Y., Tsunoda, T., Taira, H., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Nakamura, Y., Morishita, S., Okubo, K., Suyama, A. and Sugano, S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Typenson 1.0 22)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CBIO 15A, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                       AU107932 50 bp mRNA EST 05-APR-2001
AU107932 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ZRV62008, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TA140A04P 22 bp DNA GSS 13-DEC-2000 T brucei sheared genomic DNA clone 140a04, forward sequence, genomic survey sequence.
AL466405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Sugano Homo sapiens cDNA library"
19 c 15 g 9 t 1 others
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       Indels
     5,
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ZRV62008"
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85.7%;
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Trypanosoma brucei
  Conservative
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                                                                              30 CGGGGTCACAGAGG 17
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Best Local Similarity
Matches 12; Conserv
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Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:

www-bio.linl.gov/bbrp/image/image.himl
Seq primer: -40n13 fwd. Er from Amersham.
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                       Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA934014 48 bp mRNA EST 27-APR-1998 om58ell.sl NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1551404 3/ similar to gb:X01683 ALPHA-1-ANTITRYPSIN PRECURSOR (HUMAN);, mRNA sequence.
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1 (bases 1 to 48)

NCI-OGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/db_xref="taxon:9606"
/clone="InMoE:1531404"
/clone_lib="NCI_CGAP_GC4"
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/lab_host="DH108"
                                                                                           1. .44
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="233a12"
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Email: nelsayed@tigr.org
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85.7%;
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Best Local Similarity 85.7
Matches 12; Conservative
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RESULT 10 AA934014/c LOCUS

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ORGANISM

ACCESSION VERSION KEYWORDS SOURCE AUTHORS TITLE

REFERENCE

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FEATURES

BASE COUNT

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Gaps

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31 bp
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               Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.corg
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wesser Bloome Center
University of Utah
Weise Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Slam, H., Longarers, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
'M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1M0572G03F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0572G03 F, DNA sequence.
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/clone="UUGC1M0572603"
/clone_11b="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.3%; Score 10.4; DB 258; Length 22; 91.7%; Pred. No. 1.1e+05; 1ve 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                      /organism≔"Trypanosoma brucei"
/strain="TREU927"
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Insert Length: 10000 Std Error: 0.00
Plate: 0572 row: G column: 03
Seg primer: CGTTGTAAAACGACGGCCAGT
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    /organism="Mus musculus".
    /strain="C57BL/6J"

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/clone="140a04"
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Fax: 801 585 7177
nhl@sanger.ac.uk
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high modar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 fgblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rose, M., Rose, M., Rose, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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/lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGC1M0080114"
/clone=lib="Mouse 10kb plasmid UUGC1M library"
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Pred. No. 1.1e+05;
0; Mismatches 1; Indels 0;
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Fax: 801 585 7177
Email: ddun@genetics.utah.edu
Diacri Length: 10000 Std Error: 0.00
Plate: 0080 row: I column: 14
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University of Utah Genome Center
University of Utah
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Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                                                  (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4. polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil47321H gblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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University of Utah
Rm. 300, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ497161 35 bp DNA GSS 05-OCT-2000 MIN0333G2ZR Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0333G2Z R, DNA sequence.
/lab_host-"E. Coli strain XL10-Gold, T1-resistant, F-"
/note-"Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/63 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0333G22"
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Contact: Robert B. Weiss
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114)fplAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Description

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Walsh, T.A., Hey, T.D. and Morgan, A.E.R.
Walsh, T.A., Hey, T.D. and Morgan, A.E.R.
Ribosome-inactivating proteins, inactive precursor forms thereof, process for making and a method of using Patent: US 5646026-A 45 08-JUL-1997;

Location/Qualifiers
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Edwards, C.A., Cantor, C.R., Andrews, B.M., Turin, L.M. and Fry, K.E.
Method of determining DNA sequence preference of a DNA-binding
molecule
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                      07-OCT-1997
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Sequence 486 from patent US 5869241.
AR032874
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Sequence 487 from patent US 5869241.
AR032875.1 GI:5948480
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Sequence 45 from patent US 5646026.
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152125.1 GI:2473126
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182910 Sequence 12
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18290 Sequence 78
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Walsh,T.A., Hey,T.D. and Morgan,A.E.R.
Ribosome-inactivating proteins, inactive precursor forms thereof, a
process for making and a method of using
Patent: US 5635384-A 45 03-JUN-1997;
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                                                                                                                                                                                                       Unknown.
Unknown.
Unclassified.
1 (bases 1 to 50)
Edwards,C.A., Cantor,C.R., Andrews,B.M. and Turin,L.M.
Edwards,C.B.
Screening assay for the detection of DNR-binding molecules
Patent: US 5726014-A 486 10-MAR-1998;
Location/Qualifiers
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Edwards,C.A., Cantor,C.R., Andrews,B.M. and Turin,L.M.
Screening assay for the detection of DNA-binding molecules
Patent: US 5726014-A 487 10-MAR-1998;
Location/Qualifiers
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86.7%; Pred. No. 1.4e+04;
iive 0; Mismatches 2;
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86.7%; Pred. No. 1.4e+04;
ive 0; Mismatches 2;
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191289
191289.1 GI:3918785
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Sequence 486 from patent US 5726014.
191288 1191288 1 GI:3935758
     0; Mismatches
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Sequence 23 from Patent W00118250.
AX094845 GI:13511048
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Unclassified.
1 (bassi to 50)
Edwards,C.A., Cartor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
Sequence-directed DNN-binding molecules compositions and methods
Patent: US 5578444-A 487 26-NOV-1996;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 50)
Edwards, C.A., Cantor, C.R., Andrews, B.M., Turin, L.M. and Fry, K.E. Sequence-directed DNA-binding molecules compositions and methods Patent: US 5578444-A 486 26 NOV-1996;
Location/Qualifiers
Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E. Method of determining DNA sequence preference of a DNA-binding molecule Patent: US 5869241-A 487 09-FEB-1999;
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Pred. No. 1.4e+04;
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Pred. No. 1.4e+04;
0; Mismatches 2;
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Sequence 486 from patent US 5578444.
129614
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Best Local Similarity 86.7
Matches 13; Conservative
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Best Local Similarity 86.7
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TITLE JOURNAL

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Tucker,W., Huttner,E., Ignart,F. and Vermeulen,A.
Ribozymes capable of conferring resistance to potyvirus infection, and plants expressing said ribozymes
Patent: Wo 9928485-A 46 10-JUN-1999;
GENE SHEARS PTY LTD (4U); TUCKER WILLIAM (AU); HUTTNER ERIC (FR);
IGNART FREDERIC (FR); VERMEULEN AGNES (FR)
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1 (bases 1 to 25)

1 (llaponteau, B., Feng, J., Funk, W. and Andrews, W.H. Assays for the DNA component of human telomerase Patent: US 5776679-A 26 07-JUL-1998;
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1 (bases 1 to 25)

1 (bases 1 to 25)

Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H. Mammallan telomerase
Patent: US 5958680-A 27 28-SEP-1999;
Location/Qualifiers
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Pred. No. 2.5e+04;
0; Mismatches 1;
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Pred. No. 2.5e+04;
0; Mismatches 1;
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Sequence 26 from patent US 5776679.
AR016058
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Sequence 27 from patent US 5958680.
AR075530 GI:10002278
                                                                                                                      /organism="unidentified"
/db_xref="taxon:32644"
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                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 21)
Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
Mcarthy,J.J.
Single nucleotide polymorphisms in genes
Patent: WO 0118250 A 23 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
Pharmaceuticals, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tucker, W. and Huttner, E. Tucker, W. and Huttner, E. Ribozymes capable of conferring resistance to potyvirus infection, and plants expressing said ribozymes Patent: EP 0922767-A 616-JUN-1999; GENE SHEARS PTY LTD (AU)
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Pred. No. 2.5e+04;
0; Mismatches 1; Indels
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AX022755
AX022755.1 GI:10046280
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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A80791
A80791.1 GI:6731415
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/organism="unidentified"
/db_xref="taxon:32644"
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Best Local Similarity 80.0
Matches 12; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
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JP 1993091876-A/13.

Synthetic construct.

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artificial sequence.

I (bases I to 26)

Takinishi,E., Kakinuma,S., Takemoto,A., Miyoda,Y. and Fukuyama,S.

PROTEASE, ITS PRODUCTION AND USE
PROTEAT: JP 1993091876-A 13 16-APR-1993;
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C C12N9/54,C11D3/386,C12N1/21,C12N15/57,(C12N9/54,C12R1:07), PC
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Synthetic DNA for site directed mutagenesis of protease derived
from Bacillus NKS-21.
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Artifical sequence: Genes.
Bacillus NKS-21
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02-OCT-1991 JP 1991280313
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KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
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                                        Score 11.4; DB 9; Length 25;
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0; Mismatches 1; Indels
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/organism="synthetic construct"
/db_xref="taxon:32630"
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strandedness: Single;
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hypothetical: No;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

JOURNAL Unpublished (1997)  COMMENT Contact: Robert Strausberg, Ph.D.  Email: cgapbs-r@mail.nih.gov Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.  Emmert-Buck, M.D., Ph.D.	CDNA Library Preparation: Stratagene, Inc.  CDNA Library Arrayed by: Greg Lennon, Ph.D.  DNA Sequencing by: Washington University Genome Sequencing Center  Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  www-bio.llnl.gov/bbrp/image/image.html	Trace considered overall poor quality Insert Length: 660 Std Brror: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. FEATURES Location/Qualifiers Source //cranism="Homo sanions"	/db_xref="taxon.96ptc	GAATTCGGCACGAG 3' 3' adaptor sequence: 5' CTCCAGTTTTTTTTTTTTTTT 3' Average inser JNT 10 a 6 c 11 g 14 t L	Similarity 86.7%; Score 11.0; 3; Conservative 0; Mismatches gcagctgccatt 15 GAGCCACATT 5	SULT 2 662608 CUS AA662608 FINITION nr16a12.s1 NCI similar to SW:	ACCESSION AA662608.1 GI:2615457 VERSION AA662608.1 GI:2615457 KEYWORDS EST. SOURCE human. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	REFERENCE Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE 1 (bases 1 to 50) AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), TUMOR Gene Index JOURNAL Unpublished (1997) COMMENT Enal: Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D., Ph.D.	cDNA Library Preparation: David B. Krizman, Ph.D.  cDNA Library Arrayed by: Greg Lennon, Ph.D.  DNA Sequencing by: Washington University Genome Sequencing Center  Clone distribution: NCI-CEAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  www-bio.lln.gov/bbrp/image.html Seq primer: -40ml3 fwd. ET from Amersham.  FEATURES  Location/Qualifiers
SUMMARIES Result Query No. Score Match Length DB ID Description	11.8 78.7 41 12 AA829551 11.8 78.7 50 10 AA662608 11.4 76.0 45 12 AA794942 11.4 76.0 47 143 BF03638 11 73.3 47 158 H59245 11 73.3 50 107 AU103473	7 11 73.3 50 10 8 10.8 72.0 19 24 9 10.8 72.0 28 10 10 10.8 72.0 40 12 11 10.8 72.0 41 25 13 10.8 72.0 44 91	72.0 44 9 AA600013 72.0 44 11 AA713885 72.0 44 14 AA899114 72.0 50 20 A1476044 72.0 50 107 AU102666 72.0 50 107 AU104066 72.0 50 107 AU107071 69.3 20 243 AZ43787	10.4 69.3 21 24 10.4 69.3 22 24 10.4 69.3 22 24 10.4 69.3 26 24 10.4 69.3 31 15	10.4 69.3 34 4 AA282064 10.4 69.3 34 249 A2785014 10.4 69.3 38 249 A2759713 10.4 69.3 41 241 AZ37077 10.4 69.3 41 241 AZ34745 10.4 69.3 42 249 AZ760286	10.4 69.3 45 188 T17561 10.4 69.3 49 1. AA047951 10.4 69.3 49 13 AA914273 10.4 69.3 50 107 AU102448 10.4 69.3 50 107 AU103448 10.4 69.3 50 107 AU103390 10.4 69.3 50 107 AU103390 10.4 69.3 50 107 AU103390	44 10.4 69.3 50 107 AU103487 AU103487 45 10.4 69.3 50 107 AU103487 AU103487 ALIGNMENTS	RESULT 1  AA829551/c LOCUS LOCUS LOCUS DEFINITION of099h01.51 NCI_CGAP_C012 Homo sapiens CDNA clone IMAGE:1420657 3'  MRNA sequence. ACCESSION AA829551 VERSION AA829551. GI:2902650 KEYWORDS EST.	SOURCE . human. ORGANISM Homon sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 41) AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

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/clone_lib="NIH_MGC_66"
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/tissue_type="adenocarcinoma"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
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S NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTP/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM9604 row: d column: 09

High quality sequence stop: 47.

Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                    BF036368 47 bp mRNA EST 20-OCT-2000 601460534F1 NIH_MGC_66 Homo sapiens CDNA clone IMAGE:3863768 5',
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Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

E. [Obases 1 to 45]

Marra, M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HHMI Mouse EST Project

L. Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

WashU-HHMI Mouse EST Project

WashU-HHMI Mouse EST Project

WashU-HHMI Mouse EST Project

WashU-HMI Mouse EST Project

Fax: 314 286 1810

Fax: 314 286 1810
1. .50
/organism="Homo sapiens"
/organism="Homo sapiens"
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/clone="Inb="NoI_CGAP_Ew1"
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/note="Vector: pAMP10; mRNA made from Ewing's sarcoma,
Slze=selected on agarose gel, average insert size 600 bp.
Reference: Rizman et al. (1996) Cancer Research
56:5380-5383."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA794942 45 bp mRNA EST 09-FEB-1998 vr05903.rl Knowles Solter mouse blastocyst B3 Mus musculus cDNA clone IMAGE:1110964 5' similar to gb:M76124 Mus musculus EGP314 precursor mRNA, complete cds (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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/clone="IMAGE:1110964"
/clone=lib="Knowles Solter mouse blastocyst B3"
/tissue_type="blastocyst"
/dev_stage="embryo (pre-implantation)"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                     Score 11.8; DB 10; Length 50;
Pred. No. 3.3e+04;
0; Mismatches 2; Indels
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/strain="B6D2 F1/J"
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86.78;
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Best Local Similarity 86.7
Matches 13; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 50)

Suzuki,Y., Taunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata.

K., Suyama,A. and Sugano,S.

Fine Structural analysis of transcription start sites of human
mRARs using full-length enriched and 5'-end enriched cDNA libraries

Unpublished (2001)

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
1 Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukielms.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                         Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Brail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y. Yoshitcmo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
              1 (bases 1 to 50)
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Cta,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries
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AU104774 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC05287, mRNA sequence.
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21 c 15 g 9 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.3%; Score 11; DB 107; Length 50; 100.0%; Pred. No. 9e+04; ive 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
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12 c 11 g 1
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1419
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1419 Std Error: 0.00
Seq primer: Promega -21ml3
High quality sequence stop: 1.
Location/Qualifiers
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1 (bases 1 to 47)
1 Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M.; Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
Unpublished (1995)
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AU103473 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone
HEP17451, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/db_xref="taxon:9606"
/clone="IMAGE:204269"
/clone_lib="Soares fetal liver spleen lNFLS"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 47;
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; Mismatches 1;
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    .47
    /organism="Homo sapiens"

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Best Local Similarity 91.7%;
Matches 11; Conservative
                       GI:1012077
                                                                                                                                                                                                                                                                                                                       Contact: Wilson RK
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                                                                                         Homo sapiens
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H59245.1
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Gaps

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RESULT 8 AZ481008/c

ò 셤 DEFINITION ACCESSION

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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Direct, Suppose the Wellcome brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO isA, E-mail: barrell@sanger.ac.uk and nhlsganger.ac.uk constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTAT 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing projects. In Genome Sequencing Projects. In Genome Sequencing Projects. In Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA806226 40 bp mRNA EST 12-FEB-1998 oe29f12.s1 NCI_CGAP_Pr25 Homo sapiens cDNA clone IMAGE:1409999 3's similar to 9b:M33552 LYMPHOCYTE-SPECIFIC PROTEIN LSP1 (HUMAN);
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                                                                                                                                                                                                                                                                                                  TA355F03Q 28 bp DNA GSS 13-DEC-2000 T. brucei sheared genomic DNA clone 355f03, reverse sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (pases 1 to 28)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S. E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                    Score 10.8; DB 244; Length 19; Pred. No. 9.8e+04;
                                                                        Indels
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/clone="355f03"
5 c 4 q
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                       72.0%;
85.7%;
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85.7%;
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                                                                                                                                                                                                                                                                 AZ481008 19 bp DNA GSS 04-OCT-2000 1M0302N15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0302N15 R, DNA sequence. AZ481008 GI:10641989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
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                                              0;
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/clone="UUGCIM0302N15"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0302 row: N column: 15
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                       9e+04;
                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                       Pred. No.
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Location/Qualifiers
100.08; Pic
                                           11; Conservative
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Fax: 801 585 7177
Email: ddunn@genet
                                                                                            2 aagcagctgcc 12
                                                                                                                                             36 AAGCAGCTGCC 26
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                       Best Local Similarity
Matches 11; Conserv
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source

FEATURES

BASE COUNT ORIGIN

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Gaps

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described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.anger.ac.uk/Projects/T_brucei/.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cw249855 42 bp mRNA EST 07-JAN-2000 BS1554.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821534 3', AW249855
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue_type="small_cell_carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                              Score 10.8; DB 258;
Pred. No. 1.1e+05;
0; Mismatches 2;
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/db_xref="taxon:9606"
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                                                                                                                                                              /organism="Trypanosoma/strain="TREU927"
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/clone="126907"
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Other_ESTs: 2821534.5prime
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85.7%;
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TITLE
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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1 (bases 1 to 41)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Hall,N., Bowman,S., Lennard,N.J., Marris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-BEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU957/4 GUTAT 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
                  1 (bases 1 to 40)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Suzanne L. Topalian, M.D., Robert K. Bright,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T. brucei sheared genomic DNA clone 126907, reverse sequence,
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Pred. No. 1.1e+05;
0; Mismatches 2;
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Location/Qualifiers
                                                                       Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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AL463426
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85.7%;
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Best Local Similarity 85.7
Matches 12; Conservative
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Inpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Elias Campo,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LiNIx at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 865 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
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/note="Organ: lung; Vector: poTB7; Site_1: Xho1; Site_2: ECORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/Xho1 sites using the following 5' adaptor: GGCAGCAGGGG. Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                             AA353/66 44 bp mRNA EST 08-SEP-1997 nk29h01.sl NCI_CGAP_CO11 Homo sapiens cDNA clone IMAGE:1014961 3' similar to gb:M33552 LYMPHOCYTE-SPECIFIC PROTEIN LSP1 (HUMAN);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutèleostomi;
Bammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 44)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 1.1e+05;
0; Mismatches 2; Indels 0;
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Pred. No. 1.1e+05;
0; Mismatches 2; Indels
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/clone_11b="NCI_CGAP_Col1"
/tissue_type="tumor"
/lab_host="SOLR (kanamycin resistant)"
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/db_xref="taxon:9606"
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AA553766.1 GI:2324305
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Best Local Similarity 85.7
Matches 12; Conservative
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DEMARYOTE: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.

I (Jases I to 44)

Stat., Robey, P., Young, M., Schuler, G., Powell, J., Yang, L., Lennon, G., Hillier, L., Allen, M., Bowles, L., Geisel, S., Kucaba, T., Marra, M., Martin, J., Steptoe, M., Tan, P., Theising, B., Bowers, Y., Walson, R., Martin, J., Steptoe, M., Tan, P., Theising, B., Bowers, Y., Wylie, T., Materston, R., Wilson, R. and Francomano, C., Bowers, Y., Wylie, MashU-MGB/NHGRI EST Project

AL Onpublished (1997)

Contact: Wilson RK, Jia L.

MashU-MGB/NHGRI EST Project
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810

Fax: This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.
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/dev_stage="mixed"
/lab_host="Xi.Hslue MRF'/SolR"
/note="Vector: pBluescript; Site_1: EcoRI; Site_2: XhoI;
mRNA made from human bone marrow stroma, CDNA made by
oligo-dT priming. Directionally cloned. Size-selected for average insert size >0.5 kb. Library supplied by Dr. Libin Jia (NHGRI)."
                          ag29h11.s1 Jia bone marrow stroma Homo sapiens cDNA clone
IMAGE:1091013 3' similar to gb:M33552 LYMPHOCYTE-SPECIFIC PROTEIN
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AA713885.1 GI:2726159
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1091013"
/clone_lib="Jia bone marrow stroma"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 10.8; DB 9; DP 9; DP 9; Dred. No. 1.1e+05; D; Mismatches 2;
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                                                                               LSP1 (HUMAN);, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

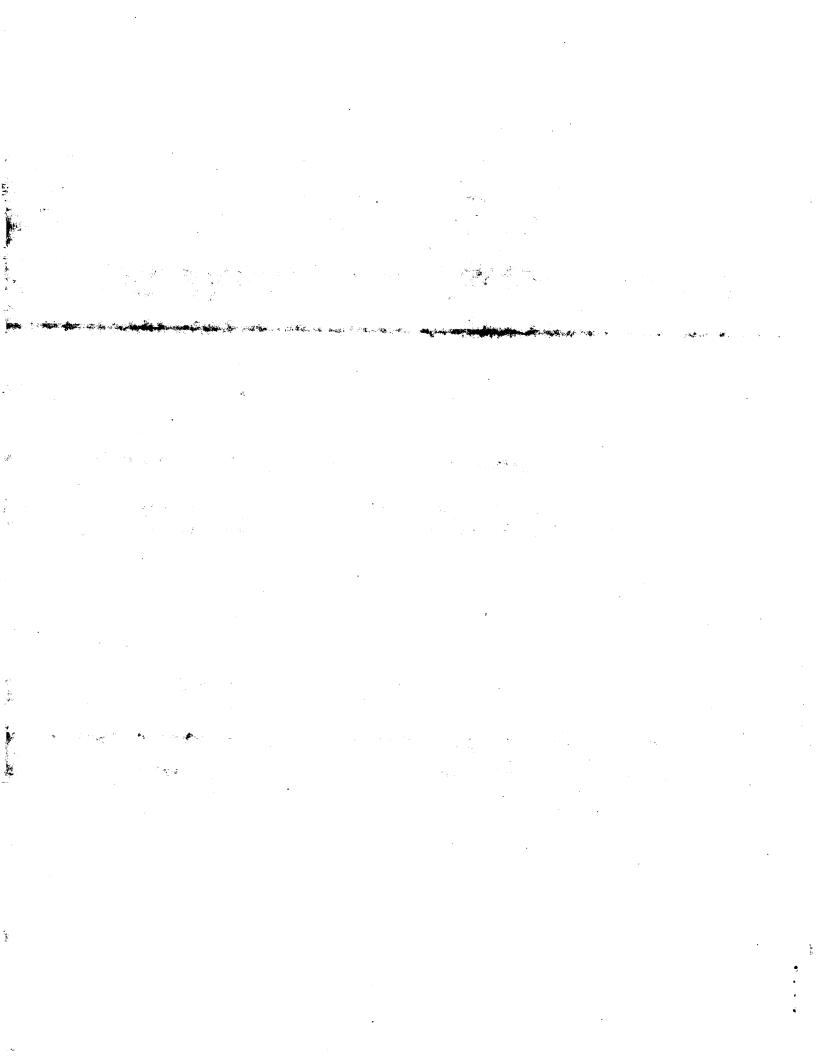
1 (bases 1 to 4)

NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Tumor Gene Index

Ontact: Robert Strausberg, Ph.D.
Email: capabs-riemail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Kristina A. Cole, M.D.,
Ph.D. student, Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck,
Ph.D. student, Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck,
Dh.D. ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CONE distribution: NCI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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//issue_trpe="normal ductal tissue"
/lab_host="DH10B"
/note="Organ: breast; Vector: pAMP10; mRNA made from
normal breast ductal tissue, cDNA made by oligo-dT
priming. Non-directionally cloned. Size-selected on
agarose gel, average insert size 600 bp. Reference:
Krizman et al. (1996) Cancer Research 56:5380-5383."
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/db_xref="taxon:9606"
/clone="IMAGE:1236011"
/clone_lib="NCI_CGAP_Br4"
/sex="female"
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Search completed: October 2, 2001, 15:01:12 Job time: 10841 sec



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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Database

AR067320 Sequence AR0775823 Sequence E30456 Method for A34802 HSV probe. 136150 Sequence 34 AR060552 Sequence 34

10 130544 9 AR067320 9 AR091705 9 AR075823 10 E30456 9 A34802 10 136150 9 AR060552

130544 Sequence 7

Description

DB

SUMMARIES

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1 (bases 1 to 22)
Evans,G.A. and Smith,M.W.
Method for generation of sequence sampled maps of complex genomes Patent: US 5851760-A 668 22-DEC-1998;
Location/Qualifiers
         29-SEP-1999
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Madeau, J.G., Pitner, J.Bruce, Linn, C.Preston and Schram, J.L.
Detection of nucleic acids by fluorescence quenching
Patent: US 5958700-A 6 28-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 34;
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Ting,J.Pan-Yung and Chin,K.
Forms of class II MHC transactivator (CIITA)
Patent: US 5994505-A 15 30-NOV-1999;
Location/Qualifiers
           PAT
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Pred. No. 5.4e+03;
); Mismatches 1;
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Pred. No. 1.3e+04;
0; Mismatches 2;
         AR067320 22 bp DNA
Sequence 668 from patent US 5851760.
AR067320
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Sequence 6 from patent US 5958700.
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5 c 4 g
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11 c 10 g
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AR091705
AR091705.1 GI:10018459
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AX015626 Sequence
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Hoke,G.D., Bradley,M.O., Williams,T.J. and Lee,C.
Antisense oligonucleotides directed against human ICAM-I RNA
Patent: US 5580969-A 7 03-DEC-1996;
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Pred. No. 5.4e+03;
0; Mismatches 1;
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130544.1 GI:1821335
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Recombinant polypeptides of the haemorrhagical septicemia virus in
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Unclassified.
Unclassified.
1 (bases 1 to 30)
Wadsworth, S., Siyder, B., Reddy, V.B. and Wei, C.
CDNA-genomic DNA hybrid sequence encoding APP770 containing a genomic DNA insert of the KI and OX-2 regions
Patent: US 5604131-A 34 18-FEB-1997;
Location/Qualifiers
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Pred. No. 2.6e+04;
0; Mismatches 1; Indels
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Eriksson, U., Olofsson, B., Alitalo, K. and Pajusola, K. Vascular endothelial growth factor-B Patent: US 5840693-A 53 24-NOV-1998;
Location/Qualifiers
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/organism="synthetic construct"
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                        Patent: EP 0377349-A 20 11-JUL-1990;
EUROGENTEC S.A
Location/Qualifiers
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Sequence 34 from patent US 5604131.
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E30456 E30456.1 GI:13025613
JP 1999056380-A/6.
                                                                                                                                                                                                                                                                                              unidentified
unclassified.
1 (bases 1 to 48)
James,G.N.J.J., Pitona,C.P.R.R. and L,S.
Wethod for detecting target nucleic acid sequence and
Patent: JP 1999056380-A 6 02-MAR-1999;
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1 (bases 1 to 18)
Renard,A. and Thiry,M.
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Unclassified.
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1 (bases 1 to 21)
Bazin, H. and Latinne, D.
Methods of inhibiting T-cell medicated immune responses with LO-CD2a specific antibodies
Patent: US 5817311-A 78 06-OCT-1998;
Location/Qualifiers
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Bazin, H. and Latinne, D.
Methods of inhibiting T-cell medicated immune responses with
                                                                                                                                                             Inflammation-induced expression of a recombinant gene Patent: US 5851822-A 4 22-DEC-1998; Location/Qualifiers
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Pred. No. 6.4e+04;
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    аки67869 28 bp DNA
Sequence 4 from patent US 5851822.
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Munford, R.S.
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Matches 11; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherita; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
Greaves, D.R., Thomsen, L., Catchpole, I.R. and Ford, M.J.
Dna constructs based on the eif4a gene promoter
Patent: WO 0102594-A 52 11-JAN-2001;
GLAXO GROUP LIMITED (GB)
                               Gaps
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73.3%; Score 11; DB 9; Length 20; 100.0%; Pred. No. 4.7e+04; rive 0; Mismatches 0; Indels
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Munford,R.S.
Inflammation-induced expression of
Patent: US 5744304-A 4 28-APR-1998;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
i a 6 c 7 g 1
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Sequence 52 from Patent WO0102594.
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AR003365.1 GI:3964624
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1 (bases 1 to 21)
Bazin H., Latinne, D., Kaplan, R., Kieber-Emmons, T., Postema, C.E. and White-Scharf, M.E.
Methods of inhibiting T cell mediated immune responses with humanized LO-CD2A-specific antibodies
Patent: US 5951983-A 78 14-SEP-1999;
Location/Qualifiers
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Bazin, H., Latinne, D., Kaplan, R., Kieber-Emmons, T., Postema, C.E. and White-Schaff, M.E.
Methods of inhibiting T cell mediated immune responses with humanized LO-CD2A-specific antibodies
Patent: US 5951983-A 79 14-SEP-1999;
Location/Qualifiers
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Pred. No. 6.4e+04;
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Pred. No. 6.4e+04;
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LO-CD2a-specific antibodies
Patent: US 5817311-A 79 06-OCT-1998;
Location/Qualifiers
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Sequence 78 from patent US 5951983.
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Sequence 79 from patent US 5951983.
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Best Local Similarity 85.7
Matches 12; Conservative
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Best Local Similarity 85.7%; Pred. No. 6.4e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Unpublished (2000) COMMENT Contact: Robert B. Weiss University of Utah Genome Center	mm. 305 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.05 15.0	Qy         3 ccaagtgagtct 15                                                 Ccaagtgagtct 17	RESULT 2 A2303920/C LOCUS DEFINITION 1M0003F19R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0003F19 R, DNA sequence. ACCESSION A2303920 VERSION A2303920 VERSION A2303920 I GI:10339372 KEYWORDS GSS. SOURCE house mouse. ORGANISM Mus musculus Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. REFERENCE (bases 1 to 32) AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
S Description	AZ303920 1M0347C11 AZ303920 1M0033F19 AZ498501 1M033IP21 AZ488625 2M0029L08 AZ381281 1M0140N08 AZ838281 1M0140N08 AZ837769 1M0229L15 AZ438946 1M0122111 WA7560 2C35a01.x1 AZ37560 2C35a01.x1 AZ480568 1M00201L11 AZ480568 1M0001L11 AZ480568 1M0003M11 AZ480568 1M00009N01 AZ3807167 AN010341 AZ827167 AN010341 AZ827167 AN01033N2 AZ827876 AN01033N2 AZ827876 AN01033N2 AZ827876 AN01033N2 AZ827876 AN01033N11 AZ333467 1M0029P06 AZ333467 1M0029P06 AZ333467 1M0029P06 AZ34567 WJ27f04.x AZ495842 1M0331L23 AZ495842 1M020488 AU102658 AU102658 AU102658 AU106203 AU100203 RZ88739 YP93C04 s1 AZ330576 IM0026F04	TS.	GSS 05-OCT-2000 guence.  Graniata; Wertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.  , Beacorn, T., Duval, B., Hamil, C.,  d. M., Meenen, E., Pedersen, T., Reilly,  R., Tingey, A., von Niederhausern, A.
SUMMARIES Query core Match Length DB ID	11.4         76.0         25         245         AZ506197           11.7         73.3         24.1         AZ5061920           10.4         69.3         34         249         AZ785625           10.4         69.3         34         249         AZ785625           10.4         69.3         34         242         AZ382781           10.4         69.3         34         AZ38781           10.4         69.3         42         AZ387696           10.4         69.3         42         AZ3877696           10.4         69.3         47         249         AZ387766           10.4         69.3         47         249         AZ387766           10.4         69.3         42         AZ3877676           10.4         69.3         42         AZ3877676           10.5         68.0         43         Z44         AZ3877677           10.5	ALIGNMENTS	AZ506197 25 bp DNA 1M0347C11F Mouse 10kb plasmid clone UUGC1M0347C11 F, DNA see AZ506197 AZ506197.1 G1:10687513 GSS. house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 25) Dunn,D., Aoyagi,A., Barber,M., Islam,H., Longacre,S., Mahmoui,M., Rose,M., Rose,R., Stokes, and Wright,D.,Welss,R.
Result No. SC	00000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		RESULT 12506197 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/G7 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonicleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gal
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil47321HJgb1AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the linsert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 43)
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Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
                                                                                                                                                                                                  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
                                                 Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
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/clone="UUGC1M0331P21"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 10.8; DB 244; Length 27;
Pred. No. 6.8e+04;
); Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0331 row: P column: 21
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"/strain="C57BL/6J"
                                                                                                                               Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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                           and Wright, D., Weiss, R.
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                                                                          plasmid inserts
Unpublished (2000)
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Best Local Similarity 85.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
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25 TACCCATGTGATTC 12
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COMMENT
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84112, USA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 27)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
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kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-" /note="Westor: PWD42Inv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
  Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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/sex="Male"
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                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Léngth: 10000 Std Error: 0.00
Plate: 0003 row: F column: 19
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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1M0331P21F Mouse 10kb plasmid UUGC1M
clone UUGC1M0331P21 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="UUGC1M0003F19"
                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 32.
Location/Qualifiers
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A2495501.1 GI:10670983
and Wright, D., Weiss, R.
                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
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//doce="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was prepared from a 6.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114) (pblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGIM0140N08"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0140 row: N column: 08
Seq primer: CGTTCTAAAACGACGCCAGT
Class: plasmid ends
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91.7%; Pred
0; }
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  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 33)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57Bix" | //db_xref="taxon:10090" | //db_xref="taxon:10090" | //clone="UGC2M0029L08" | //clone_lib="Mouse 10kb plasmid UUGC1M library" | //sex="Male"
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                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunf@qenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0029 row: L column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 43.
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Pred. No. 7e+04;
0; Mismatches
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                                                                                                                            Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
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AZ382781.1 GI:10496481
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84112, USA
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Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GEAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ438946 35 bp DNA GSS 03-OCT-2000 MO229115F Mouse 10kb plasmid UUGCIM library Mus musculus genomic Lone UUGCIM0229115 F, DNA sequence.
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Dunn,D., Aoyagi, Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="serous papillary carcinoma, high grade, 2 pooled tumors"
              NCI'cGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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84112, USA
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Seq primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualiflers
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91.7%; Pred. No. 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:2438799"
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                                                            Tumor Gene Index
Unpublished (1997)
  (bases 1 to 34)
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Best Local Similarity 91.7
Matches 11; Conservative
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Fax: 801 585 7177
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Mus musculus
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWAD42 (gil491A119491A219072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XILO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
With Stand
University of Utah
With 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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1M0132111F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                              /db.xref="taxon:10090"
/clone="UUGCIM0229L15"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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Pred. No. 1.2e+05;
0; Mismatches 1; Indels 0;
Std Error: 0.00
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                               Plate: 0229 row: L column: 15
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                  High quality sequence stop: 35.
                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                     /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ377696.1 GI:10491396
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Insert Length: 10000
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/clone_lib="Soares_senescent_fibroblasts_NbHSF"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/note="vector: pT7T3D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco RI
: 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Fm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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1 (bases 1 to 7.2).

2 (bases 1 to 7.2).

2 (bases 1 to 7.2).

3 (bases 1 to 7.2).

3 (bases 1 to 7.2).

4 (bases 1 to 7.2).

4 (bases 1 to 7.2).

5 (bases 1 to 7.2).

5 (bases 1 to 7.2).

6 (bases 1 to 7.2).

7 (bases 1 to 7.2).

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2M0051F07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Possible reversed clone: similarity on wrong strand Insert Length: 2909 Std Error: 0.00 Seq primer: mob.REGA+ET High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 10.4; DB 190; Length 46; Pred. No. 1.2e+05; 0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                           1. .46
/organism="Homo sapiens"
/db_xref="GDB:125576"
/db_xref="taxon:9606"
/clone="IMAGE:324264"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Insert Length: 10000 Std Erro
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Fax: 801 585 7177
Email: ddunn@genet
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA, was prepared from a derivative
of pWD42 (gil47321141gb]AR129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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1 (bases I to 46)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Mucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The Washu-Merck EST Project
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    zc35a01.rl Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA
clone IMAGE:324264 5' similar to PIR:S43417 S43417 RNA/DNA-binding
protein - mouse ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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0
                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCXM0132111"
/clone_lib="Mouse lOkb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 10.4; DB 242; Length 42; .Pred. No. 1.2e+05; 0; Mismatches 1; Indels 0
                                      Std Error: 0.00
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0132 row: I column: 11
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends

    .42
    /organism="Mus musculus"

                                                                                                                                                                   High quality sequence stop: 42. Location/Qualifiers
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91.7%;
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W47560.1 GI:1332239
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Best Local Similarity 91.7
Matches 11; Conservative
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114) glant29072.1), a copy number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for amplicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infe@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 1262 Std Error: 0.00
Seg primer: -400P from Gibco
High quality sequence stop: 1.
                                                                                                                                                 /db_xref="taxon:10090"
/clone="UUGC2M0091L11"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 10.4; DB 250; Length 48;
Pred. No. 1.2e+05;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource
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/db_xref="taxon:9606"
/clone="IMAGE:1723091"
                                                                                           /organism="Mus musculus"
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   ity sequence stop: 48.
Location/Qualifiers
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                                                                                                                    /strain="C57BL/6J"
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Unpublished (1997)
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Best Local Similarity 91.7
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
WR. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 48)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
181am, M., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ819513 48 bp DNA GSS 20-FEB-2001
2M0091L11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0091L11 F, DNA sequence.
                                                                                                                                                                                                                                   /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse whole genome scaffolding with paired end reads from 10\mathrm{kb} plasmid inserts
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                                                                                                                                                                          /clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                                                                                              Laboratory Mouse DNA Resource
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Insert Length: 10000 Std Error: 0.00
Plate: 0091 row: L column: 11
                                                           /organism="Mus musculus"
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Class: plasmid ends
                                                                                                                 /db_xref-"taxon:10090"
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Location/Qualifiers
                                                                                        /strain="C57BL/6J
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Best Local Similarity 91.7
Matches 11; Conservative
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Fax: 801 585 7177
Email: ddunn@qenet
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LOCUS DEFINITION

AZ819513

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VERSION KEYWORDS

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REFERENCE AUTHORS JOURNAL

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BASE COUNT

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Gaps

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EUKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 50)

2. I (Dases 1 to 50)

3. Suzuki,Y., Tsunoda,T., Tanaka,T., Makamura,Y., Morishita,S., Hata, A., T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.

Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries on Department of Virology Department of Virology Department of Virology Institute of Medical Science, University of Tokyo

4.6-1, Shirokanedai, Mnatoku, Tokyo 108-8639, Japan Enail: ysuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Mouse whole genome scaffolding with paired end reads from 10kb
                   AU105507 50 bp mRNA EST 05-APR-2001 AU105507 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone HRC12884, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A2303688 24 bp DNA GSS 29-SEP-2000
1M0003M11F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0003M11 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Sugano Homo sapiens cDNA library"
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Pred. No. 1.2e+05;
0; Mismatches 1;
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/db_xref="taxon:9606"
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91.7%;
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1 (bases 1 to 50)
Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Institute of Medical Science, University of Tokyo 4-6-1, Shizokanedai, Minatoku, Tokyo 108-8639, Japan 4-6-1, Shizokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzukitelins.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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AU105506 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC12806, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/clone="HRC12806"
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91.7%;
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Matches 11; Conservative
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Email: ddunn@genetics.utah.edu

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RESULT

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Length 50;

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/Jab host-"E. Coli strain XL10-Gold, T1-resistant, F-"
// note-"Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114(gb)AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
       Std Error: 0.00
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/db xref="taxon:10090"
/clone="UUGCIM0003M11"
Insert Length: 10000 Std Error:
Plate: 0003 row: M column: 11
Seq primer: CGTYGTAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
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Search completed: October 2, 2001, 15:01:13 Job time: 10842 sec

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Gaps

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Query Match 68.0%; Score 10.2; DB 241; Length 24; Best Local Similarity 80.0%; Pred. No. 1.5e+05; Matches 12; Conservative 0; Mismatches 3; Indels 0;

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Run on:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                               October 2, 2001, 15:56:54 ; Search time 3339.34 Seconds (without alignments) 69.480 Million cell updates/sec
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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AR042372 Sequence
AR052280 Sequence
AX09501 Sequence
AX002270 Sequence,
E28251 Purificatio
AR012670 Sequence
12036 Sequence 10

AR042372 AR052280 AX095001 AX002270 E28251 E28251 I25036 I30498

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Description

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SUMMARIES

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Eukaryotani Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [base] to 21)
Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and Mccarthy,J.J.
Single nucleotide polymorphisms in genes
Patent: WO 0118250-A 179 15-MAR-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); Millennium
                       29-SEP-1999
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                                                                                                                    Huang,S.
Retinoblastoma protein-interacting zinc finger proteins
Patent: US 5831008-A 11 03-NOV-1998;
Location/Qualifiers
                                                                                                                                                                                                                              Score 12.4; DB 9; Length 27; Pred. No. 1.5e+04; 0; Mismatches 1; Indels
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Sequence 179 from Patent W00118250.
AX095001
AX095001.1 GI:13511204
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Sequence 7 from Patent EPU881288.
AX002270
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Location/Qualifiers
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                 Sequence 11 from patent (
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1 (bases 1 to 27)
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Best Local Similarity 85.7
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AR074822 Sequence
AR035054 Sequence
I16172 Sequence 3
A42061 Sequence 4
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A27527 Synthetic B
A65367 Sequence 3
AR040914 Sequence
AR051821 Sequence
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AR001359 Sequence
AR044844 Sequence
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AR052240 Sequence
AR07839 Sequence
AR07839 Sequence
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164516 Sequence 18
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Nucleic acid molecules encoding retinoblastoma protein-interacting
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I33904 Sequence 12
 172560 Sequence 9
124623 Sequence 7
125220 Sequence 7
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Pred. No. 1.5e+04;
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Patent: US 5811304-A 11 22-SEP-1998;
Location/Qualifiers
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AR042372
AR042372.1 GI:5962868
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92.98;
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Best Local Similarity 92.9
Matches 13; Conservative
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AR012670 30 bp DNA
Sequence 9 from patent US 5763584.
AR012670.1 GI:3970988
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86.7%;
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Best Local Similarity 86.7
Matches 13; Conservative
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Bernd, K.E.B.B. and Meisterernst, G.P.
Purification of higher transcription complex from nonhuman
                                                                                                                                                                                                                                                                                                                                                                     E28251 21 bp DNA PAT 07-FEB-20
Purification of higher transcription complex from nonhuman
            unclassified.

1 (bases 1 to 21)

Berglund, E.D. and Kirschbaum, B.D.

Purification of higher order transcription complexes from transgenic non-human animals

Patent: EP 0881288-A 7 02-DEC-1998;

HOECHST AG (DE)
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Pred. No. 3.4e+04;
0; Mismatches 2; Indels
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Patent: JP 1999004638-A 3 12-JAN-1999;
HOECHST AG
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/organism="unidentified"
/db_xref="taxon:32644"
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/organism="unidentified"
//db_xref="taxon:32644"
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26-MAY-1997 DE
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C12R1:91), PC C12N15/00,
PC (C12N15/00,C12R1:91)
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location
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Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 30)
Godowski,P.J.
Receptor activation with hepatocyte growth factor agonists Patent: US 5763584-A 9 09-JUN-1998;
Location/Qualifiers
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Pred. No. 3.3e+04;
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Godowski, P. J., Lokker, N. A. and Mark, M. R.
Hepatocyte growth factor variants
Patent: US 5547856 A 10 20-AUG-1996;
Location/Qualifiers
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Unclassified.
1 (bases 1 to 30)
Godowski,P.J., Lökker,N.A. and Mark,M.R.
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Sequence 10 from patent US 5547856.
125036 125036.1 GI:1604906
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Sequence 10 from patent US 5580963.
130498
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07-0CT-1996

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1 (bases 1 to 21)
Gallie,B.L., Dunn,J.M. and Stevens,J.K.
Gallie,B.L., reagents and kit for diagnosis and targeted screening for retinoblastoma
Patent: US 5550020-A 7 27-AUG-1996;
Location/Qualifiers
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Sequence 7 from patent US 5550020.
125220
125220.1 GI:1605090
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Sequence 50 from Patent WO0118198.
AX093520
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92.3%;
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Best Local Similarity 92.3
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Unclassified.
I (bases 1 to 21)
Stevens, J. K. and Dunn, J.M.
Method for testing for mutations in DNA from a patient sample Patent: US 5545527-A 7 13-AUG-1996;
Location/Qualifiers
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Godowski.P.J.
Chimeric hepatocyte growth factor (HGF) ligand variants
Patent: USG84136-A 9 04-NOV-1997;
Location/Qualifiers
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Pred. No. 3.3e+04;
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 Single-chain hepatocyte growth factor variants
Patent: US 5580963-A 10 03-DEC-1996;
Location/Qualifiers
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92.3%; Pred. No. 5.8e+04;
tive 0; Mismatches 1;
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Sequence 7 from patent US 5545527.
124623.1 GI:1604493
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Sequence 9 from patent US 5684136.
172560
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86:78;
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Best Local Similarity 86.7
Matches 13; Conservative
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Best Local Similarity 86:7
Matches 13; Conservative
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(bases 1 to 21)
Weissenbach, J. and Hazan, J.
Cloning, expression and characterisation of the spg4 gene responsible for the most frequent form of autosomal spastic
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Patent: WO 0118198-A 50 15-MAR-2001;
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Location/Qualifiers
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Score 11.4; DB 10;
Pred. No. 5.8e+04;
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Stemmer, W.P.C. and Crameri, A.
Methods for generating polynucleotides having desired
characteristics by iterative selection and recombination
Patent: US 5811238-A 14 22-SEP-1998;
Location/Qualifiers
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1 (bases 1 to 24)
Stemmer,W.P.C.
Methods for in vitro recombination
Patent: US 5605793-A 14 25-FEB-1997;
AR040915 24 bp DNA
Sequence 14 from patent US 5811238.
AR040915.1 GI:5961411
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Sequence 14 from patent US 5830721.
AR051822 GI:5975186
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Sequence 14 from patent US 5605793.
136212.
136212.1 GI:2086725
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Unclassified.
1 (bases 1 to 24)
Stemmer,W.P.C. and Crameri,A.
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10_est48:* 10_est50:* 10_est51:* 10_est51:* 10_est51:* 10_est51:* 10_est56:* 10_est56:* 10_est56:* 10_est56:* 10_est56:* 10_est60:* 10_est60:* 10_est60:*	9b_est64:* 9cb_est65:* 9cb_est65:* 9cb_est75:* 9cb_est76:* 9cb_est76:* 9cb_est78:* 9cb_est81:* 9cb_est81:* 9cb_est81:* 9cb_est81:* 9cb_est82:*	Dest101::  Dest101::  Dest103::  Dest104::  Dest66::  Dest67::  Dest77::  De	Dest97: #   Dest98: #   m_esthum29: #   m_esthum31: #   m_esthum33: #   m_esthum33: #   m_esthum33: #   m_estro21: #   m_estro21: #   m_estro23: #   m_estro3: #   m_estro
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Unpublished (2000) COMMENT Contact: Robert B. Weiss University of Utah Genome Center	Municipal Control Cont	Oy 1 tggcttatcttcagt 15	RESULT 2 AZ830358 LOCUS LOCUS LOCUS LOCUS AZ830358 AZ830358 AZ830358 AZ830358 AZ830358 LOCUS AZCESSION AZ830358 AZ830358 LOCUS AZ830358 AZENTOR AZEN
SUMMARIES Result Query No. Score Match Length DB ID Description	c         1         11.8         78.7         21         249         AZ787920         AZ787920         AM0034M09           c         2         11.4         76.0         23         250         AZ890358         AZ69599         AZ6	ALIGNMENTS	AZ787920/c AZ787920 AZ787920 AZ787920 DEFINITION CLOSS ACCESSION AZ787920 A

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerase inchemated by repeated by the polymerase and T4 polymerase inchemated by the blunt ends in high monlar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 (gil47321). a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                       Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
   Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                     Mouse whole genome scaffolding with paired end reads from 10kb
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T. Drucei sheared genomic DNA clone 187a02, reverse sequence,
genomic survey sequence.
AL476274
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/clone="UUGCIMO519N09"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0519 row: N column: 09
Seq primer: cGTTGTAAAACGACGCCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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   ,M., Rose,M., Rose,R., and Wright,D.,Weiss,R.
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Fax: 801 585 7177
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               Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly
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/note="Westor: PWD42Iv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0109 row: M column: 04
Seg primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
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/clone="UUGC2M0109M04"
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AA906910 37 bp mRNA EST 09-JUN-1998 oj70b12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1503647 3' similar to TR:Q33565 Q33565 EATRO 164 KINETOPLAST
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 1.3e+05;
0; Mismatches 1; Indels
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/sex="male"
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/lab_host="DH108"
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/dev_stage="4 weeks"
/lab_host="DH10B"
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/clone="IMAGE:1503647"
                                                              /organism="Mus musculus"
               Location/Qualifiers
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                                                                                     /strain="C57BL/6J
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AA906910.1 GI:3042370
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91.7%;
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Best Local Similarity 91.7
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Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 ISA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
to give a tight size distribution (
the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Quallfiers
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Bukarayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukarayota; Metazoa; Chordata; Craniata; Wuridae; Murinae; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI118907 28 bp mRNA EST 02-SEP-1998 uc15767.r1 Soares_mammary_gland_NDAMG Mus musculus cDNA clone IMAGE:1398085 5' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ; mRNA sequence.
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Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10.8; DB 258; Length 40; Pred. No. 8e+04; 0; Mismatches 2; Indels 0
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Sossible reversed olone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
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/db_xref="taxon:5691"
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85.7%;
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Best Local Similarity 85.7
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Pred. No. 1.3e+05;
                     Mismatches
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/db_xref="taxon:9606"
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     91.78;
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Best Local Similarity 91.7%;
Matches 11; Conservative (
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1106 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 37)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
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/db_xref="taxon:9606"
/clone="IxAGE:1590073"
/clone_lib="NCI_CGAP_Kid5"
/iisaue_type="2 pooled tumors (clear cell type)"
/lab_host="DH108"
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Pred. No. 1.3e+05;
0; Mismatches 1; Indels (
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AA946896
AA946896.1 GI:3110291
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91.7%;
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DB 14; Length 37;

Score 10.4;

69.38;

Query Match

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LMSS03019 Human adult lung 3' directed Mbol cDNA Homo sapiens cDNA D45802 D45802.1 G1:662756
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Morimyo,M. and Mita,K.
Identification of expressed sequence tags of Schizosaccharomyces
  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Human adult lung 3' directed MboI cDNA"
/note="Adult human lung, 3' directed MboI"
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National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 38)
Itoh, K., Okubo, K., Yosii, J., Yokouchi, H. and Matsubara, K. An expression profile of active genes in human lung 95236275
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Pred. No. 1.3e+05;
0; Mismatches 1; Indels 0
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Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Institute for Molecular and Cellular Biology
Osaka University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3-1, Yamadaoka, Suita, Osaka, 565, Japan
Tel: 06-877-5111 x3910
Fax: 06-877-1922
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with 74 bNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114|gb|RF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplicillin resistance."
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12, USA
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Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.; Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ324419 46 bp DNA GSS 29-SEP-2000
1M0046B20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0046B20 F, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 10.4; DB 249; Length 45; Pred. No. 1.4e+05; 0; Mismatches 1; Indels 0
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Fax: 801 585 7177
Famil: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

    .46
    /organism="Mus musculus"
/strain="C57BL/6J"

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/clone="UUGC1M0046B20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 69.3%;
Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                                                                                                                                                   Choice—"Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the Smal site of M13mp19 DNA and the direction of DNA agequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the Wcold Wide Web. (URL, http://www.nirs.go.jp)"
                                                                  Rm.\ 308,\ \dot{B}lomedical Polymers Research Bldg.,\ 20 S.\ 2030 E.,\ SLC,\ UT 84112,\ USA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 45)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Slam,H., Longacres,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D.,Weiss,R.
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(http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ772066 45 bp DNA GSS 16-FEB-2001
1M0574L08R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0574L08 R, DNA sequence.
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/db_xref="taxon:10090"
/clone="UGCIM0574L08"
/clone_lib="Mouse lOkb plasmid UUGCIM library"
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Pred. No. 1.3e+05;
0; Mismatches 1; Indels 0,

    .42
    /organism="Schizosaccharomyces pombe"

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Insert Length: 10000 Std Error: 0.00
Plate: 0574 row: L column: 08
Seq primer: CACAGGAAACAGCTATGACC
Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Best Local Similarity 91.77
Matches 11, Conservative
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Fax: 801 585 7177
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            was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chancally-competent E. coli XL10-Gold (Stratagene) cells and selected for amplcillin resistance."
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Mm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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(http://www.jax.org/resources/documents/dnares/). The DNA
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longarere, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/clone="UUGC2M0046D07"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.3%; Score 10.4; DB 241; Length 46; 91.7%; Pred. No. 1.4e+05; ive 0; Mismatches 1; Indels 0;
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Insert Length: 10000 Std Error: 0.0
Plate: 0046 row: D column: 07
Seq primer: CACACGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 46.
Location/Qualifiers
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Matches 11; Conservative
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 gplAF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLLO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Tumor Gene Index

Orpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCT-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov

Seq primer: -40RP from Gibco.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (GGAP),
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 0.8 kb."
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/tissue_type="hepatic adenoma"
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Laboratory Mouse DNA Resource
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project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TRED927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v +i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
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Fine Structural analysis of transcription start sites of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries of nupublished (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
108-8639, Japan
Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitcmo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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                                                                                                                                                                                                           AU103710 50 bp mRNA EST 05-APR-2001
AU103710 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HEP14727, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
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T. Drucel sheared genomic DNA clone 288e04, forward sequence, Qenomic survey sequence.
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(bases 1 to 22)

Hall, N. Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Hallingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S. E., Rajandream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Pred. No. 1.4e+05;
0; Mismatches 1; Indels 0
         Score 10.4; DB 120; Length 49;
Pred. No. 1.4e+05;
0; Mismatches 1; Indels 0
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/db_xref="taxon:9606"
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/clone=lib="Sugano Homo sa
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Matches 11; Conservative
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Gaps

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Length 22;

Score 10.2; DB 258; Length Pred. No. 1.6e+05; 0; Mismatches 3; Indels

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11908, A 2, Appli 7807, Ap 7807, Ap 10084, A 13218, A 13218, A 7, Appli 1511, Ap 14337, A

13, Appl 15, Appl 18, Appl 2269, Ap

US-09-877-804-10

ALIGNMENTS

Sequence Seq

US-09-818-875-2710 US-09-818-875-2714 US-09-818-875-2714 US-09-818-875-2714 US-09-866-108-11908 US-09-371-7728-7807 US-09-371-7728-7807 US-09-371-7728-7807 US-09-371-7728-7807 US-09-371-7728-7807 US-09-371-7728-7807 US-09-371-7728-7807 US-09-371-7728-7807 US-09-25-592-13218 US-09-921-1511 US-09-921-515-13 US-09-921-515-18 US-09-921-515-18

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GRUERAL INTORNATION:

GRUERAL INTORNATION:

APPLICANT: 01, Yoogang
APPLICANT: 01, Yoogang
APPLICANT: HANEL, David K.

APPLICANT: SANDANON, Mark T.

CURRENT FILING DATE: 2001-05-25

FRIOR PAPLICATION NUMBER: US 60/236.6

FRIOR APPLICATION NUMBER: US 60/236.359

FRIOR APPLICATION NUMBER: BCT/US01/00666

FRIOR APPLICATION NUMBER: PCT/US01/00666

FRIOR APPLICATION NUMBER: PCT/US01/00666

FRIOR FILING DATE: 2001-01-30

FRIOR FIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-866-108-7017/c; Sequence 7017, Application US/09866108; GENERAL INFORMATION:
  00000000
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APPLICANT: GU, YIZADON
APPLICANT: GI, YIZADON
APPLICANT: JI, YONGGANG
APPLICANT: JI, YONGGANG
APPLICANT: JI, YONGGANG
APPLICANT: PENN, Sharron G
APPLICANT: RANK, David R.
APPLICANT: GHEN, WENDREN: US/09/866,108
CURRENT: SHANNON, MAIK
TITLE OF INVENTION: MYOBER: US/09/866,108
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT PALLCATION NUMBER: US/09/866,108
FRIOR PELICATION NUMBER: US/09/05/26
PRIOR PLICANTION NUMBER: PCT/USO1/00666
PRIOR PLICANTION NUMBER: PCT/USO1/00667
PRIOR PLICANTION NUMBER: PCT/USO1/00669
PRIOR PLICANTION NUMBER: PCT/USO1/00660
PRIOR PLICANTION NUMBER: PCT/USO1/00660
PRIOR PLICANTION NUMBER: PCT/USO1/00660
PRIOR PLICANTION NUMBER: PCT/USO1/00670
PRIOR PLILANG DATE: 2001-01-30
PRIOR PRIOR PLILANG DATE: 2001-01-30
PRIOR PLILANG DATE: 2001-01-30
PRIOR PRILANG DATE: 2001-01-30
PRIOR PRIPARE: PRI
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Pred. No. 3.2e+03;
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US-09-866.108-11910/c
; Sequence 11910, Application US/09866108
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
                                                                                                                                                                                                                           ; Sequence 11909, Application US/09866108; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.0%;
87.5%;
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Best Local Similarity 87.5
Matches 14; Conservative
      4 aagcagctgccattat 19
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                                    16 AAGCAGCTGCCACCAT 1
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US-09-866-108-11909/c
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; ORGANISM: HOMO :
US-09-866-108-11909
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SEQ ID NO 11909
LENGTH: 25
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APPLICARY: GU, YIZhong

APPLICARY: HANKEL, David K.

APPLICARY: HANKEL, David K.

APPLICARY: SHANNO, Wark

TITLE GE INVESTION WORSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

TITLE REPERBURE: ADMICA-7.

CURRENT FILING DAFE: 2001-05-25.01

PRIOR FILING DAFE: 2001-06-25

PRIOR FILING DAFE: 2001-06-25

PRIOR FILING DAFE: 2001-06-25

PRIOR FILING DAFE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/0066

PRIOR PLING DAFE: 2001-01-30

PRIOR FILING DAFE: 2001-01-30

PRIOR PRIOR PRIOR DAFE: 115752

SOFTWARE: ABOUTD SOFTWARE: ABOUTD SO
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Pred. No. 3e+03;
0; Mismatches 2; Indels
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87.5%;
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                       TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-7017
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; ORGANISM: Homo sapiens
US-09-866-108-7018
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Best Local Similarity
Matches 14; Conserva
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Best Local Similarity
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-09-866-108-7018/c
LENGTH: 17
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Sequence 11912, Application US/09866108
GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
CURENT BANKO, Mark
TITLE OF INVENTION: MACONIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-27
PRIOR PRILING DATE: 2000-10-27
PRIOR PRILING DATE: 2000-10-27
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-09-27
PRIOR PELLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-
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Best Local Similarity 87.5
Matches 14; Conservative
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US-09-866-108-11912/c
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; ORGANISM: HOMO s
US-09-866-108-11911
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                                                               APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MARK
APPLICANT: SHANNON, MARK
TITLE OF INVENTION: MYCSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AECMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR PAPLICATION NUMBER: US 60/2307,456
PRIOR PAPLICATION NUMBER: US 60/230,6
PRIOR APPLICATION NUMBER: US 60/230,6
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PRIOR DATE: 2001-01-30
PRIOR PLIING DATE: 2001-01-30
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GENERAL INFORMATION:
APPLICANT: GU, YIZHONG
APPLICANT: JI, YONGGANG
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: SHANNON, Mark
TITLE OF INVERTION: WOOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ABOMIGA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
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Pred. No. 3.2e+03;
0; Mismatches 2; Indels
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SOFTWARE: Acomica Sequence Listing Engine
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PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PLICATION WUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
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87.5%;
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Matches 14; Conservative
                                                   RANK, David R.
CHEN, Wensheng
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; ORGANISM: Homo sapiens
US-09-866-108-11910
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LENGTH: 25
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Sequence 11914, Application US/09866108

GENERAL INFORMATION:
APPLICANT: G1, Yizhong
APPLICANT: J1, Yongaang
APPLICANT: D1, Yongaang
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David K.
APPLICANT: BHANDEN, David R.
APPLICANT: BHANDEN, David R.
APPLICANT: BHANDEN, DAVIG R.
APPLICANT: BHANDEN, DAVIG R.
APPLICANT: BHANDEN, DAVIG R.
APPLICANT: APPLICATION: WORSHENG
APPLICANT: BHANDEN, DAVIG R.
APPLICANT: BHANDEN, DAVIG R.
APPLICANT: BHANDEN, DAVIG R.
APPLICANT: BHANDEN, DAVIG R.
APPLICANT: CHEN, WENSHENG
APPLICANTON NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING PRIOR PLING PUMBER: PCT/US01/00665
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Pred. No. 3.2e+03;
); Mismatches 2;
                              PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION UNMER: PCT/US01/00661
PRIOR APLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SEQ ID NO 11913
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   APPLICATION NUMBER: PCT/US01/00662
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
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FILING DATE: 2000-09-21
APPLICATION NUMBER: US 60/266,860
FILING DATE: 2001-02-05
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87.5%;
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Best Local Similarity 87.5
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108-11913
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GU YIZHONG
APPLICANT: GU YIZHONG
APPLICANT: BENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: RANK, David K.
APPLICANT: RANK, David K.
APPLICANT: GENN, Wensheng
APPLICANT: GHEN, Wensheng
APPLICANT: SHANNON, MAIK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEGMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2000-105-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00665
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                                                  PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-03-31
PRIOR PILING DATE: 2001-03-31
PRIOR PILING DATE: 2001-03-31
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RAPLICATION NUMBER: PCT/US01/00665

RAPLICATION NUMBER: PCT/US01/00668

RAPLICATION NUMBER: PCT/US01/00668

RELING DATE: 2001-01-30

RAPLICATION NUMBER: PCT/US01/00663

RAPLICATION NUMBER: PCT/US01/00663

RAPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 11912
LENGTH: 25
APPLICATION NUMBER: PCT/US01/00664
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Best Local Similarity 87.5
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108-11912
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE TELE REFERENCE: AROMCA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
      Pred. No. 3.2e+03;
); Mismatches 2;
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2001-03-7
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MARK
Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                Query Match 64.0
Best Local Similarity 87.5
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108-11916
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US-09-866-108-11916/c
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APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MAIN
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ABOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
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Pred. No. 3.2e+03;
0; Mismatches 2;
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PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELICATION NUMBER: US 60/207,456
PRIOR PELICATION NUMBER: GB 24263.6
PRIOR FILLING DATE: 2000-10-04
PRIOR FILLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PELING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
                              SOFTWARE: Aeomica Sequence Listing Engine SEQ ID NO 11914
LENGTH: 25
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PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SSOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 11915
LENGTH: 25
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11915, Application US/09866108
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                            Query Match 64.0%;
Best Local Similarity 87.5%;
Matches 14; Conservative
   NUMBER OF SEQ ID NOS: 15752
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; ORGANISM: Homo sapiens
US-09-866-108-11915
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  Length 25;
                     Indels
Score 12.8; DB 6;
Pred. No. 3.2e+03;
0; Mismatches 2;
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US-09-866-108-11917/c
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Length 25;

64.0%; Score 12.8; DB 6;

Query Match

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Squence 10, Application US/09930251

GENERAL INFORMATION:
APPLICANT: Matsuo, Masafumi; Kamei, Shoichiro
TITLE OF INFORMON: Pharmaceutical Composition for Treatment of Duchenne Muscular
FILE REFERENCE: P21360
CURRENT APPLICATION NUMBER: US/09/930,251
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: JP2000-256547
PRIOR PILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 10
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Pred. No. 7.1e+03;
0; Mismatches 3;
              FILE REFERENCE: ACOUSTICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-07
PRIOR PRILING DATE: 2000-10-27
PRIOR PRILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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SEQ ID NO 11918
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llarity 82.4%;
Conservative
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nes 14; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108-11918
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                           APPLICANT: HANELL, David K.

APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
TTTLE OF INVENTION, MAIK
TTTLE OF INVENTION, MAIK
TTTLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT PELLON NUMBER: US 60/205, 456
PRIOR PAPLICATION NUMBER: US 60/207, 456
PRIOR PAPLICATION NUMBER: GB 2426. 6
PRIOR APPLICATION NUMBER: GB 2426. 6
PRIOR PLICATION NUMBER: CB 2000-10-04
PRIOR PLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PLICATION NUMBER: PCT/US01/00669
PRIOR PLILING DATE: 2001-01-30
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
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Pred. No. 3.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aeomica Sequence Listing Engine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11918, Application US/09866108
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: RANK. David K.
APPLICANT: RANK. David R.
APPLICANT: CHEN Wensheng
APPLICANT: SHANNON, MATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
Sequence 11917, Application US/09866108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.0%;
87.5%;
                                                                  APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
PPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence I
SEQ ID NO 11917
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Matches 14; Conservative
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CORGANISM: Homo sapiens
US-09-866-108-11917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 AAGCAGCTGCCACCAT
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US-09-866-108-11918/c
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49 GTAAGCCGAAGCCATTA 33

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Search completed: October 2, 2001, 16:55:02 Job time: 17665 sec
            g
                                                                                                                                                                                                                                            Sequence 6257, Application US/60278561

Sequence 6257, Application US/60278561

Sequence 6257, Application US/60278561

Sequence 6257, Application US/60278561

APPLICANT: Morris, MacConald
APPLICANT: Lal, Preeti
APPLICANT: Die, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polymorphisms Identified Thereby
FILE REFERENCE: GX-0012-1 P
CURRENT APPLICATION NUMBER: US/60/278,561
CURRENT APPLICATION NUMBER: US/60/278,561

KUMBER OF SEQ ID NOS: 15598
SOFTWARE: PERL Program
SEQ ID NO 6257

LENGTH: 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 42;
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Pred. No. 7.5e+03;
0; Mismatches 3;
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OTHER INFORMATION: Incyte ID No: SNP00060057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: snp

: LOCATION: 26

: OTHER INFORMATION: 229652.27, 1901, A->G

0S-60-278-561-6257
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82.4%;
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Query Match
Best Local Similarity 82.49
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 82.49
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                            RESULT 14
US-60-278-561-6257/c
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/ cgn2_6/ptodata///pna/uS6013_COMB.seq:
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/ cgn2_6/ptodata///pna/uS6016_COMB.seq:
/ cgn2_6/ptodata///pna/uS6019_COMB.seq:
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US-60-233-620-16838

US-60-233-620-16838

US-60-234-017-209206

US-60-234-017-209206

US-60-234-618-83

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US-09-377-310-29
US-09-757-100B-29
PCT-USOO-18999-8
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PCT-US99-18603-16
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16.701 Million cell updates/sec
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    /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Sequence 9, Appli Sequence 9, Appli Sequence 29, Appli Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl

Description

Sequence 8, Appli Sequence 16838, A Sequence 16838, A Sequence 209206, Sequence 20420, A Sequence 50420, A Sequence 5139, Appl Sequence 1519, Appl Sequence 1519, Appl Sequence 1519, Appl Sequence 16193, Appl Sequence 16193, Appl Sequence 28, Appl Sequence 21960, A Sequence 21960, A

Sequence 27969, Sequence 352215,

Sequence 15, Sequence 16,

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                                                                                                                                            APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0476
CURRENT PILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310A
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 9
LENGTH: 20
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ALIGNMENTS
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                                                                                                                                  : Isis Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: antisense sequence PCT-US00-18999-9
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                                                                                          Sequence 9, Application PC/TUS0018999
GENERAL INFORMATION:
APPLICANT: Isis Pharmaceuticals, In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09377310A GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO
LENGTH: 20
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Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity
Matches 20, Conserv
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US-09-757-100B-9
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APPLICANT: Garde, William A.

APPLICANT: Garde, William A.

APPLICANT: Nero, Pamela S.

TITLE OF INVENTION: Expression

FILE REFERENCE: ISPH-0476

CURRENT APPLICATION NUMBER: PCT/US00/18999

CURRENT APPLICATION NUMBER: 09/377,310

PRIOR APPLICATION NUMBER: 09/377,310

PRIOR APPLICATION NUMBER: 09/377,310

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 29

LENGTH: 15
APPLICANT: Monia, Brett P.
APPLICANT: Garde, William A.
APPLICANT: Garde, William A.
APPLICANT: Garde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase;
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0533
CURRENT APPLICATION NUMBER: US/09/757,100B
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 2001-03-15
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 9
LENGTH: 20
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: antisense sequence PCT-US00-18999-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
100.0%;
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity
Matches 20; Conserv
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Gaps

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; Sequence 8, Application US/09377310A; GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase; TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389; CURRENT APPLICATION NUMBER: US/09/377,310A; CURRENT FILING DATE: 1999-08-19; NUMBER OF SEQ ID NOS: 43; SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8; SEQ ID NO 8: 2.0
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APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Nero, Pamela S.
TILE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase TILE OF INVENTION: Expression
FILE REFERENCE: ISPH-0533
CURRENT APPLICATION NUMBER: US/09/757,100B
CURRENT APPLICATION NUMBER: 09/377,310
PRIOR PILING DATE: 1999-08-19
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  CURRENT APPLICATION NUMBER: PCT/USO0/18999
CURRENT FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
LENGTH: 20
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PRIOR FILING DATE: 2000-07-13
                                                                                                                                                                                                                                        ; OTHER INFORMATION: antisense sequence PCT-US00-18999-8
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COTHER INFORMATION: antisense sequence
US:09-377-310-8
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100.0%; Pre
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                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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US-09-757-100B-8
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APPLICANT: Gaarde, William A.

APPLICANT: Gaarde, William A.

APPLICANT: Gaarde, William A.

APPLICANT: Mero, Pamela S.

TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase;

TITLE OF INVENTION: Expression

FILE REFERENCE: ISPH-0533

CURRENT FAPLICATION NUMBER: US/09/757,100B

PRIOR APPLICATION NUMBER: 09/377,310

PRIOR PELING DATE: 1999-08-19

PRIOR FILING DATE: 1999-08-19

PRIOR FILING DATE: 2000-07-13

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 29

LENGTH: 15
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APPLICANT: ISIS PHARMACEUTICALS, INC.
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase FILE REFERENCE: ISPH-0476
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-03189
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: antisense sequence US-09-377-310-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 29, Application US/09757100B GENERAL INFORMATION:
                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 15; Conservative
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US-09-757-100B-29
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                                                                                                                                                                        SEQ ID NO 29
LENGTH: 15
                                                                                                                                                                                                                    TYPE: DNA
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; DATABASE ACCESSION NUMBER: SGD YER050C US-60-232-638-58459
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Best Local Similarity
Matches 16; Conserva
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Best Local Similarity
Matches 15; Conserv
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LENGTH: 25
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET 0200cpl
CURRENT APPLICATION NUMBER: US/09/422,978
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-04-21
MUMBER OF SEQ ID NOS: 11796

SEQ ID NO 407

LENGTH: 47
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GENERAL INFORMATION:
APPLICANT: Mittmann
I APPLICANT: Mittmann
CHARL INFORMATION:
TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
CURRENT APPLICATION NUMBER: US/60/232,638
CURRENT FILING DATE: 2000-09-14
NUMBER OF SEQ ID NOS: 138410
SOCTUMENT: FastSEQ for Windows Version 4.0
SEQ ID NO 58459
LENGTH: 25
                                                                                                                                                                       Length 20;
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Pred. No. 2.3e+03;
0; Mismatches 2;
                                                                                                                                                                     Query Match 75.0%; Score 15; DB 29; 18est Local Similarity 100.0%; Pred. No. 1.6e+03; Matches 15; Conservative 0; Mismatches 0;
                                                                        FEATURE:
CTHER INFORMATION: antisense sequence US-09-757-100B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Saccaromyces cerevisiae PUBLICATION INFORMATION:
                                   TYPE: DNA ORGANISM: Artificial Sequence
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88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
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ORGANISM: Homo Sapiens
FEATURE:
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LOCATION: 24
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SEQ ID NO 8
LENGTH: 20
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  Length 25;
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Sequence 209206, Application US/60234017
GENERAL INFORMATION:
APPLICANT: Mithmann, M
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of Mus;
TITLE OF INVENTION: Methods of Genetic Analysis of Mus;
FILE REFERENCE: 3115
CURRENT APPLICATION NUMBER: US/60/234,017
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: FastSEQ for Windows Version 4.0
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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APPLICANT: Mittnann
APPLICANT: Mittnann
TITLE OF INVENTION: Methods of Genetic Analysis of
TITLE OF INVENTION: Methods of Genetic Analysis of
TITLE OF INVENTION: Machinopsis thaliana
FILE REFERENCE: 3116
CURRENT APPLICATION NUMBER: US/60/233,620
CURRENT FILING DATE: 2000-110-24
NUMBER OF SEQ ID NOS: 131820
SOFTWARR: FastSEQ for Windows Version 4.0
SEQ ID NO 16838
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14.4; DB 55;
Pred. No. 3.4e+03;
0; Mismatches 1;
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Pred. No. 4.3e+03;
0; Mismatches 3;
Score 14.4; DB 55
Pred. No. 3.4e+03;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AC005499
US-60-233-620-16838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CREANISM: MUS MUSCULUS
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank AI504141
US-60-234-017-209206
                                                                                                                                                                                                                ; Sequence 16838, Application US/60233620; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Arabidopsis thaliana
72.0%;
93.8%;
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93.8%;
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84.2%;
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Best Local Similarity 93.8
Matches 15; Conservative
                                       Conservative
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Search completed: October 2, 2001, 21:50:12
Job time: 24525 sec
                                                                                                                  GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: HARDA, Hidepuki

APPLICANT: TAGASHIRA, Shuzo

APPLICANT: TAGASHIRA, Masashi

APPLICANT: NAKATSUKA, Masashi

TITLE OF INVENTION: DNA Participating In Regulation of Expression of PEBPZalphaA Ge

TITLE OF INVENTION: Thereof

TITLE OF INVENTION: Thereof

FILE REFERENCE: 0020-4685P

CURRENT APPLICATION NUMBER: 254250/1997 Japan

PRIOR FILING DATE: 1997-10-15

PRIOR APPLICATION NUMBER: 29407/1997 Japan

PRIOR FILING DATE: 1998-04-08

PRIOR FILING DATE: 1998-04-08

PRIOR PELING DATE: 1998-04-08
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APPLICANT: Affymetrix, Inc.
TTLE OF INVENTION: Methods of Genetic Analysis of Yeast
FITLE OF INVENTION: Methods of Genetic Analysis of Yeast
FILE REFERENCE: 3110
CURRENT FILING DATE: 2000-09-14
NUMBER OF SEQ ID NOS: 138410
SOFTWARE: FALSEQ for Mindows Version 4.0
SEQ ID NO 50420
LENGTH: 25
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Pred. No. 6.6e+03;
0; Mismatches 2;
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; ORGANISM: Other nucleic acid, synthetic DNA
US-09-486-816-26
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: SGD YDR240C
US-60-232-638-50420
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                                                                      Sequence 26, Application US/09486816
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 26
LENGTH: 20
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Best Local Similarity 88.2%;
Matches 15; Conservative
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3 tttgataaatgctaggt 19
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Best Local Similarity 88.23
Matches 15; Conservative
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2052, Ap 116945, A 17300, A 18915, A 20162, A 5680, Ap 6194, Ap 6484, Ap 6683, Ap 7183, Ap

24, Appl 6, Appli 3901, Ap 13773, A

7502, A 8470, A 25152,

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

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Sequence 6107, Application US/60278258

SEGURAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Morris, MacDonald
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polymorphisms Identified Thereby
CURRENT APPLICATION NUMBER: US/60/278,258
CURRENT APPLICATION NUMBER: US/60/278,258
NUMBER OF SEQ ID NOS: 17730
SEQ ID NO 6107
TENCH: APPLICATION OF 107
   Seduence Sequence Seq
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GRNERAL INFORMATION:
APPLICANT: Warrington, Janet
APPLICANT: Shah, Nila
APPLICANT: Gingeras, Thomas Raymond
APPLICANT: Affymetrix, Inc.
APPLICANT: Affymetrix, Inc.
FILE OF INVENTION: Human Lymphoblast Polymorphisms
FILE REPERENCE: 3229.2
CURRENT APPLICATION NUMBER: US/09/574,376B
Score 13.8; DB 8;
Pred. No. 8.8e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: SNP00057112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: 350403.1, 20, G->A US-60-278-258-6107
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Best Local Similarity 88.2
Matches 15; Conservative
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   RESULT 2
US-09-574-376B-1127/c
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Sequence 557, Appl
Sequence 557, App
Sequence 9054, App
Sequence 11076, Appl
Sequence 173, Appl
Sequence 773, Appl
Sequence 1751, Appl
Sequence 12658, Appl
Sequence 12658, Appl
Sequence 96, Appl
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Sequence 96, Appl
Sequence 212658, Appl
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Sequence 1127, Ap
Sequence 1141, Ap
Sequence 1801, Ap
Sequence 5496, Ap
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8122, Ap
                                                                                                                                                                                                    Search time 2173.58 Seconds (without alignments) 19.290 Million cell updates/sec
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Sequence 1
Sequence 4
Sequence 8
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/USOG_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

8: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq2:*

8: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq2:*
                            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-811-274-1141

US-09-811-274-1141

US-09-817-879-481

US-09-817-879-481

US-09-817-879-6920

US-09-817-879-6920

US-09-817-879-6920

US-09-817-879-6920

US-09-817-879-6920

US-09-817-879-6920

US-09-23-1107-20

US-09-23-170-20

US-09-801-273-105-80

US-09-801-273-105-80

US-09-801-255-89-1265-80

US-09-801-285-80

US-09-817-879-2431

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 50
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Match 1
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1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.0%;
87.5%;
                                                                                 Query Match 64.0%;
Best Local Similarity 77.8%;
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                                                                                                                                                                ; OTHER INFORMATION: DNAZyme US-09-817-879-5496
                                                                                                                        14; Conservative
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Best Local Similarity 87.5
Matches 14; Conservative
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US-09-801-274-1801
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US-09-817-879-5496
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GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Leander, Eric S.
APPLICANT: Lender, Eric S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2825.2009-001
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/187,510
PRIOR APPLICATION NUMBER: US 60/206,129
PRIOR PILING DATE: 2000-03-07
PRIOR PLICATION NUMBER: US 60/206,129
PRIOR FILING DATE: 2000-05-22
NUMBER OF SED ID NOSS: 1802
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1801
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1141, Application US/09801274
GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Lander, Eric S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2255.2009-001
CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT APPLICATION NUMBER: US 60/187,510
PRIOR PILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 1802
SOFTHARE: PRESENCE TO NOS: 1802
SOFTHARE: PRESENCE TO WINDOWS VERSION 4.0
SEQ ID NO 141
                                                                                                                                                                                                                            Length 31;
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Pred. No. 2.8e+03;
1; Mismatches 3
                    NUMBER OF SEQ ID NOS: 1330
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1127
LENGTH: 31
2000-05-19
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Best Local Similarity 77.8%;
Matches 14; Conservative
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8 ttgccaaaygctcggtat 25
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Best Local Similarity 75.0
Matches 15; Conservative
                                                                                                                      ORGANISM: Homo sapiens;
PUBLICATION INFORMATION:
US-09-574-376B-1127
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US-09-801-274-1141
  CURRENT FILING DATE:
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US-09-801-274-1801
                                                                                                        TYPE: DNA
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APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBHBO0-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5496
LENGTH: 31
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GENERAL INFORMATION:
APPLICANT: Silhay, Daniel
APPLICANT: Silhay, Daniel
APPLICANT: Silhay, Daniel
APPLICANT: Siraman, Priya
ITILE OF INVENTION: Plastid Promoters for Transgene
ITILE OF INVENTION: Expression in the Plastids of Higher Plants
CURRENT APPLICATION NUMBER: US/09/445,283B
CURRENT FILING DATE: 1998-12-03
PRIOR PILING DATE: 1998-06-03
PRIOR FILING DATE: 1998-06-03
PRIOR FILING DATE: 1999-09-12
PRIOR FILING DATE: 1997-09-12
SPIOR PRIOR APPLICATION NUMBER: 60/048,376
PRIOR FILING DATE: 1997-06-03
SOFTWARR: FASTSEQ for Windows Version 3.0
SEQ ID NO 47

LENGTH: 27
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Score 12.8; DB 6; Pred. No. 2.8e+03;
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Pred. No. 2.8e+03;
0; Mismatches 2;
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TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBBBO0-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFFWARE: Patentin version 3.0
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CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
SEQ ID NO 9054
LENGTH: 31
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GENERAL INFORMATION:
APPLICANT: Havukkala, 11kka J
TITLE OF INVENTION: Polynucleotides isolated from plants; TITLE OF INVENTION: and methods for their use.
FILE REFERENCE: 1054P3
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Pred. No. 5.8e+03;
); Mismatches 3;
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Pred. No. 5.8e+03;
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                                                                                 APPLICANT: Ribozyme Pharmaceuticals Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ribozyme Pharmaceuticals Inc.
                                         ; Sequence 6920, Application US/09817879 ; GENERAL INFORMATION:
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82.4%;
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82.4%;
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US-09-817-879-9054
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Best Local Similarity 82.4
Matches 14; Conservative
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Best Local Similarity
Matches 14; Conserva
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                       US-09-817-879-6920
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                                                                                                                                                                                                                                                         APPLICANT: Ribozyme pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate TITLE OF INVENTION: Hepatitis C Virus Infection FILE REFERENCE: MBH800-801-F CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT APPLICATION NUMBER: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
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                                         Indels
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  Score 12.4; DB 6;
Pred. No. 4.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12.2; DB 6;
Pred. No. 5.8e+03;
                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ribozyme Pharmaceuticals Inc.
                                                                                                                                                                                                                        Sequence 4811, Application US/09817879 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5557, Application US/09817879 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.0%;
82.4%;
  62.0%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.0%;
82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 ttgctagatgctaggta 19
||||||| | ||||| ||
1 ttgctataggctagcta 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: DNAZyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 ttgctagatgctaggta 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: DNAZyme US-09-817-879-5557
Query Match 62.0
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 61.0
Best Local Similarity 82.4
Matches 14; Conservative
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                                                                               3 ttgctagatgctag 16
                                                                                                                     17 TTGCTAGATTCTAG 4
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                       US-09-817-879-4811
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US-09-817-879-5557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-817-879-4811
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LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
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     APPLICANT: Poque, Gregory P.

TITLE OF INVENTION: METHOD OF DEFERMINING THE FUNCTION OF

TITLE OF INVENTION: METHOD OF DEFERMINING THE FUNCTION OF

TITLE OF INVENTION: TRANSFECTING THE SAME INTO A HOST

TITLE OF INVENTION: TRANSFECTING THE SAME INTO A HOST

CURRENT APPLICATION NUMBER: US/09/232,170

CURRENT FILING DATE: 1999-01-15

NUMBER OF SEQ ID NOS: 49

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 36
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APPLICANT: Gearing, David P.
TITLE OF INVENTON: MUCLEIC ACID MOLECULES DERIVED FROM A
TITLE OF INVENTON: NUCLEIC ACID MOLECULES DERIVED FROM A
TITLE OF INVENTON: NUCLEIC ACID MOLECULES DERIVED FROM A
TITLE OF INVENTON: NUCLEIC ACID MOLECULES DERIVED FROM A
TITLE OF INVENTON: NUCLEIC ACID MOLECULES DERIVED FROM A
TITLE OF INVENTON: NUMBER: US 60/084,098
CURRENT FILING DATE: 1098-03-08
PRIOR APPLICATION NUMBER: US 60/123,523
PRIOR APPLICATION NUMBER: US 60/123,523
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-05-04
NUMBER OF SEQ ID NOS: 1311
SOFTWARRE: FASLESEQ FOR WINDOWS VERSION 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 11.8; DB 6;
Pred. No. 9.6e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)...(38)
; OTHER INFORMATION: n = A,T,C or G
US-09-840-424-773
                                                                                                                                                                                                                                                                                                                                                                                                             59.0%;
86.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 86.7
Matches 13; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 TCTTGCTAGATTCTA 10
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                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: VIRAL
US-09-232-170-20
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US-09-801-274-1751
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US-09-840-424-773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16613, Application US/09708690
; Sequence 16613, Application US/09708690
; GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Bavco, pam
APPLICANT: Bavco, pam
APPLICANT: Baccobcdo, Jaim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Scobcdo, Jaim
APPLICANT: Scobcdo, Jaim
APPLICANT: Baccobcdo, Jaim
APPLICANT: Baccobcdo, Jaim
APPLICANT: Baccobcdo, Jaim
APPLICANT: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHBDO, 976-L (400/002)
CURRENT APPLICATION NUMBER: US 60/708, 690
PRIOR PILING DATE: 1995-10-26
PRIOR PILING DATE: 1995-01-08
PRIOR PILING DATE: 1996-01-08
PRIOR PILING DATE: 1996-01-08
PRIOR PILING DATE: 1990-08-10
PRIOR PILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 20828
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16613
LENGTH: 31
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US-09-708-690-16613
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                                                                                                                                                                                                                                                                 60.0%; Score 12; DB 8; Length 36; 75.0%; Pred. No. 7.5e+03; ive 0; Mismatches 5; Indels
CURRENT APPLICATION NUMBER: US/60/253,378
CURRENT FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 40367
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11076
LENGTH: 36
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US-09-232-170-20/C
; Sequence 20, Application US/09232170
; GENERAL INFORMATION:
; APPLICANT: Erwin, Robert L.;
; APPLICANT: Erwin, Robert L.;
; APPLICANT: Hanley, Kathleen M.;
APPLICANT: Hanley, Kathleen M.;
APPLICANT: Lindbo, John A.;
; APPLICANT: Lindbo, John A.;
; APPLICANT: MGGee, David R.
                                                                                                                                                                                                                                                                                                                                                                1 ttttgctagatgctaggtat 20
                                                                                                                                                                                                                                                                                                                                                                                       32 TITGLCCTGTIGCTAGGTAT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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86.7%;
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Best Local Similarity 75.0
Matches 15; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
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                                                                                                                                              ; TYPE: DNA
; ORGANISM: Pinus radiata
US-60-253-378-11076
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US-09-708-690-16613
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## APPLICANT: Lander, Eric S.
### TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
### FILLE REPERENCE: 2825.2009-00.
### CURRENT APPLICATION NUMBER: US 60/187,510
### PRIOR APPLICATION NUMBER: US 60/206,129
### PRIOR PILING DATE: 2000-05-22
### PRIOR PILING DATE: 2000-05-23
### PRIOR PILING DATE: 2000
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64.0
12.8
12.8
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(cgn2_6/ptodata1/pna/US06_COMB.seq:*

(cgn2_6/ptodata1/pna/US08_COMB.seq:*

(cgn2_6/ptodata1/pna/US081_COMB.seq:*

(cgn2_6/ptodata1/pna/US0801_COMB.seq:*

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/cgn2_6/ptodata/1/pna/US6007_COMB.seq:*
/cgn2_6/ptodata/1/pna/US6008_COMB.seq:*
/cgn2_6/ptodata/1/pna/US6009_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US6011_COMB.seq:*
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                            14155048 segs, 7388405095 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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                                                                                                                                                         October 2, 2001, 21:50:10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                       1 ctagatgctaggtatctgtc 20
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20
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Perfect score:
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                                                                                                                                                                                                                                                                                                       Sequence:
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44: /cgn2_6/ptodata/1/pna/US6012_COMB.seq:*
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46: /cgn2_6/ptodata/1/pna/US6014_COMB.seq:*
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60: /cgn2_6/ptodata/1/pna/US602_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	8	ednence 8,	ednence 8,	ednence 73	edneuc	edneuc	Sequence 101590,	Sequence 28, Appl	Sequence 28, Appl	Seguenc	dneuce	Sequence 9, Appli	Sequence 3, Appril	Sequence 48863, A	equenc	equenc	edneuc	Sequence 218150,	edneuc	edneuc	ednenc	sednenc	dneuce	Sequence 17, Appl	Sequence 48858, A	Sequence /1961, A	Sequence 123/13,	35924	38163	e 65887,	equence 65897,	ີ ເ	equence 2229	equence 45867	equence 532, A	equence 58459,	equence 5, Appl	equence 14687,	equence 6840	equence 13600,	13607,	Sequence 13608, A
SUMMARIES	QI	PCT-US00-18999	S-09-377-310-8	S-09-757-100B-8	0-233-620-73	S-60-233-620-7349	8-60-216-745-2764	33-620-101	1-18999-2	177-310-28	57-100B-	-18999-	77-310-9	37-100B-9	50-220-	32-638-9916	22-978-8159	33-166-17515	33-166-218	33-166-29586	33-166-32158	33-620-8944	34-01/-9483	8-747A-1	14-117-17	00-220-4885	32-638-/1961	33-166-27	33-166-35924	33-620-38163	33-620-6588	33-620-6589	34-01/-460/	34-017-458	34-017-45867	00-106-532	32-638-58	68-416-5	60-220-1468	60-220-6840	33-62U-136	-60-233-620-1360	0-13
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	Length	20	20	20	25	25	47	25	15	15	15	20	0 0	2 2	25	25	21	25	25	25	25	2.2	C7	4.	43	2.5	72	2.5	25	25	25	25	27	2 5	25	20	25	24	25	25	07	27	C7
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;	Result No.	1	7	m ·	4.		9 U		80	6	10	Ţ	7 [	77	c 15	c 16	17	18	7	c 50	~ (	77	7 (		N	N (	27	1 C	l M	c 31	3	m c	(s)	יי רי	37	38	c 39		4			44.	45

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                                                                                Sequence 8, Application PC/TUS0018999
GENERAL INFORMATION:
APPLICANT: ISIS Pharmaceuticals, Inc.
APPLICANT: Baret P.
APPLICANT: Gaarde, William A.
APPLICANT: Garde, William A.
APPLICANT: Nero, Pamela S.
ITILE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
ITILE OF INVENTION: Expression
FILE REFERENCE: ISPH-0476
CURRENT APPLICATION NUMBER: PCT/US00/18999
CURRENT APPLICATION NUMBER: PCT/US00-07-13
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 20
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Sequence 8, Application US/09377310A

Sequence 8, Application US/09377310A

Sequence 8, Application William A.

APPLICANT: Garde, William A.

TITLE OF INVENTION: Expression

TITLE OF INVENTION: Expression

TITLE OF INVENTION: Expression

TITLE OF INVENTION: Expression

CURRENT APPLICATION NUMBER: US/09/377,310A

CURRENT PILING DATE: 1999-08-19

NUMBER OF SEO ID NOS: 43

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 8

LENGTH: 20
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100.0%; Pred. No. 1.6;
Live 0; Mismatches
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ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: antisense sequence PCT-US00-18999-8
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US-09-757-100B-8
; Sequence 8, Application US/09757100B
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 20; Conservative
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APPLICANT: Monia, Brett P.
APPLICANT: Garde, William A.
APPLICANT: Garde, William A.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase;
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0533
CURRENT APPLICATION NUMBER: US/09/757,100B
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 2000-07-13
NUMBER: OF SEQ ID NOS: 44
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 8
LENGTH: 20
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PAPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of
TITLE OF INVENTION: Arabidopsis thaliana
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GENERAL INFORMATION:
APPLICANT: Mittmann
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of
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Pred. No. 3.2e+02;
0; Mismatches 2;
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Pred. No. 1.6;
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; DATABASE ACCESSION NUMBER: GenBank AC003672
US-60-233-620-73486
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CURRENT APPLICATION NUMBER: US/60/233,620
CURRENT FILING DATE: 2000-10.24
NUMBER OF SEQ ID NOS: 131820
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 73486
LENGTH: 25
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
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Best Local Similarity 89.5%
Matches 17; Conservative
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APPLICANT: Monia, Brett P.
APPLICANT: Garde, William A.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
FILE REFERENCE: ISPH-0476
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APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310A
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 15
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                                                                                                                    76.0%; Score 15.2; DB 55;
85.0%; Pred. No. 6.9e+02;
Live 0; Mismatches 3;
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100.0%; Pred. No. 8.2e+02;
iive 0; Mismatches 0;
      ; ORGANISM: Arabidopsis thaliana
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AF096373
US-60-233-620-101590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: PCT/US00/18999
CURRENT FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
SUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: antisense sequence PCT-US00-18999-28
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; GENERAL INFORMATION:
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Best Local Similarity 85.0
Matches 17; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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PCT-US00-18999-28
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SOFTWARE: Par
SEQ ID NO 28
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US-09-377-310-28
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APPLICANT: Cohen, Daniel
APPLICANT: Chumenfeld, Marta
APPLICANT: Chumenfeld, Marta
APPLICANT: Chumencov, IIya
APPLICANT: Chumencov, IIya
APPLICANT: Chumencov, IIya
TITLE OF INVENTON: BIALLELIC MARKER MAPS FOR USE IN CONSTRUCTING A HIGH DENSITY...
FILE REFERENCE: 84 USI.PRO
CURRENT PAPPLICATION NUMBER: US/60/216,745
CURRENT FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 13665
SEQ ID NO 2764
LENGTH.
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GENERAL INFORMATION:
APPLICANT: Mittmann
APPLICANT: Mittmann
TITLE OF INVENTION: Methods of Genetic Analysis of
TITLE OF INVENTION: Arabidopsis thaliana
FILE REFERENCE: 3116
CURRENT PAPLICATION NUMBER: US/60/233,620
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 131820
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 101590
TYPE: DNA
TYPE: DNA
                                                                                                                                                                                                                                                     Score 15.8; DB 55;
Pred. No. 3.2e+02;
0; Mismatches 2;
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Pred. No. 5.9e+02;
1; Mismatches 2;
                                                                                                                                                    PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank AC003672
US-60-233-620-73499
CURRENT APPLICATION NUMBER: US/60/233,620
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 131820
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 73499
LENGTH: 25
                                                                                                                    TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                     79.0%;
89.5%;
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84.2%;
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Best Local Similarity 89.55
Matches 17; Conservative
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Best Local Similarity 84.2<sup>§</sup>
Matches 16; Conservative
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ORGANISM: Homo Sapiens
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APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
APPLICANT: Brook pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase;
TITLE OF INVENTION: Expression
FILE REPRENCE: ISPH-0533
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: US/09/757,100B
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LIGHTHAND 9
                                                                                                                                                               Sequence 9, Application US/09377310A
GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION UNMER: US/09/377,310A
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
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100.0%; Pred. No. 8.6e+02;
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100.0%; Pred. No. 8.6e+02;
iive 0; Mismatches 0;
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COTHER INFORMATION: antisense sequence
US-09-377-310-9
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100.0%; Pre-
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Best Local Similarity 100.
Matches 15; Conservative
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Matches 15; Conservative
                                     1 ctagatgctaggtat 15
                                                       6 ctagatgctaggtat 20
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| ctagatgctaggtat 20
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                                                                                                                                                             RESULT 10
US-09-757-100B-28
US-09-757-100B-28
Sequence 28, Application US/09757100B
GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Mero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase:
TITLE OF INVENTION: Expression
FILE REPRENCE: ISPH-053
CURRENT APPLICATION NUMBER: US/09/757,100B
CURRENT APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PartentIn Ver: 2.0
SEQ ID NO 28
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application PC/TUS0018999
GENERAL INFORMATION:
APPLICANT: Isis Pharmaceuticals, Inc.
APPLICANT: Monia, Brett P.
APPLICANT: Garde, William A.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Expression
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                                   Indels
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                 Pred. No. 8.2e+02;
Mismatches 0;
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CURRENT APPLICATION NUMBER: PCT/USOO/18999
CURRENT FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN Ver. 2.0
SSOTUNO 9
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION: antisense sequence US-09-757-1008-28
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100.08; Pie
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ORGANISM: Artificial Sequence
FEATURE:
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               Best Local Similarity 100.
Matches 15; Conservative
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Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserva
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; Sequence 48863, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mitthann et al.; APPLICANT: Mitthann et al.; APPLICANT: Mitthann et al.; TITLE OF INVENTION: Methods of Genetic Analysis of Human FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,220
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SED ID NOS: 140981
; SOFUMARE: EastSEQ for Windows Version 4.0
; SEQ ID NO 48863
; LENGTH: 25
                                                        APPLICANT: Mittann et al.
APPLICANT: Mittann et al.
APPLICANT: Mittann et al.
TITLE OF INVENTION: Methods of Genetic Analysis of Human FILE REFERNCE: 3102.1
CURRENT APPLICATION NUMBER: US/09/660,220
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/164,973
PRIOR FILING DATE: 1999-11-11
NUMBER OF SEQ ID NOS: 140981
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11883
LENGTH: 25
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84.2%; Pred. No. 2.4e+03;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 71.0%; Score 14.2; DB 26; Best Local Similarity 84.2%; Pred. No. 2.4e+03; Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo Sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank M14338
US-09-660-220-48863
                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
OCGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank D63881
US-09-660-220-11883
                     Sequence 11883, Application US/09660220 GENERAL INFORMATION:
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Best Local Similarity 84.29
Matches 16; Conservative
US-09-660-220-11883
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Search completed: October 2, 2001, 21:50:11 Job time: 24524 sec

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32, Appl 10, Appl 26932, A

Appli

87, Appl 191, App 22107, A 16933, A 17980, A

Sequence Seq

34, Appl 235, App 3466, Ap

Sequence Sequence Sequence

2187, Ap

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Sequence 773, Application US/09840424

GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Macarthy, Sean A.
TITLE OF INVENTION: HUMAN MICHOVASCULES DERIVED FROM A
TITLE OF INVENTION: HUMAN MICHOVASCULAR ENDOTHELIAL LIBRARY
FILE REFERENCE: 1600.1010-002
CURRENT APPLICATION NUMBER: US/09/840,424
CURRENT FILING DATE: 2001-04-23
FRIOR PAPLICATION NUMBER: US 60/123,523
FRIOR PAPLICATION NUMBER: US 60/123,523
FRIOR FILING DATE: 1999-03-08
FRIOR PLING DATE: 1999-03-08
FRIOR FILING DATE: 1999-03-30
FRIOR PLING DATE: 1999-03-30
FRIOR FILING DATE: 1999-05-04
FRIOR PLING DATE: 1999-05-04
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FRIOR PLING DATE: 1999-05-04
FRIOR PLING DATE: 1999-05-04
FRIOR APPLICATION NUMBER: US 60/126,974
FRIOR PLING DATE: 1999-05-04
FRIOR APPLICATION NUMBER: US 60/126,974
FRIOR PLING DATE: 1999-05-04
FRIOR APPLICATION NUMBER: US 09/304,649
FRIOR PLING DATE: 1999-05-04
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FRIOR PLING DATE: 1999-05-04
FRIOR APPLICATION NUMBER: US 09/304,649
              US-09-708 690-8033
US-09-546-745A-3189
US-09-625-255-3
US-09-625-251A-10
US-09-545-551A-10
US-09-725-3-651-26932
US-09-724-750-22107
US-09-724-750-22107
US-09-708-690-16933
US-09-708-690-16933
US-09-708-690-18029
US-09-708-690-18029
US-09-744-671-235
US-09-744-671-235
US-09-7866-108-2603
US-09-866-108-2603
US-09-866-108-2603
US-09-866-108-2603
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Pred. No. 1.5e+03;
0; Mismatches 2;
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APPLICANT: MORTIS, MacDonald; APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
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. OTHER INFORMATION: n = A,T,C or
US-09-840-424-773
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87.5%;
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16 ctagatgttacgtatc 31
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
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Matches 14; Conserv
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US-60-278-258-6107/c
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10.00.88
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Sequence 7, Appl1
Sequence 7, Appl1
Sequence 43320, A
Sequence 2604, Ap
Sequence 2605, Ap
Sequence 2606, Ap
Sequence 2606, Ap
Sequence 5534, Ap
                                                                                                                                                                                       (without alignments)
19.290 Million cell updates/sec
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Sequence 6107, Ap
Sequence 3190, Ap
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Sequence 5533, A
Sequence 5533, A
Sequence 5534, A
Sequence 5535, A
Sequence 5535, A
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/USOG_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/USOR_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/USOR_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/USOR_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/USOS_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/USOS_NEW_COMB.seq:*

8: /cgn2_6/ptodata/2/pna/USOS_NEW_COMB.seq2:*
                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-048-473-3

US-09-048-473-3

US-09-048-473-3

US-09-086-108-2604

US-09-866-108-2605

US-09-866-108-5533

US-09-866-108-5534

US-09-866-108-5534

US-09-866-108-5536

US-09-866-108-5536

US-09-866-108-5536

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US-08-798-074B-7431
US-08-798-074C-7431
US-09-839-976-3279
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Maximum DB seq length: 50
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Match I
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TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using TITLE OF INVENTION: Polymorphisms Sequence Databases, and Single Nucleotide FILE OF INVENTION: Polymorphisms Identified Thereby
FILE REFERENCE: GX-00.10-1 P
CURRENT PAPLICATION NUMBER: US/60/278,258
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 1730
SOFTWARE: PERL Program
SEQ ID NO 6107
LENGTH: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3190, Application US/09546745A
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Zwick, Michael
APPLICANT: Pavco, Pam
APPLICANT: MocSaigen, Jim
TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules
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APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
TITLE OF INVENTION: Regulation of Repressor Genes using Nucleic Acid Molecules
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58.3%; Pred. No. 3.8e+03;
ive 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: US-09-546-745A-3190
                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: SNP00057112
NAME/KEY: snp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/546,745A CURRENT FILING DATE: 2000-04-11 NUMBER OF SEQ ID NOS: 7043 SOFTWARE: Patentin version 3.0 SEQ ID NO 3190 LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3191, Application US/09546745A
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: 350403.1, 20, G->A US-60-278-258-6107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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Best Local Similarity 58.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ctagatgctaggtatct 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 CTAGATGGTAGTTATGT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blatt, Larry
Zwick, Michael
                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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3 cuagguaucugu 14
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US-09-546-745A-3190
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US-09-546-745A-3191
                                                                                                                                                                                                                                                                                                                      NAME/KEY: snp
LOCATION: 20
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                                                                                                                                                                                                                    TYPE: DNA
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Gaps
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* OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-546-7458-3191
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                                                                                                                                                                                                                                                                                                                      Score 12; DB 6; Length 17;
Pred. No. 3.8e+03;
5; Mismatches 0; Indels
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CORRUTER: IBM Compatible
COERATING SYSTEM: DOS
SOFTWARE: FASEEGO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,473
FILING DATE: 26-Mar-1998
PRIOR APPLICATION NUMBER: 07/214,237
FILING DATE: 01-JUL-1992
APPLICATION NUMBER: 07/931,123
FILING DATE: 17-AUG-1992
APPLICATION NUMBER: 08/345,018
FILING DATE: 23-NOV-1994
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ADDRESSE: Genencor International, Inc.
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
FILE REFERENCE: 237/193
CURRENT APPLICATION NUMBER: US/09/546,745A
CURRENT FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 7043
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3191
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ASPARTIC PROTEINA FILAMENTOUS FUNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: GC45-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAMÉ: Glaister, Debra J.
REGISTRATION NUMBER: 33,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayenga, Kirk J.
Lawlis, Virgil B.
Ward, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09048473 GENERAL INFORMATION:
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ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Berka, Randy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 3:
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LENGTH: 36 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                      60.0%;
58.3%;
                                                                                                                                                                  TYPE: RNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 58.3
Matches 7; Conservative
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US-09-048-473-3/C
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Gaps

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APPLICANT: SHANNON, MARK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
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                         TITLE OF INVENTION: Polynucleotides, isolated from plants TITLE OF INVENTION: and methods for their use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT PELLING DATE: 2001-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-07
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRILCATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
                                                                     FILE REFERENCE: 1054P2
CURRENT APPLICATION NUMBER: US/60/253,457
CURRENT FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 48893
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 43320
LENGTH: 39
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SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 2604
LENGTH: 17
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US-09-866-108-2604
; Sequence 2604, Application US/09866108
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Conservative
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                                                                                                                                                                                                                                                                    ; TYPE: DNA; ORGANISM: Pinus radiata
US-60-253-457-43320
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Best Local Similarity
Matches 15; Conserv
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APPLICANT:
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                         Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ASPARTIC PROTEINASE DEFICIENT FILAMENTOUS FUNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRSLSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,473
FILING DATE: 26-Mar-1998
PRIOR APPLICATION DATA:
60.0%; Score 12; DB 7; Ler
75.0%; Pred. No. 4.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc.
STREET: 925 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/214,237
FILING DATE: 01-JUL-1992
APPLICATION NUMBER: 07/931,123
FILING DATE: 17-AUG-1992
APPLICATION NUMBER: 08/345,018
FILING DATE: 23-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATORNEY/AGENT INFORMATION:
NAME: Glaister, Debra J.
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC45-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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Sequence 43320, Application US/60253457
GRERAL INFORMATION:
APPLICANT: HAVUKABLA, IIkka J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09048473
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
Hayenga, Kirk J.
Lawlis, Virgil B.
Ward, Michael
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ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-845-6504 INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 36 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                1 ctagatgctaggtatctgtc 20
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Best Local Similarity 75.0°
Matches 15; Conservative
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
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                                         Best Local Similarity
Matches 15; Conserv
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US-09-048-473-7/c
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                         Query Match
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APPLICAMY: GU, Yizhong
APPLICAMY: GU, Yizhong
APPLICAMY: Ju, Yongang
APPLICAMY: Ju, Yongang
APPLICAMY: David R.
APPLICAMY: PENN, Sharron G.
APPLICAMY: RANK, David R.
APPLICAMY: RANK, David R.
APLICAMY: GINN, MAIN-INGER, GO, 106
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT APPLICATION NUMBER: US/00/866,108
CURRENT APPLICATION NUMBER: US/00/20,2456
PRIOR FILING DATE: 2000-09-24
PRIOR PLING DATE: 2000-09-24
PRIOR PLING DATE: 2000-09-26
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PLING DATE: 2001-01-30
PRIOR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 4.9e+03;
0; Mismatches 2;
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                                                                                                                                                             Sequence 2606, Application US/09866108
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86.7%;
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 15752
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Best Local Similarity 86.7
Matches 13; Conservative
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   2 agatgctgggcatct 16
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US-09-866-108-2606
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GERREAL INFORMATION:
APPLICANT: 100, VIZIONG
APPLICANT: 101, VIZIONG
APPLICANT: 101, VIZIONG
APPLICANT: 102, VIZIONG
APPLICANT: BENN, Sharron G.
APPLICANT: RANK, David R.
APPLICANT: RANK, David R.
APPLICANT: SHANKON, MAIK
APPLICANT: SHANKON, MAIK
FILIKO BERERREE: AECOMICA-7
CURRENT APPLICATION NUMBER: US/09/866.108
PRIOR APPLICATION NUMBER: US/09/36.359
PRIOR APPLICATION NUMBER: US/00/207, 456
PRIOR APPLICATION NUMBER: US/00/207, 456
PRIOR APPLICATION NUMBER: US/09/36.359
PRIOR APPLICATION NUMBER: US/09/36.359
PRIOR PELING DAPE: 2000-10-0-0-0
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR PELING DAPE: 2001-0-1-30
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR PELING DAPE: 2001-0-1-30
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR APPLICATION NUMBER: PCT/US01/0067
PRIOR PELING DAPE: 2001-0-1-30
PRIOR APPLICATION NUMBER: PCT/US01/0067
PRIOR PELING DAPE: 2001-0-1-30
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                                                                                                                                  Length 17;
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Pred. No. 4.9e+03;
0; Mismatches 2;
                                                                                                                            Score 11.8; DB 6;
Pred. No. 4.9e+03;
0; Mismatches 2;
                                                                                                                        Query Match 59.0
Best Local Similarity 86.7
Matches 13; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
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; ORGANISM: Homo sapiens US-09-866-108-2604
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CORGANISM: Homo sapiens
US-09-866-108-2605
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APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MARK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEGMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 60/207,456
PRIOR APPLICATION NUMBER: GB 60/207,456
PRIOR PILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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Pred. No. 5.3e+03;
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                        PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-01-31
PRIOR RELING DATE: 2001-01-31
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FILING DATE: 2001-01-30
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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CORGANISM: Homo sapiens
US-09-866-108-5534
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Best Local Similarity
Matches 13; Conserv
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                                                              APPLICANT: SHANNON, MAIK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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5.3e+03;
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                                                                                                               THILE REPERENCE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2001-01-30

PRIOR PRILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/USO1/0661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/USO1/0670

PRIOR APPLICATION NUMBER: PCT/USO1/0661

PRIOR PRILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/USO1/06670

PRIOR APPLICATION NUMBER: PCT/USO1/06670

PRIOR APPLICATION NUMBER: PCT/USO1/06670

PRIOR APPLICATION NUMBER: PCT/USO1/06670
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CURRENT FILING DATE: 2001-05-25
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86.7%;
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence
RANK, David R. CHEN, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 59.0
Best Local Similarity 86.7
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-09-866-108-5533
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APPLICANT: CHEM, WEASABAGG

APPLICANT: GIRANON, MAIK

TITLE OF INVERTION: WYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ADOMICA-7

CURRENT APPLICATION UNMER: US/09/866,108

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-04

PRIOR PELLING DATE: 2001-01-30

PRIOR PLILNG DATE: 2001-01-30

PRIOR PLILNG DATE: 2001-01-30

PRIOR PLILNG DATE: 2001-01-30

PRIOR PLILNG DATE: 2001-01-30

PRIOR PPLICATION NUMBER: PCT/US01/00669

PRIOR PLILNG DATE: 2001-01-30

PRIOR PLILNG DATE: 2
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Pred. No. 5.3e+03;
); Mismatches 2; Indels
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 5536
LENGTH: 25
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SOFTWARE: Acomica Sequence Listing Engine
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Best Local Similarity 86.7
Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108-5536
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APPLICANT: HANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MAIK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: ADONICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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                                                                       PRIOR PELICATION NUMBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/USO1/00662
PRIOR PELLING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-03-30
PRIOR PILING DATE: 2000-03-30
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-20
PRIOR PILING DATE: 2000-09-20
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SEQ ID NO 5535
LENGTH: 25
        APPLICATION NUMBER: PCT/US01/00669
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Best Local Similarity 86.7
Matches 13; Conservative
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9 agatgctgggcatct 23
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/cgn2_6/ptodata/1/pna/US6008_COMB.seq:
/cgn2_6/ptodata/1/pna/US6019_COMB.seq:
/cgn2_6/ptodata/1/pna/US6010_COMB.seq:
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Copyright (c) 1993 - 2000
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Listing first 45 summaries
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/cgn2_6/ptodata/1/pna/US6026_COMB.seq:
/cgn2_6/ptodata/1/pna/US6026_COMB.seq:
/cgn2_6/ptodata/1/pna/US6028_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
APPLICANT: Garde, William A.
APPLICANT: Garde, William A.
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0333
CURRENT APPLICATION NUMBER: US/09/757,100B
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEO ID NOS: 44
SOCTUMARE: Patentin Ver. 2.0
SEO ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: antisense sequence US-09-757-1008-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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CURRENT FILING DATE: 1999-08-19

PRIOR APPLICATION NUMBER: 09/377,310

PRIOR APPLICATION NUMBER: 09/377,310

PRIOR APPLICATION NUMBER: 09/377,310

SOFTWARE: PATENTIN OF THE STATE 
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APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310A
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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15;
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100.0%; Pred. No. 15;
Live 0; Mismatches
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              ALIGNMENTS
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US-09-757-100B-7
: Sequence 7, Application US/09757100B
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity 100.
Matches 20; Conservative
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US-09-377-310-7
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LENGTH: 20
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GENERAL INFORMATION:
APPLICANT: BOTSGOOT THO:
TITLE OF INVENTION: RICIA-LIKE TOXIN VARIANTS FOR TREATMENT OF CANCER,
TITLE OF INVENTION: VIRAL OR PARASITIC INFECTIONS
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     Length 20;
                                                                                                                                                                                                         Sequence 486, Application US/09310298
GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Wang, David G.
TITLE OF INVENTION: PRIMER SEQUENCES FOR SINGLE NUCLEOTIDE
TITLE OF INVENTION: POLYMORPHISMS
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Pred. No. 2.7e+03;
0; Mismatches 1;
     Score 20; DB 29;
Pred. No. 15;
                                          Mismatches
                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: WHIFG90-07pA
CURRENT APPLICATION NUMBER: US/09/310,298
CURRENT FILICATION NUMBER: 055-12
EARLIER PELING DATE: 1998-05-12
NUMBER OF SEQ ID NOS: 5968
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 486
LENGTH: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Oligonucleotide primer US-09-310-298-486
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     100.0%;
100.0%;
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94.18;
Ouery Match
Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity
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Gaps

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: General Antisense Modulation of Focal Adhesion Kinase:
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0533
CURRENT APPLICATION NUMBER: US/09/757,100B
CURRENT APPLICATION NUMBER: US/09/7757,100B
CURRENT APPLICATION NUMBER: US/09/777,310
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 15
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TITLE OF INVENTION: Methods of Genetic Analysis of the Rat TITLE OF INVENTION: Genome FILE REFERENCE: 3112
CURRENT APPLICATION NUMBER: US/60/233,166
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 420907
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 25
                                                                                                                                                                                     Length 15;
                                                                                                                                                                                   75.0%; Score 15; DB 17; I 100.0%; Pred. No. 3.5e+03; tive 0; Mismatches 0;
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Pred. No. 3.5e+03;
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DATABASE ACCESSION NUMBER: GenBank AA818353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                ; OTHER INFORMATION: antisense sequence US-09-377-310-27
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Best Local Similarity 100.
Matches 15; Conservative
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                                        TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 15; Conserv
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  NO 27
FH: 15
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                                                                                   FEATURE:
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; ORGANISM: Human Prostate-Specific Antigen linker region of pAP-290
US-09-403-752A-115
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TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
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GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ALISENSE Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310A
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
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76.0%; Score 15.2; DB 18;
Best Local Similarity 85.0%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 3;
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              CURRENT APPLICATION NUMBER: US/09/403,752A
CURRENT FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: U.S. 60/045,148
PRIOR FILING DATE: 1997-04-30
PRIOR FILING DATE: 1997-04-30
PRIOR FILING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 142
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 115
LENGTH: 36
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CURRENT APPLICATION NUMBER: PCT/US00/18999
CURRENT FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27, Application PC/TUS0018999 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Monia, Brett P. APPLICANT: Gaarde, William A.
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SOFTWARE: PatentIn Ver. 2.0
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10447-005
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Best Local Similarity
Matches 15; Conserv
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APPLICANT: Brett P. Monia APPLICANT: Lex M. Cowsert TITLE OF INVENTION: ANTISENSE MODULATION OF UBIQUITIN PROTEIN LIGASE WWP1 AND TITLE OF INVENTION: EXPRESSION FILE REFERENCE: RTS-0087 CURRENT APPLICATION NUMBER: US/09/657,481A CURRENT FILING DATE: 2000-09-07 NUMBER OF SEQ ID NOS: 93
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GENERAL INFORMATION:
APPLICANT: Mittmann
APPLICANT: Mittmann
TITLE OF INVENTION: Genome
TITLE OF INVENTION: Genome
FILE REPERBENCE: 3112
CURRENT APPLICATION NUMBER: US/60/233,166
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 420907
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 108604
LENGTH: 25
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GENERAL INFORMATION:
APPLICANT: Mittmann:
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
TITLE OF INVENTION: Genome
FILE REFERENCE: 3112
CURRENT APPLICATION NUMBER: US/60/233,166
CURRENT FILING DATE: 2000-10-24
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Pred. No. 1.4e+04;
0; Mismatches 2;
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Pred. No. 1.4e+04;
0; Mismatches 2;
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; DATABASE ACCESSION NUMBER: GenBank AA860043
US-60-233-166-108604
                                 US-09-657-481A-39/c; Sequence 39, Application US/09657481A; GENERAL INFORMATION:
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88.2%;
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88.2%;
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Best Local Similarity 88.2
Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserv
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LENGTH: 20
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US-60-233-166-280120
Sequence 280120, Application US/60233166
Sequence 280120, Application US/60233166
GENERAL INFORMATION:
APPLICANT: Mittmann
APPLICANT: Mittmann
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
TITLE OF INVENTION: Genome
FILE REFERENCE: 3112
CURRENT APPLICATION NUMBER: US/60/233,166
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 420907
SOTUMENT: SEQ ID NOS: 420907
LENGTH: 25
LENGTH: 25
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US-60-234-017-131414
; Sequence 131414, Application US/60234017
; GENERAL INFORMATION:
    APPLICANT: Mittmann, M
    APPLICANT: Affymetrix, Inc.
    TITLE OF INVENTION: methods of Genetic Analysis of Mus
    TITLE OF INVENTION: methods of Cenetic Analysis of Mus
    TITLE REPERBENCE: 3115
CURRENT APPLICATION NUMBER: US/60/234,017
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 131414
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                                                     Score 14.8; DB 55;
Pred. No. 4.8e+03;
); Mismatches 2;
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Pred. No. 4.8e+03;
0; Mismatches 2;
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84.2%; Pred. No. 9.2e+03;
ive 0; Mismatches 3;
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank AA600645
SC-234-017-131414
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; PUBLICATION INFORMATION:
US-60-233-166-280120
                                                   74.0%;
88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
US-60-233-166-23007
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| US-60-234-017-425796/c
| Sequence 425796, Application US/60234017
| GENERAL INFORMATION:
| APPLICANT: Mittmann, M
| APPLICANT: Mittmann, M
| TITLE OF INVENTION: Methods of Genetic Analysis of Mus
| TITLE OF INVENTION: Methods of Genetic Analysis of Mus
| TITLE REPERBENCE: 3115
| CURRENT APPLICATION NUMBER: US/60/234,017
| CURRENT FILING DATE: 2000-09-20
| NUMBER OF SEQ ID NOS: 605887
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 425796
| LENGTH: 25
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; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 167371
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AA926247
US-60-233-166-167371
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CRGANISM: Mus musculus
PUBLICATION INFORMATION:
LATABASE ACCESSION NUMBER: Genbank AV102460
US-60-234-017-425796
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Best Local Similarity 88.29
Matches 15; Conservative
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Query Match
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US-09-726-774-70
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LENGTH: 36
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Sequence 18891, A
Sequence 1781, Ap
Sequence 22, App
Sequence 22, Appl
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32245, A
Appl
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7, Appli
                                                                                                  Search time 2173.58 Seconds (without alignments) 19.290 Million cell updates/sec
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14008, A
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Sequence 70, Appl
Sequence 83, Appl
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Sequence 14008, A
Sequence 15489, A
Sequence 90, Appl
Sequence 1240, Ap
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Sequence 36,
Sequence 74,
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Sequence 5
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/cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
/cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq1:*
/cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq2:*
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-60-252-833-32245
US-60-278-561-675
US-09-516-667-73
US-09-516-667-35
US-09-516-667-35
US-09-516-667-74
US-09-516-667-74
US-09-516-667-74
US-09-516-667-74
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US-09-514-8833-9824
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US-09-747-391-16
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Listing first 45 summaries
                                                                       OM nucleic - nucleic search, using sw model
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22, Appl
247, App
13, Appl
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US-09-343-126B-50

US-09-488-265-63

US-09-801-274-736

US-09-801-274-736

US-09-801-274-1470

US-09-69-101A-293

US-09-546-745A-5238

US-09-546-745A-5238

US-09-546-745A-5238

US-09-546-745A-5238

US-09-69-011A-293

US-09-69-011A-293

US-09-69-011A-293

US-09-708-690-18282

US-09-708-690-1822

US-09-708-690-1822

US-09-708-690-18274

US-09-708-690-18274

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US-09-708-690-18274

US-09-708-690-18274

US-09-708-690-18274

US-09-708-690-18274
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; OTHER INFORMATION: Human Prostate-Specific Antigen linker region of pAP-290 US-09-551-151-115
                                                                                                                                                                 APPLICANT: Borgford, Thor
TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
TITLE OF INVENTION: Viral or Parasitic Infections
FILE REPERENCE: 10447-011
CURRENT APPLICATION NUMBER: US/09/551,151
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 142
SOFTWARE: Patentin Ver. 2.0
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Actick L.
TITLE OF INVENTION: Composition
TITLE OF INVENTION: Composition
FILE REFERENCE: 0450-0032.30
CURRENT FILING DATE: 2000-11-29
FILE PAPLICATION NUMBER: US/09/726,774
CURRENT FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 139
SEQ ID NOS: 139
SECTION 10 70
SEQ ID NO 70
LENGTH: 21
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85.0%; Pred. No. 4.9e+02;
Live 0; Mismatches 3;
ALIGNMENTS
                                                                                                                   ; Sequence 115, Application US/09551151; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
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Gaps
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Manbeck, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701-E
CITY: Washington
STATE: DC
COMPUTRY: USA
ZIP: 2000A
ZIP: 2000A
COMPUTER: Flopy disk
COMPUTER: Flopy disk
COMPUTER: Flopy STEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NDATE: US/08/850,062A
FILING DATE: 02-May-1997
CLASSIFICATION: <UNKNOWN>
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                                                                                                                                                                                                                                                                                                                                                                                      Length 36;
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                                   Score 13.6; DB 8;
Pred. No. 2.8e+03;
); Mismatches 4;
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Futreal, P. Andrew
TITLE OF INVENTION: 179-Linked Breast ar
Susceptibility Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,554
FILING DATE: 06-JUN-1995
FILING DATE: 24-MAR-1995
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 16-SEP-1994
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 29-NOV-1994
APPLICATION NUMBER: US 08/308,104
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US-08-850-062A-75
Sequence 75, Application US/08850062A;
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Skolnick, Mark H. Goldgar, David E. Miki, Yoshio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Swenson, Jeff
Kamb, Alexander
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match 68.0
Best Local Similarity 80.0
Matches 16; Conservative
                       US-60-252-833-32245/c
                                                                                                                                                                                                                                                                                                            ORGANISM: Bovine US-60-252-833-32245
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Sequence 83, Application US/09900590
GENERAL INFORMATION:
APPLICANT: Huse, William D.
Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
Anti-Alpha V Beta 3 Recombinant Human
Anti-Alpha V Beta 3 Recombinant Human
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                                                                                                                                   69.0%; Score 13.8; DB 6; Length 21; 88.2%; Pred. No. 2.1e+03; Live 0; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/900,590
FILING DATE: 06-Jul-2001
CLASSIFICATION: CUNKNOWN>
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ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 13.8; DB 6;
Pred. No. 2.2e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 83:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LUCATION: 1..33
; SEQUENCE DESCRIPTION: SEQ ID NO: 83: US-09-900-590-83
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APPLICATION NUMBER: 09/016,061
FILING DATE: CURRIGH
                                                         ; OTHER INFORMATION: antisense oligomer US-09-726-774-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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LENGTH: 33 base pairs
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Matches 15; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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APPLICANT: Wang, Nan APPLICANT: Wang, Nan APPLICANT: Wang, Nan APPLICANT: Yamanaka, Kunitoshi APPLICANT: Yamanaka, Kunitoshi TITLE OF INVENTION: COLD-SHOCK REGULATORY ELEMENTS, CONSTRUCTS THEREOF, AND TITLE OF INVENTION: METHODS OF USE FILE REFERENCE: 1053-00
CURRENT APPLICATION NUMBER: US/09/516,667
CURRENT FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 87
LENGRENT FILING COLD NOS: 87
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APPLICANT: Inouye, Masayori
APPLICANT: Mang, Nanaka, Kunitoshi
TITLE OF INVENTION:
TITLE OF INVENTION: METHODS OF USE
TITLE OF INVENTION: METHODS OF USE
FLIE REFERENCE: 1053-00
CURRENT APPLICATION NUMBER: US/09/516,667
CURRENT FILING DATE: 2001-08-01
SOFTWARE: PATENTIN UNCS: 87
SEQUIPMENT APPLICATION UNC
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GENERAL INFORMATION:
APPLICANT: Inouye, Masayori
APPLICANT: Yamanaka, Kunitoshi
TITLE OF INVENTION: ColD-SHOCK REGULATORY ELEMENTS, CONSTRUCTS THEREOF, AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 1053-00
GURRENT APPLICATION NUMBER: US/09/516,667
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Pred. No. 1.3e+04;
0; Mismatches 3; Indels
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; OTHER INFORMATION: oligonucleotide
US-09-516-667-73
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA ORGANISM: Artificial Sequence
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Best Local Similarity 82.4%;
Matches 14; Conservative
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Matches 14; Conservative
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Sequence 657, Application US/60278561
Sequence 657, Application US/60278561
GENERAL INFORMATION:
APPLICANT: MOSTIS, MacDonald
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polymorphisms Identified Thereby
TITLE OF INVENTION: Polymorphisms Identified Thereby
TITLE OF INVENTION NUMBER: US/60/278,561
CURRENT APPLICATION NUMBER: US/60/278,561
CURRENT APPLICATION NUMBER: US/60/278,561
SOFTWARE: PERL PROGRAM
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                                                                            NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: SNP00057293
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-08-850-062A-75
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Best Local Similarity 78.9
Matches 15; Conservative
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Best Local Similarity 78.9
Matches 15; Conservative
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LOCATION: 21
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Best Local Similarity 82.4%;
Matches 14; Conservative
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Matches 13; Conservative
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US-60-253-652-14008
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APPLICANT: Mang, Nan
APPLICANT: Wang, Nan
APPLICANT: Yamanaka, Kunitoshi
TITLE OF INVENTION: COLD-SHOCK REGULATORY ELEMENTS, CONSTRUCTS THEREOF, AND
FILLE REFERENCE: 1053-00
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GENERAL INFORMATION:
APPLICANT: Inouye, Masayori
APPLICANT: Wang, Nan
APPLICANT: Wang, Nan
APPLICANT: Yamanaka, Kunitoshi
TITLE OF INVENTION: COLD-SHOCK REGULATORY ELEMENTS, CONSTRUCTS THEREOF, AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: 1053-00
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                                                                                                                                                                                                                                                                               3; Indels
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                                                                                                                                                                                                                                            Score 12.2; DB 6;
Pred. No. 1.3e+04;
0; Mismatches 3;
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CURRENT FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 74
LENGTH: 48
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CURRENT FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 75
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US-09-516-667-74/c
; Sequence 74, Application US/09516667
; GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 36
LENGTH: 48
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ORGANISM: Artificial Sequence
                                                                                                                     ORGANISM: Artificial Sequence
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Best Local Similarity 82.4%;
Matches 14; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity 82.4
Matches 14; Conservative
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                                                                                                      TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Gligor, Mutray R
TITLE OF INVENTION: Compositions isolated from bovine
TITLE OF INVENTION: Lissues and methods for their use.
FILE REFERENCE: 1055P2
CURRENT APPLICATION NUMBER: US/60/253,652
CURRENT APPLICATION NUMBER: 2000-11-28
NUMBER OF SEQ ID NOS: 29954
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 98.24, Application US/60252833
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions isolated from bovine
TITLE OF INVENTION: tissues and methods for their use.
FILE REFERENCE: 105.2P2
CURRENT APPLICATION NUMBER: US/60/252,833
CURRENT FILIKO DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 43535
SOFTWARE: FastSEQ for Windows Version 4.0
; FEATURE:
. OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-09-516-667-75
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Pred. No. 1.3e+04;
0; Mismatches 3;
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Pred. No. 2.4e+04;
0; Mismatches 4; Indels
      Sequence 15489, Application US/60253456
GENERAL INFORMATION:
APPLICANT: Havukkala, Ilkka J.
TITLE OF INVENTION: Polynucleotides, isolated from
TITLE OF INVENTION: Polynucleotides, isolated from
TITLE OF INVENTION: Polynucleotides, isolated from
TITLE REFERENCE: 1054P1
CURRENT APPLICATION NUMBER: US/60/253,456
CURRENT APPLICATION NUMBER: 2000-11-27
NUMBER OF SEQ ID NOS: 37096
SEQ ID NO 15489
LENGTH: 29
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US-09-574-376B-90/C
; Sequence 90, Application US/09574376B
; GENERAL INFORMATION:
; APPLICANT: Warrington, Janet
; APPLICANT: Gingeras, Thomas Raymond
APPLICANT: Gingeras, Thomas Raymond
APPLICANT: Human Lymphoblast Polymorphisms
; TILE OF INVENTION: Human Lymphoblast Polymorphisms
; FILE REFERENCE: 3229.2
; CURRENT APPLICATION NUMBER: US/09/574,376B
; CURRENT FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 1330
; SEQ ID NO 90
; LENGTH: 31

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Best Local Similarity 77.8%;
Matches 14; Conservative
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Best Local Similarity 70.09
Matches 14; Conservative
                                                                                                                                                                                                                                                             TYPE: DNA
CRGANISM: Pinus radiata
US-60-253-456-15489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CRGANISM: Homo sapiens
PUBLICATION INFORMATION:
US-09-574-376B-90
US-60-253-456-15489
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Search completed: October 2, 2001, 16:55:00 Job time: 17663 sec

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(without alignments)
16.701 Million cell updates/sec
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(cgn2_6/ptodata1/pna/US08_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US6008_COMB.seq:
/cgn2_6/ptodata/1/pna/US6009_COMB.seq:
/cgn2_6/ptodata/1/pna/US6010_COMB.seq:
/cgn2_6/ptodata/1/pna/US6011_COMB.seq:
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                      OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                      IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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/cgn2_6/ptodata/1/pna/US6025_COMB.seq:
/cgn2_6/ptodata/1/pna/US6025_COMB.seq:
/cgn2_6/ptodata/1/pna/US6026_COMB.seq:
/cgn2_6/ptodata/1/pna/US6026_COMB.seq:
/cgn2_6/ptodata/1/pna/US6026_COMB.seq:
/cgn2_6/ptodata/1/pna/US6026_COMB.seq:
444455...
5521...
5521...
5521...
5551...
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Length DB ID . Description	.0 20 1 PCT-US00-18999-6 Sequence 6	.0 20 17 US-09-377-310-6 Sequence 6,	.0 20 29 US-09-757-100B-6 Sequence 6,	.0 25 55 US-60-233-166-247462 Sequence 247	.0 15 1 PCT-US00-18999-26 Sequence 26,	.0 15 17 US-09-377-310-26 Sequence 26,	.0 15 29 US-09-757-100B-26 Sequence 26,	.0 25 55 US-60-233-166-169359 Sequence 169	.0 25 55 US-60-233-166-169364 Sequence 169	.0 25 26 US-09-660-080-2372 Sequence 2372, A	.0 25 26 US-09-660-220-7628 Sequence	.0 25 55 US-60-233-166-75968 Sequence 75968,	.0 25 55 US-60-233-166-247458 Sequence	.0 25 55 US-60-233-166-353412 Sequence 353412,	.0 25 55 US-bU-233-35/-/140 Sequence /14U, A	.0 45 I/ US-U9-3IU-298-IbU3 Sequence IbU3,	.0 20 31 05-09-044-321-10 sequence 10, App	.001-662-00-80 66 62 0.	.0 25 55 US-60-233-620-33139 Sequence 33139	.0 25 55 US-60-233-620-33145 Sequence 33145,	.0 25 55 US-60-233-620-33146 Sequence	.0 25 55 US-60-234-017-31881 Sequence 31881,	.0 25 55 US-60-234-017-31890 Sequence	.0 25 55 US-60-234-049-10183 Sequence	.0 25 55 US-60-233-166-142391 Sequence 14239	.0 25 55 US-60-233-166-35893	.0 25 55 US-60-233-357-14127 Sequence 1412	.0 25 55 US-60-234-017-150021 Sequence 1500	.0 25 55 US-60-234-017-427143 Sequence 4271	.0 25 55 US-60-234-017-427147 Sequence 4271	.0	.0 10 08 HC-00-703-708-1007/ Company 1007	.0 19 48 US-60-164-320-12274 Sequence 12274.	.0 19 50 US-60-183-791-12274 Sequence 12274,	.0 20 16 US-09-201-228A-4597 Sequence 4597,	.0 25 26 US-09-660-080-2373 Sequence 23	.0 25 55 US-60-233-166-75953	.0 25 55 US-60-233-620-33138 Sequence 33	.0 36 16 US-09-232-278A-25 Sequence 25	
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APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase;
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0533
CURRENT APPLICATION NUMBER: US/09/757,100B
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 20
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Montain Brett P.

APPLICANT: Gaarde, William A.

TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310A
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
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13;
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Pred. No. 13;
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                ALIGNMENTS
                                                                                                                                                                                                                                                                  FILE REFERENCE: ISPH-0476
CURRENY APPLICATION NUMBER: PCT/US00/18999
CURRENT FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
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                                                                                                                                                       Isis Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: antisense sequence PCT-US00-18999-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: antisense sequence US-09-377-310-6
                                                                                                           Sequence 6, Application PC/TUS0018999 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09377310A GENERAL INFORMATION:
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100.0%; Pr
tive 0;
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ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity 100.
Matches 20; Conservative
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SEQ ID NO 6
LENGTH: 20
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SEQ ID NO 6
LENGTH: 20
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APPLICANT:
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PPLICANT: Gaarde, William A.
APPLICANT: Nero, Pamela S.

TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
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                                                                                                          Length 20;
                                                                                                                                                                                                                                                                                                              Sequence 247462, Application US/60233166
GRNERAL INFORMATION:
APPLICANT: Mittenan
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
TITLE OF INVENTION: Genome
FILE REFERENCE: 3112
CURRENT FILING DATE: 2000-10-24
.NUMBER OF SEQ ID NOS: 420907
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Pred. No. 3.1e+03;
0; Mismatches 3;
                                                                                                          DB 29;
                                                                                                                                                 Mismatches
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; DATABASE ACCESSION NUMBER: GenBank AI043982
US-60-233-166-247462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 420907
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 247462
LENGTH: 25
                                                                                                          Score 20;
Pred. No.
                               ; OTHER INFORMATION; antisense sequence US-09-757-100B-6
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                                                                                                          100.0%;
100.0%;
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85.0%;
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                               20; Conservative
                                                                                                        Query Match
Best Local Similarity
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US-60-233-166-247462/c
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PCT-US00-18999-26
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APPLICANT:
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                                                                                                                                               Matches
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Sequence 6, Application US/09757100B

RESULT 3 US-09-757-100B-6

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TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 15; Conservative
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NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver.
SEQ ID NO 26
LENGTH: 15
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Matches 15; Conserv
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US-60-233-166-169359/c
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LENGTH: 25
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase; TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase; TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0533
CURRENT APPLICATION NUMBER: US/09/757,100B
CURRENT FILING DATE: 2001-03-15
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 2000-07-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Monital Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310A
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEO ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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3.5e+03;
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. 3.5e+03;
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                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
               FILE REFERENCE: ISPH-0476
CURRENT APPLICATION NUMBER: PCT/USOO/18999
CURRENT FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                           Score 15;
Pred. No.
                                                                                                                                                                                                                                      ; OTHER INFORMATION: antisense sequence PCT-USO0-18999-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: antisense sequence US-09-377-310-26
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Sequence 26, Application US/09377310A
GENERAL INFORMATION:
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100.0%;
TITLE OF INVENTION: Expression
                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                       Query Match 75.0
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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1 aactgcagaaggcac 15
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APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
TITLE OF INVENTION: Genome
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; Sequence 169364, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; TITLE OF INVENTION: Genome
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                                                                                                               Score 15; DB 29; I
Pred. No. 3.5e+03;
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100.0%; Pred. No. 3.9e+03;
Live 0; Mismatches 0;
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100.0%; Pred. No. ...
0; Mismatches
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PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: GenBank AA955408

US-60-233-166-169359
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; DATABASE ACCESSION NUMBER: Genbank AA955408
US-60-233-166-169364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 3112
CURRENT APPLICATION NUMBER: US/60/233,166
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 420907
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 169359
LENGTH: 25
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CURRENT APPLICATION NUMBER: US/60/233,166
CURRENT FILING DATE: 2000-10-24
SUUMBER OF SEC ID NOS: 420907
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                        Sequence 169359, Application US/60233166; GENERAL INFORMATION:
FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-26
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100.0%; P1.
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TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Mittmann et al.
TITLE OF INVENTION: Methods of Genetic Analysis of Human
FILE REFERENCE: 3102.1
CURRENT APPLICATION NUMBER: US/09/660,220
CURRENT FILING DATE: 2000-09-12
PRIOR FILING DATE: 1999-11-11
NUMBER OF SEQ ID NOS: 140981
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7628
   Length 25;
                                   Indels
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TITLE OF INVENTION: Methods of Genetic Analysis of Rat
TITLE OF INVENTION: Toxicology
FILE REFRENCE: 3109.1
CURRENT APPLICATION NUMBER: US/09/660,080
CURRENT FILING DATE: 2000-09-12
PRIOR PELLING DATE: 1999-10-28
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Pred. No. 4.9e+03;
); Mismatches 2;
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Pred. No. 4.9e+03;
0; Mismatches 2;
75.0%; Score 15; DB 55; 100.0%; Pred. No. 3.9e+03; 1ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DATABASE ACCESSION NUMBER: GenBank AA819500 US-09-660-080-2372
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SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2372
LENGTH: 25
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US-09-660-220-7628
                                                                                                                                                                       US-09-660-080-2372/c
; Sequence 2372, Application US/09660080
; GENERAL INFORMATION:
; APPLICANT: Mittmann et al.
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88.9%;
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
                 Best Local Similarity 100.
Matches 15; Conservative
                                                                      1 gaaactgcagaaggc 15
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   Query Match
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US-60-233-166-247458, Application US/60233166

Sequence 247458, Application US/60233166

SEMERAL INFORMATION:
SPELICANT: Mittmann
APPLICANT: Mittmann
TITLE OF INVENTION: Genome
FILE REPERENCE: 3112
CURRENT APPLICATION UNBER: US/60/233,166
CURRENT FILING DATE: 2000-10-24
SUMBER OF SEQ ID NOS: 420907
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 247458
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 25;
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                                                           APPLICANT: Mittenin
APPLICANT: Mittenin
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
TITLE OF INVENTION: Gene
FILE REFRENCE: 3112
CURRENT APPLICATION UNMBER: US/60/233,166
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 420907
SOFTHARE: FastsEQ for Windows Version 4.0
LENGTH: 25
LENGTH: 25
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Sequence 353412, Application US/60233166
Sequence 353412, Application US/60233166
Sequence 353412, Application US/60233166
APPLICANT: Mittmann
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Genome
TITLE OF INVENTION: Genome
FILE REPERENCE: 3112
CURRENT APPLICATION NUMBER: US/60/233,166
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Pred. No. 7.7e+03;
); Mismatches 1;
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Pred. No. 4.9e+03;
0; Mismatches 2;
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; DATABASE ACCESSION NUMBER: GenBank AA819500
US-60-233-166-75968
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; DATABASE ACCESSION NUMBER: GenBank AI043982
US-60-233-166-247458
US-60-233-166-75968/c
; Sequence 75968, Application US/60233166
; GENERAL INFORMATION:
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93.8%;
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88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 93.8
Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7140, Application US/6023357
GENERAL INFORMATION:
APPLICANT: Mittmann
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
TITLE OF INVENTION: Methods of Cenetic Analysis of Rat
TITLE OF INVENTION: Meurobiology
FILE REFERENCE: 3114
CURRENT APPLICATION NUMBER: US/60/233,357
CURRENT PILLING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 21305
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 25
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 420907
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 25
                                                                                                  TYPE: DNA
ORGANISM: Rattus norvegicus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank U59126
US-60-233-166-353412
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ORGANISM: Rattus norregicus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank D49836
US-60-233-357-7140
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Best Local Similarity 84.29
Matches 16; Conservative
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US-09-866-108-4949 US-09-928-614-2 US-09-923-170-7 US-09-806-769-33 US-09-806-769-33 US-09-866-174-223 US-09-866-174-223 US-09-866-174-223 US-09-866-174-223 US-09-866-174-277 US-09-893-238-45 US-09-893-238-45 US-09-891-274-1777 US-09-124-1777 US-09-124-1757 US-09-124-1757 US-09-124-1757

Appli

18382, 2, Appl 39, App

US-09-700-360-2 US-09-929-404-39

ALIGNMENTS

Appli

Appl

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APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE. ABOMICAT
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-03-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-05-25
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-010-04
PRIOR PELING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PELING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/00665
PRIOR PELING DATE: 2001-01-30
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
  US-09-866-108-2022/c
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  4.22.22.21
2.22.22.21
2.22.22.22.21
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19.290 Million cell updates/sec
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Sequence 4953,
Sequence 4954,
Sequence 4955,
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Sequence 4957,
Sequence 4959,
Sequence 4960,
Sequence 1959,
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

8: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq2:*
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-866-108-4955
US-09-866-108-4955
US-09-866-108-4956
US-09-866-108-4956
US-09-866-108-4956
US-09-866-108-4956
US-09-866-108-4959
US-09-866-108-4950
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US-09-724-648-6
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US-09-919-478-15
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                                                                                                                                                            October 2, 2001, 16:54:59
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                   - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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### PRPLICANT; CHEN, Wenshing
### PREPLICANT; CHEN, Wenshing
### PRILICANT; CHEN, Wenshing
### TILIRE REPERENCE: ### APPLICANTON, WASIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
CURRENT APPLICANTON NUMBER: US/09/866,108
### CURRENT FILING DATE: 2001-05-25
### PRIOR PILING DATE: 2000-10-04
### PRIOR FILING DATE: 2000-10-04
### PRIOR PILING DATE: 2000-10-04
### PRIOR PILING DATE: 2000-10-04
### PRIOR PILING DATE: 2000-10-10-10
### PRIOR PILING DATE: 2001-01-30
### PRIOR PILING DATE: 2001-01-30
### PRIOR PPLICATION NUMBER: PCT/US01/00669
### PRIOR PPLICATION NUMBER: PCT/US01/00669
### PRIOR PPLING DATE: 2001-01-30
## PRIOR PPLING DATE: 2001-01-30
### PRIOR PPLING DATE: 2001-01
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Pred. No. 1.1e+03;
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SOFTWARE: Acomica Sequence Listing Engine
                                                                                                                                                                                         US-09-866-108-4951/c; Sequence 4951, Application US/09866108; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4952, Application US/09866108; GENERAL INFORMATION:
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93.8%;
                                                                                                                                                                                                                                                                                                     APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 72.0
Best Local Similarity 93.8
Matches 15; Conservative
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CHEN, Wensheng
5 ctgcagaaggcactga 20
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                                      16 CTGCAGAAGGCACCGA 1
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US-09-866-108-4952/c
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US-09-866-108-4951
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APPLICANT: TO, YIZIDONG
APPLICANT: HANEL, David K.
APPLICANT: HANEL, David K.
APPLICANT: PENN, Sharron G.
APPLICANT: HANEL, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: RAKY, David R.
APPLICANT: CHEN, Wensheng
APPLICANTON NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR PLICANTON NUMBER: US 60/230,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-27
PRIOR FILING DATE: 2000-03-7
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLICANTON NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR PLICANTON NUMBER: PCT/US01/00665
PRIOR PLICANTON NUMBER: PCT/US01/00667
PRIOR PRICA PLICANTON NUMBER: PCT/US01/00667
PRIOR PRICA PRICA PLICANTON NUMBER: PCT/US01/00670
PRIOR PRICA PURPARE PCT/US01/00670
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Pred. No. 1e+03;
0; Mismatches 1;
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SOFTWARE: Acomica Sequence Listing Engine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2023, Application US/09866108 GENERAL INFORMATION:
                                                                                                                                                                                                72.0%;
93.8%;
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Best Local Similarity 93.8
Matches 15; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108-2022
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CORGANISM: Homo sapiens
US-09-866-108-2023
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LENGTH: 17
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APPLICANT: RANK, DAVID R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MARK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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Pred. No. 1.1e+03;
0; Mismatches 1;
                   CURRENT APPLICATION NUMBER: US/09/866,108 CURRENT FILING DATE: 2001-05-25
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR PLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-01-04
PRIOR PLILING DATE: 2000-01-04
    FILING DATE: 2000-05-26
APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4954, Application US/09866108 GENERAL INFORMATION:
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, Dayld K.
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US-09-866-108-4953
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Best Local Similarity
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE REFERENCE: ABOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
                                                                       APPLICANT: CHEN, Wensheng
APPLICANT: SHAMNON, Mark
TITLE OF INVENTION: MASIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
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Pred. No. 1.1e+03;
0; Mismatches 1; Indels
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CURRENT FILING DATE: 2001-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-04

PRIOR PLILING DATE: 2000-10-04

PRIOR PLILING DATE: 2000-10-04

PRIOR PELING DATE: 2000-10-07

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/USO1/00663

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/USO1/00661

PRIOR APPLICATION NUMBER: US 60/284,687

PRIOR APPLICATION NUMBER: US 60/286,860

PRIOR PELING DATE: 2001-01-30

PRIOR PELICATION NUMBER: US 60/286,860

PRIOR PELICATION NUMBER: US 60/286,960
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SEQ ID NO 4952
LENGTH: 25
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Sequence 4953, Application US/09866108
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: CHEN, Wensheng
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93.8%;
PENN, Sharron G.
HANZEL, David K.
RANK, David R.
CHEN, Wensheng
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Best Local Similarity 93.8
Matches 15; Conservative
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24 CTGCAGAAGGCACCGA 9
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; ORGANISM: Homo sapiens
US-09-866-108-4952
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APPLICANT:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: 31, Yazhong
APPLICANT: 31, Yazhong
APPLICANT: 31, Yazhong
APPLICANT: 41, Yanggang
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David K.
APPLICANT: SHANK, David R.
APPLICANT: SHANKON, Wark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILER REFERENCE: ADMICA-7
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR PILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
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Pred. No. 1.1e+03;
); Mismatches 1;
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PRILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Acomica Sequence Listing Engine
SCOT ID NO 4955
LENGTH: 25
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APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 60/234,687
ELLING DATE: 2000-09-21
APPLICATION NUMBER: US 60/266,860
FILING DATE: 2001-02-05
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Best Local Similarity 93.8%;
Matches 15; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108-4955
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APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                   PRIOR FILING DATE: 2001-01-30
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PRIOR PILING DATE: 2000-09-21
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PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-20
PRIOR PILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
LENGTH: 25
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CURRENT FILING DATE: 2001-05-25
PRIOR PLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-27
PRIOR PLICATION NUMBER: US 60/236,359
PRIOR PELICATION NUMBER: PCT/US01/00666
PRIOR PELICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
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FLING DAFE: 2010-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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93.8%;
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APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 93.8
Matches 15; Conservative
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; ORGANISM: Homo sapiens
US-09-866-108-4954
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APPLICANT: CHEN, WENSINGON,
TITLE OF INVERTION: WOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AECMICA-7
CURRENT APPLICATION: WOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT APPLICATION NUMBER: US/02/456
PRIOR APPLICATION NUMBER: US/02/456
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-0
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                                                 Indels
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           Pred. No. 1.1e+03;
0; Mismatches 1;
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Pred. No. 1.1e+03;
0; Mismatches 1;
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LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                  Sequence 4958, Application US/09866108
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
   93.88;
       Best Local Similarity 93.8
Matches 15; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
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19 CTGCAGAAGGCACCGA 4
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; ORGANISM: Homo sapiens
US-09-866-108-4958
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US-09-866-108-4959/c
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APPLICANT: JI, Yonggang
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David K.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, MARK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
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Pred. No. 1.1e+03;
0; Mismatches 1;
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NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 4956
LENGTH: 25
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LENGTH: 25
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93.8%;
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Best Local Similarity 93.8
Matches 15; Conservative
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US-09-866-108-4956
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US-09-866-108-4957/c
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                                                          APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANSEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
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Pred. No. 1.1e+03;
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Sequence 4959, Application US/09866108
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GENERAL INFORMATION:
APPLICANT: GU, Yizhong
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93.8%;
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PENN, Sharron G.
HANZEL, David K.
RANK, David R.
CHEN, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 93.8
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 CTGCAGAAGGCACCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-866-108-4959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-866-108-4960/c
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APPLICANT
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Gaps
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GENERAL INCOMMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Lander, Elic S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2825.2009-001
CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/187,510
PRIOR PLICATION NUMBER: US 60/187,510
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 25;
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Pred. No. 1.1e+03;
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                    PRIOR APPLICATION NUMBER: GS 24263.6
PRIOR APPLICATION NUMBER: GS 24263.6
PRIOR FILING DATE: 2000-05-04
PRIOR PLING DATE: 2000-09-07
PRIOR PELICATION NUMBER: GS 60/236,359
PRIOR PLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 1802
SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 93.8
Matches 15; Conservative
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US-09-801-274-1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: HOMO
US-09-866-108-4960
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LENGTH: 31
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APPLICANT: SHANNON, MATK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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Pred. No. 3.2e+03;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT AFFILCATION NUMBER: US/09/060/100
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-05-25
PRIOR PELICATION NUMBER: GB 24263.6
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR PELICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2001-01-30
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                                                Application US/09866108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.0%;
93.3%;
                                                                                                               APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
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Best Local Similarity 93.3
Matches 14; Conservative
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US-09-866-108-2024
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APPLICANT: JI, YONGGANG
APPLICANT: HAWKEL, David K.
APPLICANT: HAWKEL, David R.
APPLICANT: HAWKEL, David R.
APPLICANT: HAWKEL, David R.
APPLICANT: HAWKEL, David R.
APPLICANT: RANK, WENSHORD
APPLICANT: CHEN, WENSHORD
APPLICANT: SHANNON, MAIK
TITLE REPRENCE: ADDITCA-7
CURRENT: SHANNON, MAIK
TITLE OF INVENTION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR PELICANTION NUMBER: US/09/866,108
CURRENT FILING DATE: 2000-06-36
PRIOR FILING DATE: 2000-06-36
PRIOR FILING DATE: 2000-09-37
PRIOR FILING DATE: 2000-09-37
PRIOR FILING DATE: 2000-00-39
PRIOR PLICANTION NUMBER: PCT/US01/0066
PRIOR PLICANTION NUMBER: PCT/US01/0066
PRIOR PLICANTION NUMBER: PCT/US01/0066
PRIOR FILING DATE: 2001-01-30
PRIOR PLICANTION NUMBER: PCT/US01/0066
PRIOR FILING DATE: 2001-01-30
PRIOR PLICANTION NUMBER: PCT/US01/0066
PRIOR FILING DATE: 2001-01-30
PRIOR PLICANTION NUMBER: PCT/US01/00663
PRIOR PLICANTION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR PLICANTION NUMBER: PCT/US01/00663
PRIOR PLICANTION NUMBER: PCT/US01/0067
PRIOR PRIOR PLICANTION NUMBER: PCT/US01/0067
PRIOR PRIOR PLICANTION NUMBER: PCT/US01/0067
PRIOR PLICANTION NUMBER: PCT/US01/0067
PRIOR PLICANTION DATE: 2001-01-30
PRIOR P
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Query Match
69.0%; Score 13.8; DB 6; Length 31;
Best Local Similarity 78.9%; Pred. No. 2.3e+03;
Matches 15; Conservative 1; Mismatches 3; Indels
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Pred. No. 3.2e+03;
0; Mismatches 1; Indels
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LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                        US-09-866-108-2021/c; Sequence 2021, Application US/09866108; GENERAL INFORMATION:
                                                                                                                                                                                         2 gacactgcaggaggmgctg 20
                                                                                                                                                    1 gaaactgcagaaggcactg 19
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; ORGANISM: Homo sapiens
US-09-866-108-2021
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Best Local Similarity
Matches 14; Conserv
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Gaps

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6 tgcagaaggcactga 20 

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Length 17;

Wed Oct 3 08:30:52 2001

3865, Ap 6, Appli 14335, A 14335, A 23884, A 19893, A 19893, A 19893, A 19893, A 1985, Appl 1025, Ap 1025, Ap 1025, Ap 1025, Ap 1025, Ap 1026, Appl 1086, Appl 1086,

sednence sed

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APPLICANT: Garner, Harold R.
APPLICANT: Garner, Harold R.
APPLICANT: Wren, Johathan D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTSD0667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILMS DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SEQ ID NO 204
LENGTH: 35
                                                                                                                                                                                                                                                                                                                      APPLICANT: Grigor, Murray R
TITLE OF INVENTION: Compositions isolated from bovine
TITLE OF INVENTION: Compositions isolated from bovine
TITLE OF INVENTION: tissues and methods for their use.
FILE REFERENCE: 1052P2
CURRENT APPLICATION NUMBER: US/60/252,833
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 43535
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26301
      US-09-559-639-6

US-09-711-772B-12058

US-09-718-620-14335

US-09-880-50-23884

US-09-880-50-81

US-09-633-739-10

US-09-633-739-10

US-09-633-634-19893

US-09-774-553C-155

US-09-774-553C-1025

US-09-774-7879-1280

US-09-817-879-1280

US-09-817-879-1280

US-09-817-879-1377

US-09-863-806-186

US-09-863-806-186

US-09-863-806-186

US-09-863-806-186

US-09-863-806-186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 12.2; DB 8;
Pred. No. 9.1e+03;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                      Sequence 26301, Application US/60252833; GENERAL INFORMATION: APPLICANT: Glenn, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 204, Application US/09475947A; GENERAL INFORMATION:
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1 ggcgccgtgcaccgagg 17
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Best Local Similarity
Matches 14; Conserv
 ; ORGANISM: Bovine US-60-252-833-26301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: human
                                                                                                                                                                                                                                                                              US-60-252-833-26301
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US-09-475-947A-204
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 TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26, Appl
282, App
1, Appli
1, Appli
23, Appl
6500, Appl
185, Appl
10876, A
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22, Appl
                                                                      Search time 2173.58 Seconds (without alignments) 19.290 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 282,
Sequence 1, A
Sequence 1, A
Sequence 53,
Sequence 6500
Sequence 185,
Sequence 185,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
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                                                                                                                                                                                                                                                                                                           Pending_Patents_NA_New:*

1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/USOG_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq:*

8: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq2:*

8: /cgn2_6/ptodata/2/pna/USOB_NEW_COMB.seq2:*
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-145-916B-22
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US-09-817-879-6300
                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                         1895189 seqs, 1048201267 residues
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                                                                       2001, 16:54:58
                                                                                                                                                                                                                                                                                        Listing first 45 summaries
                                                   OM nucleic - nucleic search, using sw model
                                                                                                                                       1 ggcgccgtgaagcgaaggca 20
                                                                                                                                                         IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                              Maximum Match 100%
                                                                                                             US-09-757-100B-4
20
                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
                                                                       October 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                  Minimum DB seq length: 0 Maximum DB seq length: 50
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Match 1
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                                                                                                                 Title:
Perfect score:
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                                                                                                                                                                                         Searched:
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Gaps

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5 ccgtgaagcgaaggc 19
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LOCATION:
ORGANISM: Homo sapiens
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US-09-817-879-1504/c
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TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide
TITLE OF INVENTION: Polymorphisms and Methods of Use Thereof
FILE REFERENCE: 15966-534C
CURRENT FILING DATE: 1999-11-17
PRIOR FILING DATE: 1999-11-17
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-16
PRIOR APPLICATION NUMBER: 09/443,199
PRIOR FILING DATE: 1999-11-16
PRIOR FILING DATE: 1999-11-16
SPRIOR FILING DATE: 1999-11-16
SOFTWARE: Curaden Patent Formatter Version 0.9
SEQ ID NO 1086
LENTH: 50
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GENERAL INFORMATION:
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Leach, Martin
TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide
TITLE OF INVENTION: Polymorphisms and Methods of Use Thereof
TITLE OF INVENTION: Polymorphisms and Methods of Use Thereof
FILE REFERENCE: 15966-334A
CURRENT FILING DATE: 1999-11-16
PRIOR FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 1272
SOFTWARE: Curaden Patent Formatter Version 0.9
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LOCATION: (26)...(0)
OTHER INFORMATION: 2 of 2 allelic variants (1085 is other entry)
NAME/KEY: misc_feature
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OTHER INFORMATION: nucleotide deleted between bases 25 and 26
LOCATION: (0)...(0)
                   Length 35;
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                                                              5; Indels
                60.0%; Score 12; DB 7;
75.0%; Pred. No. 1.1e+04;
iive 0; Mismatches 5
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                                      Local Similarity 75.0 nes 15; Conservative
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                Query Match
Best Local S
Matches 15
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RESULT 5
US-09-817-879-1279/C
Squence 1279, Application US/09817879
Squence 1279, Application US/09817879
SGUENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Brazymatic Nucleic Acid Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REPERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: PATENTIN VETSION 3.0
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GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals Inc.
APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel:
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
SEQ ID NO 1504
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LOCATION: (26)...(0)
OTHER INFORMATION: 2 of 2 allelic variants (1085 is other entry)
NAME/KEY: misc_feature
LOCATION: (25)...(25).
OTHER INFORMATION: nucleotide deleted between bases 25 and 26
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Pred. No. 1.4e+04;
0; Mismatches 2;
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COTHER INFORMATION: Accession number cg44923068
US-09-443-199C-1086
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ORGANISM: artificial sequence
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ORGANISM: artificial sequence
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Best Local Similarity 75.0°
Matches 15; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
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APPLICANT: Ribozyme Pharmaceuticals Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3276
LENGTH: 17
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APPLICANT: Shah, Nila
APPLICANT: Shah, Nila
APPLICANT: Glageras, Thomas Raymond
APPLICANT: Affgrers, Thomas Raymond
APPLICANT: Affgrers, Inc.
TITLE OF INVENTION: Human Lymphoblast Polymorphisms
FILE REFERENCE: 3229.2
CURRENT APPLICATION NUMBER: US/09/574,376B
CURRENT FILLING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 1330
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 157
LENGTH: 31
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Pred. No. 1.4e+04;
1; Mismatches 2;
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Pred. No. 1.4e+04;
0; Mismatches 2;
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; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-3276
                                                                                          RESULT 9
8.09-817-879-3276
Sequence 3276, Application US/09817879
GENERAL INFORMATION:
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; GENERAL INFORMATION:
; APPLICANT: Watson, James D
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80.0%;
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86.7%;
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Best Local Similarity 80.0
Matches 12; Conservative
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; PUBLICATION INFORMATION:
US-09-574-376B-157
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Best Local Similarity
Matches 13; Conserv
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US-09-724-671-4282/c
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US-09-574-376B-157
-- 167 AD
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TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                              Sequence 1505, Application US/09817879
GENERAL INFORMATION:
FOR TITLE OF INVENTION: BARD THE CONDITIONS Relate
TITLE OF INVENTION: Hepatitis C Virus Infection
FILE REFERENCE: MBHB00-801-F
CURRENT APPLICATION NUMBER: US/09/817,879
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 9703
SOFTWARE: Patentin version 3.0
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                                                                                      Score 11.8; DB 6;
Pred. No. 1.4e+04;
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86.7%; Pred. No. 1.4e+04;
tive 0; Mismatches 2;
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Pred. No. 1.4e+04;
0; Mismatches 2;
   ; OTHER INFORMATION: oligonucleotide substrate US-09-817-879-1505
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                                                                                        Query Match 59.0%;
Best Local Similarity 86.7%;
Matches 13; Conservative
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Best Local Similarity 86.7%;
Matches 13; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
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LENGTH: 17
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LOCATION:
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TTILE OF INVENTION: Transfection, Storage and Transfer of
TTILE OF INVENTION: Transfection, Storage and Transfer of
TTILE OF INVENTION: Transfection, Storage and Transgenic Stem
TTILE OF INVENTION: Cells
TTILE OF INVENTION: Cells
TTILE OF INVENTION: Cells
FILE REPERENCE: 18810-81602
CURRENT APPLICATION NUMBER: US/09/919,042
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1998-11-13
PRIOR PRICATION NUMBER: US 60/065,825
PRIOR FILING DATE: 1997-11-14
PRIOR APPLICATION NUMBER: US 60/065,825
SPRIOR APPLICATION NUMBER: US 60/065,825
SPRIOR APPLICATION NUMBER: PS/11-13
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 22
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
TITLE OF INVENTION: CAPACID DISEASES
FILE REFERENCE: P2833R1C1
CURRENT APPLICATION NUMBER: US/09/929,404
CURRENT PILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 310
SEQ ID NO 282
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Pred. No. 1.7e+04;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 282, Application US/09929404; GENERAL INFORMATION:
       Koeffler, H. Phillip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Watanabe, Colin K.
Wood, William
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Kabokoff, Rhona C.
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Best Local Similarity 77.8
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pennica, Diane
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Pan,James
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APPLICANT: Murison, James G
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: by the polynucleotides and methods for their use.
FILE REFERENCE: 105002
CURRENT APPLICATION NUMBER: US/09/724,671
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US. No. 60/171,678
PRIOR FILING DATE: 1999-12-23
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                                                                                                                                                                                                                                                                                                                                                                                                                              Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26, Application US/09918889
GENERAL INFORMATION:
APPLICANT: Readhead, Carol W.
APPLICANT: Winston, Robert
APPLICANT: Winston, Robert
APPLICANT: Winston, Robert
APPLICANT: Winston, Robert
APPLICANT: Willer, Carsten
TITLE OF INVENTION: CYCLIN A1 PROMOTER, AND KIT
FILE REFERENCE: 18810-81603
CURRENT APPLICATION NUMBER: US/09/918,889
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US 09/191,920
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-11-13
PRIOR FILING DATE: 1998-11-13
PRIOR FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 32
SOFFWARE: FEASTSED for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 11.8; DB 7; Length 3 Pred. No. 1.4e+04; Dred. Mismatches 2; Indels
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                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 21907
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4282
LENGTH: 31
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GENERAL INFORMATION:
APPLICANT: Readhead, Carol W.
APPLICANT: Winston, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                           59.0%;
86.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 59.0
Best Local Similarity 86.7
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 CGGGAGGCGAAGGCA 6
                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Mouse
US-09-724-671-4282
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US-09-919-042-26/c
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GENERAL INFORMATION:
APPLICANT: Setera Sciences, Inc.
TILE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
FILE REFERENCE: SIER 005M0
CURRENT APPLICATION NUMBER: PC/TUS01/25861
CURRENT PILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/237,865
PRIOR PILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
TYPE: DNA
TYPE: DNA
CRGANISM: human
PCT-US01-25861-1
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                       0; Gaps
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Pred. No. 1.8e+04;
0; Mismatches 4; Indels
Best Local Similarity 77.8%; Pred. No. 1.8e+04; Matches 14; Conservative 0; Mismatches 4; Indels
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77.8%;
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6 gtcgctgtgaagccaacg 23
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Best Local Similarity 77.84
Matches 14; Conservative
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PCT-US01-25861-1/c
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Search completed: October 2, 2001, 16:54:59 Job time: 17662 sec

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16.701 Million cell updates/sec
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/cgn2_6/ptodata/1/pna/US6010_COMB.seq:
/cgn2_6/ptodata/1/pna/US6011_COMB.seq:
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                           14155048 seqs, 7388405095 residues
                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                          2, 2001, 21:50:08
                                        OM nucleic - nucleic search, using sw model
                                                                                                                 1 ggcgccgtgaagcgaaggca: 20
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.: /cgn2_6/ptodata/1/pna/
:: /cgn2_6/ptodata/1/pna/
:: /cgn2_6/ptodata/1/pna/
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Gapop 10.0 , Gapext 1.0
                                                                                            US-09-757-100B-4
20
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55: /cgn2_6/ptodata/1/pna/US6022_COMB.seq:*
56: /cgn2_6/ptodata/1/pna/US6025_COMB.seq:*
57: /cgn2_6/ptodata/1/pna/US6025_COMB.seq:*
58: /cgn2_6/ptodata/1/pna/US6025_COMB.seq:*
59: /cgn2_6/ptodata/1/pna/US6025_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Sequence 4, Appli	. 4	24,	24,	4	equence 13,	Sequence 14,	Sequence 949	5 Sequence 3520	Sequence 11, App	Sequence 4017	Sequence 40466,	Sequence 45792	Sequence 1049	Sequence 10497	Sequence 10498	Sequence 10501	Sequence 5687	8 Sedneuce 56872	Sequence 568	4 Sequence 568734,		Sequence 12063,	9 Sequence 200	1 Sequence 309711	2588,	Sequence 2593	. Sequence 78332,	Sequence 83352,	4741,	4743,	e 4744,	4746,	4754,	4788,	4789,	4790,	91,	equence 4792,	93,	equence 4795,	Sequence 5481,	Sequence 29410,	Sequence 73099,
ID	PCT-US00-18999-4	-09-757-100B	-US00-18999-2	8-09-377-310-2	US-09-757-100	-08-448-223-1	-08-448-223-14	S-60-234-017-949	S-60-234-017-3520	S-09-812-913-11	S-09-404-520-4017	S-09-404-520-404	S-60-232-638-4579	8-60-233-166-1049	S-60-233-166-104	-60-233-166-10	S-60-233-166-1050	60-234-017-5	50-234-017-5687	50-234-017-5687	S-60-234-017-5687	09-660-080-1959	-09-660-220-1206	60-233-166-2005	-60-233-166-3	-60-233-620-258	-60-233-620-2593	-233-620-783	-60-233-620-8335	0-234-049-474	-60-234-049-474	-60-234-049-474	-60-234-049-474	-60-234-049-475	-60-234-049-4	-60-234-049-478	-60-234-049-479	US-60-234-049-4791	-60-234-049-4	-234-049-479	-60-234-049-479	-60-234-049-5481	-60-234-049-2941	0-234-049-73
DB	1	53		17		ω																					22																	
Length		20	15	15	15	45	45	25	25	30	41	41	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25
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Result No.		ım	4	ស	9	7	ω.		c 10	-	12	13	14	c 12	Н,	Η,	Η,	19	20	21	22	~	0	7	~	c 27	c 28	29	m	c 31	(A)	. س	m ·	m	36	37	38	39	40	41	42		44	c 45

## GENERAL INFORMATION: FEATURE: δλ QQ Dp ö ö SUBLEMAL INFORMATION: APPLICANT: Monia, Brett P. APPLICANT: Monia, Brett P. APPLICANT: Monia, Brett P. APPLICANT: Monia, Brett P. APPLICANT: Garade, William A. APPLICANT: OBERCH. APPLICANT: OBERCH. TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase TITLE OF INVENTION: Expression FILE REFERENCE: ISSH-0476 CURRENT APPLICATION NUMBER: PCT/US00/18999 CURRENT FILING DATE: 1999-08-19 PRIOR FILING DATE: 1999-08-19 NUMBER OF SEQ ID NOS: 43 SOFWWARE: Patentin Ver. 2.0 SEQ ID NO 4 LENGTH: 20 Gaps Gaps APPLICANT: Monia, Brett P. APPLICANT: Monia, Brett P. APPLICANT: Gaarde, William A. TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase TITLE OF INVENTION: Expression FILE REFERENCE: ISPH-0389 CURRENT APPLICATION NUMBER: US/09/377,310A CURRENT FILING DATE: 1999-08-19 NUMBER OF SEQ ID NOS: 43 SOFTHARE: Patentin Ver. 2.0 SED ID NO 4 LENGTH: 20 ö ö Query Match 100.0%; Score 20; DB 17; Length 20; Best Local Similarity 100.0%; Pred. No. 14; Matches 20; Conservative 0; Mismatches 0; Indels Length 20; Indels ); DB 1; ). 14; Mismatches ALIGNMENTS 100.0%; Score 20; 100.0%; Pred. No. ; OTHER INFORMATION: antisense sequence PCT-USO0-18999-4 CTHER INFORMATION: antisense sequence US-09-377-310-4 Sequence 4, Application PC/TUS0018999 GENERAL INFORMATION: Sequence 4, Application US/09377310A GENERAL INFORMATION: Sequence 4, Application US/09757100B ö 1 ggcgccgtgaagcgaaggca 20 1 ggcgccgtgaagcgaaggca 20 1 ggcgccgtgaagcgaaggca 20 TYPE: DNA ORGANISM: Artificial Sequence 1 ggcgccgtgaagcgaaggca 20 TYPE: DNA ORGANISM: Artificial Sequence Query Match 100. Best Local Similarity 100. Matches 20; Conservative RESULT 3 US-09-757-1008-4 RESULT 2 US-09-377-310-4 ò 셤 ô g

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APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Garde, William A.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFREENCE: ISPH-0533
CURRENT APPLICATION NUMBER: US/09/757,100B
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR APPLICATION NUMBER: PCT/US00/18999
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
APPLICANT: Garde, William A.
APPLICANT: Nero, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase TITLE OF INVENTION: Expression
FILLE DE INVENTION: Expression
CURRENT APPLICATION NUMBER: PCT/USOO/18999
CURRENT FILLING DATE: 2000-07-13
PRIOR PPLICATION NUMBER: 09/377,310
PRIOR FILLING DATE: 1999-08-19
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Pred. No. 3.8e+03;
0; Mismatches .0;
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Pred. No. 14;
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; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: antisense sequence US-09-757-100B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: antisense sequence PCT-USO0-18999-24
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APPLICANT: Monia, Brett P.
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100.08; PAN
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100.0%;
                                                                                                                                                                                                                                                                                                            LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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PCT-US00-18999-24
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US-09-377-310-24
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SEQ ID NO 24
LENGTH: 15
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Length 45;
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APPLICANT: Gelfand, David H.
APPLICANT: Kalman, Lisa V.
APPLICANT: Reichert, Fred L.
TITLE OF INVENTION: Thermostable DNA Polymerases With
TITLE OF INVENTION: Altered Discrimination Properties
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                             COMPUTER TREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Pred. No. 4.9e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/448,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Hoffmann-La Roche Inc.
340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08448223
GENERAL INFORMATION:
APPLICANT: Abramson, Richard D.
                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
NAME: Sias, Stacey R.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 9134
TELEPHONE: (510) 814-2863
TELEPHONE: (510) 814-2977
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 9134
                                                   340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Sias, Stacey R.
REGISTRATION NUMBER: 32,630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.0%;
88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
                                                                      Nutley
New Jersey
RY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Jersey
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                         COUNTRY:
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US-08-448-223-14
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                                                                                                STATE:
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APPLICANT: Gazde, William A.
APPLICANT: Gazde, William A.
APPLICANT: Gazde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
TITLE OF INVENTION: 1909-08:15
CURRENT APPLICATION NUMBER: US/09/757,100B
PRIOR PELLING DATE: 2001-03:15
PRIOR FILING DATE: 1999-08:19
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.0
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310A
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match 75.0%; Score 15; DB 17; Length 15; Best Local Similarity 100.0%; Pred. No. 3.8e+03; Matches 15; Conservative 0; Mismatches 0; Indels
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APPLICANT: Gelfand, David H.
APPLICANT: Kalman, Lisa V.
APPLICANT: Reichert, Fred L.
TITLE OF INVENTION: Thermostable DNA Polymerases With
TITLE OF INVENTION: Altered Discrimination Properties
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 75.0%; Score 15; DB 29; I Best Local Similarity 100.0%; Pred. No. 3.8e+03; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                           FEATURE:
CTHER INFORMATION: antisense sequence
US-09-377-310-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-757-100B-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24, Application US/09757100B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/08448223
GENERAL INFORMATION:
APPLICANT: Abramson, Richard D.
                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 cgccgtgaagcgaag 15
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LENGTH: 15
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 45;
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SGENERAL INFORMATION:
APPLICANT: Mittmann, M
TITLE OF INVENTION:
FILE REFERENCE: 3115
CURRENT APPLICATION WUMBER: US/60/234,017
CURRENT APPLICATION WUMBER: US/60/234,017
CURRENT APPLICATION WUMBER: US/60/234,017
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mitmann, M
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of Mus
TITLE OF INVENTION: Musculus
FILE REFERENCE: 3115
CURRENT PEPLICATION NUMBER: US/60/234,017
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 94926
LENGTH: 25
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 14.8; DB 8;
Pred. No. 4.9e+03;
0; Mismatches 2;
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; DATABASE ACCESSION NUMBER: GenBank AJ243852
US-60-234-017-94926
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; DATABASE ACCESSION NUMBER: Genbank AI506367
US-60-234-017-352075
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                                 TELEPHONE: (510) 814-2863
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-448-223-14
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88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus
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US-60-234-017-352075/c
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Sequence 11, Application US/09812913

Sequence 11, Application US/09812913

GENERAL INFORMATION:
APPLICANT: Weeks, Donald
APPLICANT: Cerutti, Heriberto
TITLE OF INVENTION: Acetolactate synthase gene and construct for the transformatio
TITLE OF INVENTION: Extranuclear genomes
FILE REPERENCE: N1231-210
CURRENT FILING DATE: 2001-03-20
FRIOR PPLICATION NUMBER: 60/190,668
PRIOR FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 11
LENGTH: 30
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y AppLICANT: Gao, Yongwei
y AppLICANT: Ghodssi, Azita
APPLICANT: Ghodssi, Azita
APPLICANT: Hinkle, Gregory J.
APPLICANT: Timberlake, William E.
APPLICANT: 100 Journal State Control
CURRENT APPLICATION NUMBER: US/09/404,520
CURRENT APPLICATION NUMBER: US/09/404,520
CURRENT APPLICATION NUMBER: US/09/404,520
CURRENT FILIA DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 44345
SEQ ID NO 40172
LENGTH: 41

TYPE: DNA
ORGANISM: Aspergillus nidulans
US-09-404-520-40172
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  Length 25;
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80.0%; Pred. No. 1.9e+04;
Live 0; Mismatches 4;
Score 13.6; DB 55;
Pred. No. 1.9e+04;
0; Mismatches 4;
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Pred. No. 1.9e+04;
0; Mismatches 4;
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; ORGANISM: Chlamydomonas reinhardtii
US-09-812-913-11
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68.0%;
80.0%;
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80.0%;
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Best Local Similarity 80.0°
Matches 16; Conservative
                                          Conservative
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Best Local Similarity
Matches 16; Conserv
Query Match
Best Local Similarity
Matches 16; Conserv
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                                                                              APPLICANT: Cac, Yongwei
APPLICANT: Chocksi, Azita
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Timberlake, William E.
APPLICANT: 100 WINMER: US/09/404,520
CURRENT PILLIKG DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 44345
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US-60-232-588 45792
US-60-232-588 45792
Sequence 45792, Application US/60232638
SEMERAL INFORMATION:
APPLICANT: Mittmann
APPLICANT: Mittmann
APPLICANT: Mittmann
TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
FILE REFERENCE: 3110
CURRENT APPLICATION NUMBER: US/60/232,638
CURRENT FILING DATE: 2000-09-14
NUMBER OF SEQ ID NOS: 138410
SEQ ID NO 45792
LENGTH: 25
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GENERAL INFORMATION:
APPLICANT: Mitmann
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
FIRE REFERENCE: 3112
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Pred. No. 2.9e+04;
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CURRENT APPLICATION NUMBER: US/60/233,166
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 420907
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; DATABASE ACCESSION NUMBER: SGD YDL200C
US-60-232-638-45792
                                        Sequence 40466, Application US/09404520 GENERAL INFORMATION:
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Best Local Similarity 83.3%;
Matches 15; Conservative
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US-60-233-166-104969/c
RESULT 13
US-09-404-520-40466
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LENGTH: 41
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/pna/US6028_COMB.seq
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US-09-660-220-37376
US-09-660-220-37377
US-60-234-017-55657
US-60-234-017-55657
US-60-234-017-5527
US-60-234-017-10846
US-60-234-017-10846
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US-60-234-017-480869
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PCT-US00-18999-23
US-09-377-310-23
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US-09-377-310-3
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16.701 Million cell updates/sec
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3: (cgn2_6/ptodata/1/pna/USO8_COMB.seq:*
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Sequence 3, Appli Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl

Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli

Description

Sequence 37376, A Sequence 37377, A Sequence 18577, A Sequence 5567, A Sequence 75527, A Sequence 10846, A Sequence 2, Appli

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Sequence 18962, A Sequence 18962, A Sequence 18962, A Sequence 18062, Sequence 136549, Sequence 217856, Sequence 410831, Sequence 413818, Sequence 228334, Sequence 228334, Sequence 228330, Sequence 228330,

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Sequence 40877, 1 Sequence 185404, Sequence 235736,

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Sequence 37375, Sequence 30520,

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                                                                                                                                   APPLICANT: Isis Pharmaceuticals, Inc.

APPLICANT: Monia, Brett P.

TITLE Gaarde, William A.

TITLE OF INVENTION: Expression

FILE REFERENCE: ISPH-0476

CURRENT APPLICATION NUMBER: PCT/US00/18999

CURRENT APPLICATION NUMBER: PCT/US00/18999

PRIOR FILING DATE: 1999-08-19

PRIOR FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0

LENGTH: 20
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APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310A
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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100.0%; Pred. No. 15;
tive 0; Mismatches 0
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ALIGNMENTS
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                                                                                                 Sequence 3, Application PC/TUS0018999 GENERAL INFORMATION:
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US-09-757-100B-3
: Sequence 3, Application US/09757100B
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Matches 20; Conservative
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Best Local Similarity 100.
Matches 20; Conservative
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PCT-US00-18999-3
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US-09-377-310-3
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LENGTH: 20
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APPLICANT: Monia, Erett P.
APPLICANT: Gaarde, William A.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0476
CURRENT APPLICATION NUMBER: PCT/US00/18999
CURRENT FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
APPLICANT: Gaarde, william A.
APPLICANT: Gaarde, william A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase;
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0533
CURRENT APPLICATION NUMBER: US/09/757,100B
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver: 2.0
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Pred. No. 15;
; Mismatches 0;
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Pred. No. 4.1e+0:
0; Mismatches
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; GENERAL INFORMATION:
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APPLICANT: Monia, Brett P.
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Best Local Similarity 100.0%; Pa
Matches 15; Conservative 0;
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
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PCT-US00-18999-23
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US-09-377-310-23
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Gaps
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GENERAL INFORMATION:
APPLICANT: Mittmann et al.
APPLICANT: Mittmann et al.
TITLE OF INVENTION: Methods of Genetic Analysis of Human TITLE OF INVENTION: Methods of Genetic Analysis of Human FILE OF INVENTION: Methods of Genetic Analysis of Human CURRENT APPLICATION NUMBER: US/09/660,220
CURRENT FILING DATE: 2000-09-12
PRIOR PELLING DATE: 1999-11-11
NUMBER OF SEQ ID NOS: 140981
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mittmann
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
FITLE OF INVENTION: Genome
FILE REFERENCE: 3112
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Pred. No. 5.1e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                         Score 14.8; DB 26;
Pred. No. 5.1e+03;
0; Mismatches 2;
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US-60-233-166-185790
               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 37376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 185790 LENGTH: 25
                                                                                                            ; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank L11931
US-09-660-220-37376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank L11931
US-09-660-220-37377
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CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 420907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 185790, Application US/60233166; GENERAL INFORMATION:
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ilarity 88.9%;
Conservative
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88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity
Matches 16; Conserv
        PRIOR FILING DATE:
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US-09-660-220-37377
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APPLICANT: Monia, Brett P.
APPLICANT: Monia, Pamela S.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: 1SPH-0533
CURRENT FILING DATE: 1999-08-15
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR APPLICATION NUMBER: 09/377,310
PRIOR APPLICATION NUMBER: PCT/US00/18999
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 2000-07-13
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
LENGTH: 15
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310A
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
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APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of Human
FILE REFERENCE: 3102.1
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100.0%; Pred. No. 4.1e+03
iive 0; Mismatches 0
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                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: antisense sequence US-09-377-310-23
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; Sequence 37376, Application US/09660220
; GENERAL INFORMATION:
; APPLICANT: Mitmann et al.
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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Length 25;
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Sequence 55657, Application US/60234017

Sequence 55657, Application US/60234017

GENERAL INFORMATION:

APPLICANT: Mittann, M

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis of Mus;

TITLE OF INVENTION: Musculus

FILE REFERENCE: 3115

CURRENT FILING DATE: 2000-09-20

NUMBER OF SEQ ID NOS: 605887

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 55657

LENGTH: 25
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GENERAL INFORMATION:
APPLICANT: Mittmann, M
TITLE OF INVENTION: Methods of Genetic Analysis of Mus
TITLE OF INVENTION: Methods of Genetic Analysis of Mus
TITLE OF INVENTION: Methods of Genetic Analysis of Mus
FILE REFERENCE: 3115
CURRENT APPLICATION NUMBER: US/60/234,017
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 75527
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Score 14.8; DB 55;
Pred. No. 5.1e+03;
0; Mismatches 2;
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Pred. No. 1e+04;
0; Mismatches 3;
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Pred. No. 1e+04;
0; Mismatches 3;
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; DATABASE ACCESSION NUMBER: GenBank AF048838
US-60-234-017-75527
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; DATABASE ACCESSION NUMBER: GenBank U76759
US-60-234-017-55657
74.0%;
88.9%;
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84.2%;
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Best Local Similarity 84.2%;
Matches 16; Conservative
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Matches 16; Conserva
                   Best Local Similarity
Matches 16; Conserv
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Query Match
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US-60-233-166-279728/c

Sequence 279728, Application US/60233166

Sequence 279728, Application US/60233166

Separate National Matternan

APPLICANT: Affymetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis of the Rat

TITLE OF INVENTION: Genome

FILE REFERENCE: 3112

CURRENT APPLICATION NUMBER: US/60/233,166

CURRENT FILIG DATE: 2000-10-24

NUMBER OF SEQ ID NOS: 420907

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 279728

LENGTH: 25
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GENERAL INFORMATION:
APPLICANT: Mittmann:
APPLICANT: Mittmann:
APPLICANT: Mittmann:
APPLICANT: Mittmann:
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
TITLE OF INVENTION: Genome
FILE REPRENCE: 311
CURRENT APPLICATION NUMBER: US/60/233,166
CURRENT APPLICATION NUMBER: US/60/233,166
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 420907
SOFTWARE: FASLSEQ for Windows Version 4.0
FEMILE THE SECTION OF THE SEQ ID NOS: 420907
TYPE: DNA
TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Mittmann, M
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of Mus
TITLE OF INVENTION: musculus
FILE REFERENCE: 3115
CURRENT APPLICATION NUMBER: US/60/234,017
CURRENT FILING DATE: 2000-09-20
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Pred. No. 1.6e+04;
0; Mismatches 2;
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100.0%; Pred. No. 1.2e+04;
Live 0; Mismatches 0;
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DATABASE ACCESSION NUMBER: GenBank A1639107
US-60-233-166-279728
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88.2%;
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Best Local Similarity 100.
Matches 14; Conservative
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Best Local Similarity 88.2
Matches 15; Conservative
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i Sequence 248844, Application US/60234017

i GENERAL INFORMATION:

APPLICANT: Mittmann, M

TITLE OF INVENTION: Methods of Genetic Analysis of Mus;

TITLE OF INVENTION: Methods of Genetic Analysis of Mus;

TITLE OF INVENTION: Methods of Genetic Analysis of Mus;

TITLE OF INVENTION: Methods of Genetic Analysis of Mus;

TITLE OF INVENTION: Methods of Genetic Analysis of Mus;

TITLE OF INVENTION: Methods of Genetic Analysis of Mus;

FILE REFERENCE: 3115

CURRENT FILING DATE: 2000-09-20

NUMBER OF SEQ ID NOS: 605887

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 248844

LENGTH: 25

TYPE: DATA

ORGANISM: Mus musculus

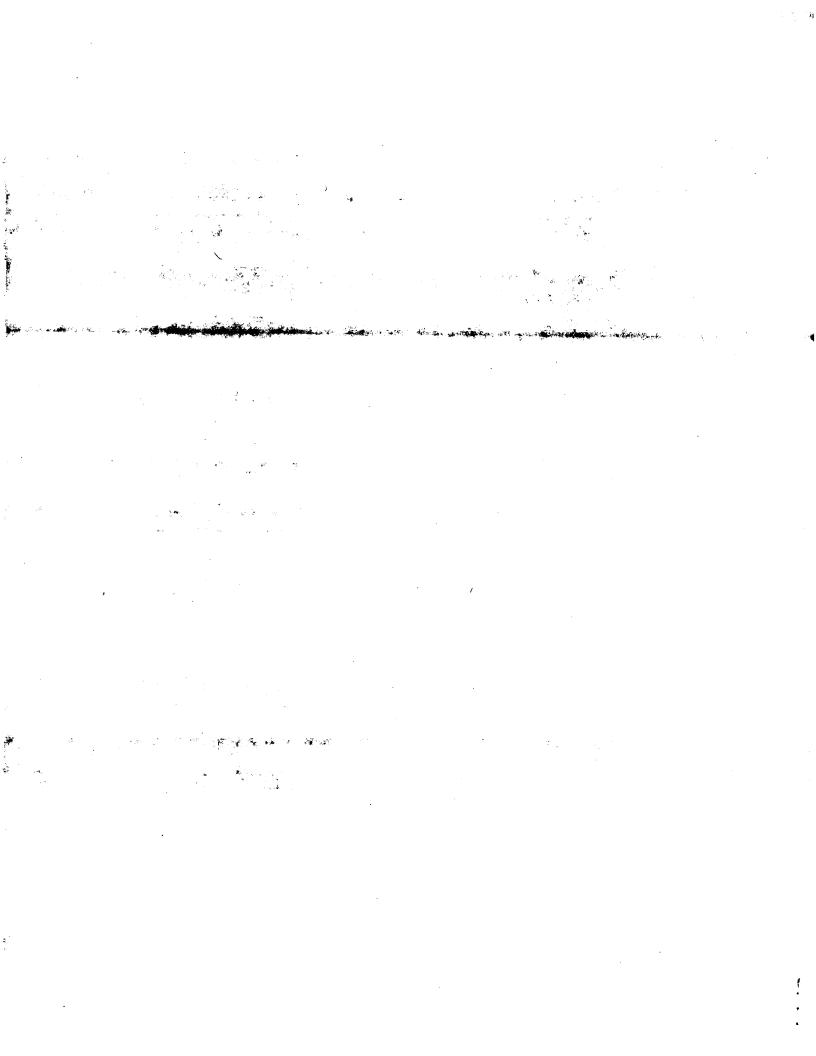
PUBLICATION INFORMATION:

BATABASE ACCESSION NUMBER: GenBank AW049900

US-60-234-017-248844
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Pred. No. 1.6e+04;
0; Mismatches 2;
                                                                                TYPE: DNA
ORGANISM: Mus musculus
POBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank AF055638
US-60-234-017-10846
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10846
LENGTH: 25
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Best Local Similarity 88.2%;
Matches 15; Conservative
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Matches 15; Conservative
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Search completed: October 2, 2001, 21:50:08 Job time: 24521 sec

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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/USOG_NEW_COMB.seq:*
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7: /cgn2_6/ptodata/2/pna/USOR_NEW_COMB.seq:*
8: /cgn2_6/ptodata/2/pna/USOR_NEW_COMB.seq2:*
                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-735-271-2037
US-09-775-271-2037
US-09-775-271-10
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US-09-915-060-43
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## ALIGNMENTS

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APPLICANT: Lassner, M.; Post-Beittenmiller, M.; Savidge, B.; Weiss, J.; Mitsky, T. APPLICANT: Lassner, M.; Post-Beittenmiller, M.; Savidge, B.; Weiss, J.; Mitsky, T. APPLICANT: Valentin, H.

TITLE OF INVERTION: Nucleic Acid Sequences to Proteins Involved in Tocopherol Synt File Reperence: 16515.055
CURRENT APPLICATION NUMBER: US/09/688,071
CURRENT APPLICATION NUMBER: US 60/129,899
PRIOR APPLICATION NUMBER: US 60/146,461
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
                                                                                                                                                                                                                           Sequence 53, Application US/09688069; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAMT: Subramaniam, S.; Slater, S.; Karberg, K.; Chen, R.; Valentin, H.; Wong,
TITLE OF INVENTION: Uncleic Acid Sequences to Proteins Involved in Tocopherol Synt,
FILE REFERENCE: 16515.054
CURRENT APPLICATION NUMBER: US/09/688,069
CURRENT FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 114
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Score 12.2; DB 7; Length 41; pred. No. 9.4e+03; 0; Mismatches 3; Indels
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Pred. No. 9.4e+03;
0; Mismatches 3;
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Pred. No. 9.4e+03;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetic Oligonucleotides US-09-688-071-53
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                                               14; Conservative
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Best Local Similarity
Matches 14; Conserv
                   Best Local Similarity
Matches 14; Conserv
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Best Local Similarity
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US-09-688-069-53
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US-09-688-071-53
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      Query Match
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TITLE OF INVENTION: Nucleic Acid Sequences to Proteins Involved in Tocopherol Synthes FILE REFERENCE: 16515.055
CURRENT APPLICATION NUMBER: US/09/688,071
CURRENT FILING DATE: 2000-10-14
PRIOR PELICATION NUMBER: US 60/129,899
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 1999-04-15
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-09-14
SEQ ID NOS: 114
SEQ ID NOS: 114
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 51, Application US/09688069
GENERAL INFORMATION:
APPLICANT: Subramaniam, S.; Slater, S.; Karberg, K.; Chen, R.; Valentin, H.; Wong, Y.
APLICANT: Subramaniam, S.; Slater, S.; Karberg, K.; Chen, R.; Valentin, H.; Wong, Y.
TILE OF INVENTION: Nucletc Acid Sequences to Proteins Involved in Tocopherol Synthes
FILE REFERENCE: 16515.054
CURRENT FILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lassner, M.; Post-Beittenmiller, M.; Savidge, B.; Weiss, J.; Mitsky, T.;
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                                                                                                                                                                       Length 50;
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                                                                                                                                                                                                              Indels
                                                                                                                                                                   Score 13.2; DB 7;
Pred. No. 2.9e+03;
0; Mismatches 3;
                                                                                   ; OTHER INFORMATION: Synthetic Oligonucleotides US-09-688-071-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Synthetic Oligonucleotides US-09-688-069-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 51, Application US/09688071; GENERAL INFORMATION:
                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.0%;
82.4%;
                                                                                                                                                                   66.0%;
ilarity 83.3%;
Conservative
                                                                                                                                                                                                                                                       1 ccgcgggctcacagtggt.18
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Best Local Similarity
Matches 15; Conserve
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Best Local Similarity
Matches 14; Conserv
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US-09-688-071-51
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    LENGTH: 50
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LENGTH: 41
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                                                                FEATURE
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kster, Hubert
TITLE OF INVENTION: DNA Diagnostics Based on Mass Spectrometry
NUMBER OF SEQUENCE: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                             ;
0
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Pred. No. 1.8e+04;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Heller Ehrman White & McAuliffe LLP
STREET: 4350 La Jolla Village Drive
CITY: San Diego
                                                                                                                                                                                                                                               Score 11.6; DB 6;
Pred. No. 1.8e+04;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24736-2002M
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/879,341 FILING DATE: 11-Jun-2001 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/786,416
FILING DATE: 28-FEB-2001
APPLICATION NUMBER: 09/287,679
FILING DATE: 06-APR-1999
APPLICATION NUMBER: 08/617,256
FILING DATE: 18-ARR-1996
APPLICATION NUMBER: 08/406,199
FILING DATE: 03-MAR-1996
                                                                                        ; TOPOLOGY: linear; SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-879-341-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-879-341-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09879341 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (617)227-7400
TELEPKX: (617)227-5941
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                              LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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77.8%;
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Best Local Similarity 77.8
Matches 14; Conservative
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Best Local S
Matches 14
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TITLE OF INVENTION: DNA Diagnostics Based on Mass Spectrometry
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Haller Ehrman White & McAuliffe LLP
STREET: 4350 La Jolla Village Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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COMPUTER: IBM Compatible

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/879,341

FILING DATE: 11-Jún-2001

APPLICATION NUMBER: 09/786,416

FILING DATE: 28-FEB-2001

APPLICATION NUMBER: 09/287,679

FILING DATE: 06-APR-1999

APPLICATION NUMBER: 08/617,256

FILING DATE: 18-MAR-1996

APPLICATION NUMBER: 08/406,199

FILING DATE: 103-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
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REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24736-2002M
                                                                                                                                                  APPLICANT: Rioux, John APPLICANT: Siminovitch, Kathy TITLE OF INVENTION: IBD-RELATED POLYMORPHISMS FILE REFERENCE: 2825.1025-002 CURRENT APPLICATION NUMBER: US/09/735,271 CURRENT FILING DATE: 2000-12-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.5e; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 2058
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/170,257
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 60/196,046
PRIOR FILING DATE: 2000-04-10
                                         Sequence 2037, Application US/09735271
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TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/09879341 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.0%;
86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 92122-1246
COMPUTER READABLE FORM:
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Best Local Similarity 86.7
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-735-271-2037
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US-09-879-341-12
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LENGTH: 25
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN GROWTH FACTOR WITH HOMOL
TITLE OF INVENTION: EPIDERMAL GROWTH FACTOR, BGS-8, EXPRESSED HIGHLY IN IMMUNE TI
FILE REFERENCE: D0166 PSP
CURRENT APPLICATION NUMBER: US/60/298,340
CURRENT FILING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
SEQ ID NO 21
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Sequence 17, Application US/09787252

Sequence 17, Application US/09787252

GENERAL INFORMATION:
APPLICANT: Lex M. COWSETt

TITLE OF INVENTION: ANTISENSE MODULATION OF RhOG EXPRESSION
FILE REFERENCE: RTSP-0106

CURRENT APPLICATION NUMBER: US/09/787,252

CURRENT FILING DATE: 2001-03-15

PRIOR APPLICATION NUMBER: 09/161,015

PRIOR FILING DATE: 1998-09-25

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 17

LENGTH: 18
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GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Lander, Eric S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2825.2009-001
CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT FILING DATE: 2001-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 1802
NUMBER OF SEQ ID NOS: 1802
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 39;
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Pred. No. 1.9e+04;
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Pred. No. 2.3e+04;
0; Mismatches 1;
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92.3%;
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Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-298-340-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 cgggctcacagtg 16
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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SOFTWARE: Patentin version 3.1

SEQ ID NO 43

LENGTH: 30
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                                                                                                                                                                                                   Sequence 9. Application US/09915060
GENERAL INFORMATION:
APPLICAMY: Valams Internulversitair Instituut voor Biotechnol
TITLE OF INVENTION: thereof
TITLE OF INVENTION: thereof
TITLE OF INVENTION: thereof
TITLE OF INVENTION: thereof
TITLE OF INVENTION: 000401 internal ribosome entry site, vector containing same and t
TITLE OF INVENTION: 000401 internal ribosome entry site, vector containing same and t
TITLE OF INVENTION: 000401 internal ribosome entry site, vector containing same and t
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Pred. No. 1.9e+04;
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US-60-298-340-21/c
; Sequence 21, Application US/60298340
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; Sequence 43, Application US/09915060
; GENERAL INFORMATION:
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US-09-915-060-9
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 77.8%;
Matches 14; Conservative
      3 gegggeteacagtggteg 20
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                                                20 GCGGCAAACAGTCGTTG 3
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Matches 14; Conservative
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Pred. No. 2.4e+04;
0; Mismatches 1; Indels
                                                                                                                                     Score 11.4; DB 6; Length 31;
Pred. No. 2.3e+04;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-09-735-271-1558/C

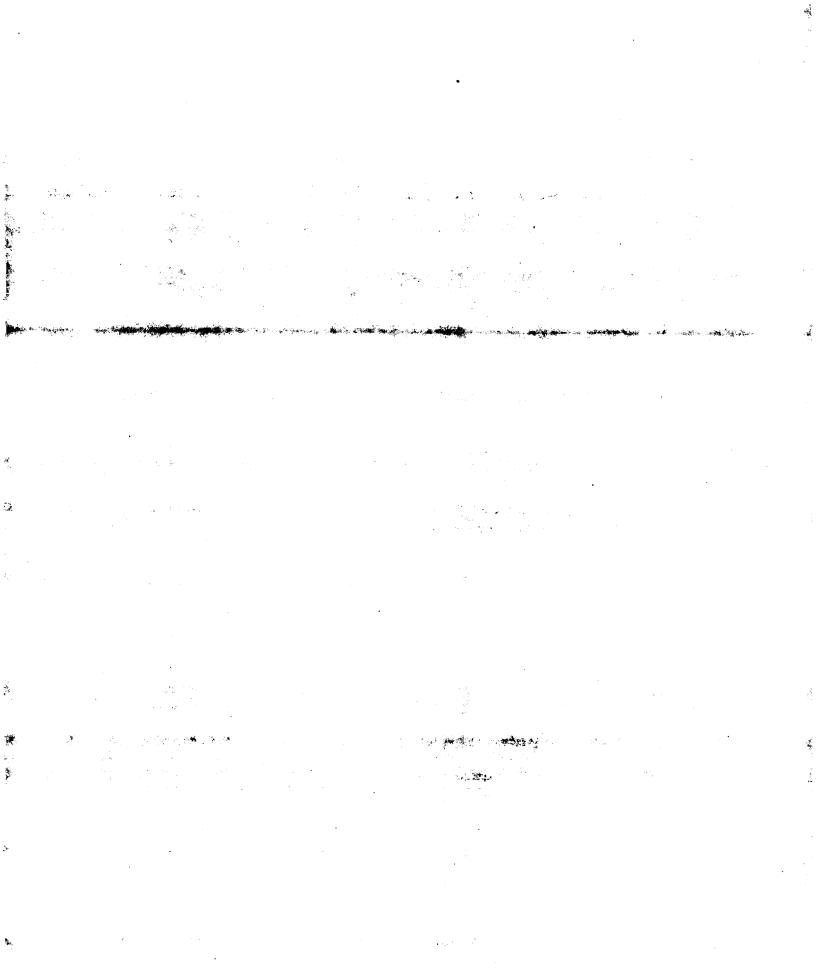
Sequence 1558, Application US/09735271

GENERAL INFORMATION:
APPLICANT: Hudson, Thomas J.
APPLICANT: Lander, Eric S.
APPLICANT: Rioux, John
TITLE OF INVENTION: Ender, Rathy
TITLE OF INVENTION: 180-RELATED POLYMORPHISMS
FILE REFERENCE: 2825.1025-002
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 60/170,257
PRIOR FILING DATE: 1999-12-10
PRIOR FILING DATE: 2000-12-11
PRIOR FILING DATE: 2000-12-11
PRIOR FILING DATE: 2000-12-10
PRIOR FILING DATE: 2000-12-10
SPRIOR FILING DATE: 2000-12-10
SPRIOR FILING DATE: 2000-04-10
SPECIFICATION NUMBER: US 60/196,046
SEQ ID NOS: 2058
SEQ ID NOS: 2058
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SEQ ID NOS: 2058
FIRENTH: 40
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NAME/KEY: misc_feature
LOCATION: (1)...(40)
OTHER INFORMATION: n = A,T,C or G
US-09-735-271-1558
                                                                                                                                     Query Match 57.0%;
Best Local Similarity 80.0%;
Matches 12; Conservative
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Best Local Similarity 92.3%;
Matches 12; Conservative
                                                                                                                                                                                                                              6 ggctcacagtggtcg 20
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3 gggtcacagtggcsg 17
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-629
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35 GCGGGTCACAGT 23
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ORGANISM: Homo sapiens
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Fatent NO. 6133031
GENERAL INFORMATION:
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Expression
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION UNMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 20
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Sequence
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Patent No. 6133031
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
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100.0%; Pred. No. 0.041;
live 0; Mismatches 0; Indels
             US-08-471-791-39
PCT-US91-01746-39
PCT-US91-01750-10
US-08-781-891-3
US-08-445-4638-63
US-08-445-4638-63
US-08-445-4638-63
US-08-445-4638-62
US-08-790-963-2
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US-08-790-774-2
US-08-790-774-2
US-08-790-774-2
US-08-790-774-2
US-08-790-774-2
US-08-790-774-041-31
US-08-795-401-040
US-08-379-0818-117
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 RESULT 2
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SEQ ID NO 29
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                                                                                                              Search time 417.38 Seconds
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Sequence 3
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
           version 4.5
- 2000 Compugen Ltd.
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US-09-377-310-8
US-09-377-310-8
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US-09-03-05-83-15
US-09-03-05-83-15
US-08-686-968C-32
US-08-686-968C-32
US-08-686-968C-32
US-08-686-968C-32
US-08-292-597-8
US-08-292-597-8
US-08-293-898-8
US-08-157-985-8
US-09-087-716-8
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Maximum Match 100%
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Copyright (c) 1993
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length: 50
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Result Š. Pred.

Minimum DB Maximum DB

Database

Searched:

Gaps

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Length 31;
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APPLICANT: Gold, Larry
APPLICANT: Gold, Larry
APPLICANT: Tanjic, Nebojsa
APPLICANT: Tasset, Diane
TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND
TITLE OF INVENTION: THROMBIN
NUMBER OF SEQUENCES: 445
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette, 3.5 inch, 1.44 MB storage
                                                                                                                                                                                                                                                                                                                 DB 1;
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8400 E. Prentice Avenue, Suite 200
                                                                                                                                                                                                                                                                                                               Score 13.6; DI
Pred. No. 98;
0; Mismatches
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SUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,421
FILING DATE: 08-MAY-1996
CLASSIFFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: 08/195,005
FILING DATE: 10-FEBRUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
PRIOR APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,333
FILING DATE: 11-NOVEMBER-1992
PRIOR APPLICATION DATA:
FILING DATE: 10-UNBER: 07/714,131
FILING DATE: 10-UNBER: 07/714,131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 227, Application US/08687421 Patent No. 6177557
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APPLICATION NUMBER: 08/219,012
FILING DATE: 28-MARCH-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07/536,428
                                                       REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9900
TELEFAX: (303) 850-9401
INPORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                 68.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 11-JUNE-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             2 rrrrggraraggcraggrgr 21
     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             1 ttttgctagatgctaggtat
                         NAME: Barry J. Swanson
REGISTRATION NUMBER: 3
                                                                                                                                                                         LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                         Conservative
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                         linear
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-08-687-421-227
                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                           US-08-219-012-39
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APPLICANT: Montal, Brett P.
APPLICANT: Montal, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 20
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                                                                                                 DB 3; Length 15;
17;
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17;
                                                                                                                                       0; Indels
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APPLICANT: Larry Gold
APPLICANT: Dane Tasset
TITLE OF INVENTION: Ligands of Thrombin
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beaton & Swanson, P.C.
STREET: 4582 South Ulster Street Parkway, Suite #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.0%; Score 15; DB 100.0%; Pred. No. 17; Live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense sequence
US-09-377-310-8
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-29
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,012
                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09377310B Patent No. 6133031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 39, Application US/08219012 Patent No. 5543293
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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PRIOR APPLICATION DATA:
                                                                                                                                                                           6 ctagatgctaggtat 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Denver
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-219-012-39
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Pred. No. 5.3e+02;
0; Mismatches 3; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OHKAWA, HIDEO
APPLICANT: IMAISHI, HIROMASA
TITLE OF INVENTION: NOVEL CYTOCHROME P450 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                               SUFIYARE: PATEBLIAN RELEASE #1.0, VETS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,832A
FILING DATE: 30-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,955
FILING DATE: 07-JUL-1995
PRIOR APPLICATION NUMBER: US 08/678,435
FILING DATE: 03-JUL-1996
ATTORNEY/AGNET INFORMATION:
NAME: Hibler, David W.
REGISTRATION NUMBER: 41,071
REGISTRATION NUMBER: 41,071
REGISTRATION NUMBER: 41,071
REFERENCE/DOCKET NUMBER: TAMK:190
TELECOMMUNICATION INFORMATION:
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NAME: PAUL E. WHITE, JR.
RECISTRATION NUMBER: 32,011
REFERNCE/DOCKET NUMBER: 9437/251563
TELECOMMINICATION INFORMATION:
TELEPHONE: (202) 861-8651
TELEFRAX: (202) 822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/033,055A
FILING DATE: MARCH 2, 1998
CLASSIFICATION: 536
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US-09-033-055A-10
Sequence 10, Application US/09033055A
Patent No. 6069241
GENERAL INFORMATION:
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82.4%;
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TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 ttgctagatgctaggta 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity
Matches 14; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-792-832A-15
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STATE:
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APPLICANT: Monia, Brett P.

APPLICANT: Gaarde, William A.

TITLE OF INVENTION: Expression
FILE REPERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 15
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Patent No. 6017734

GENERAL INFORMATION

APPLICANT: Summers Dr., Max D.

APPLICANT: Braunagel Dr., Sharon C.

APPLICANT: Hong Dr., Tao

TILLE OF INVENTION: UNIQUE NUCLEOTIDE AND AMINO ACID

TILLE OF INVENTION: SEQUENCE AND USES THEREOF

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: AROLIG, White & Durkee
                                                                                                                                                                                                                                                                                                                                     4; Indels
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; Mismatches
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                                                                                                                                                                                                                                                                                            68.0%; Score 13.6;
80.0%; Pred. No. 98
                   REFERENCE/DOCKET NUMBER: NEXO7/PCT
TELECOMONIOLEATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEPAX: (303) 793-3433
INPORMATION FOR SEQ ID NO: 227:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: antisense sequence US-09-377-310-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-377-310-28; Sequence 28, Application US/09377310B; Patent No. 6133031
  REGISTRATION NUMBER: 33,215
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                               Best Local Similarity 80.0
Matches 16; Conservative
                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
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US-08-687-421-227
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: OTHER INFORMATION: Description of Artificial Sequence: primer US-08-686-9686-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12.2; DB 4; Length 35;
Pred. No. 5.4e+02;
0; Mismatches 3; Indels
     Indels
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Pred. No. 5.4e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 34, Application US/08686968C

Patent No. 6221361

GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: Recombinant Swinepox Virus
FILE REFERENCE: 39119-H/JML
CURRENT APPLICATION NUMBER: US/08/686,968C
CURRENT FILING DATE: 1996-07-25
NUMBER OF SEQ ID NOS: 231

SEQ ID NO 34

LENGTH: 35
                                                                                                                                                                                                                      APPLICANT: Cochran, Mark D.
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: Recombinant Swinepox Virus
FILE REFERENCE: 39119-H/JML
CURRENT APPLICATION NUMBER: US/08/686,968C
CURRENT FILING DATE: 1996-07-25
NUMBER OF SEQ ID NOS: 231
SEQ ID NO 32
LENGTH: 35
     Mismatches
                                                                                                                                 RESULT 11
NS-08-6869 968C-32
Sequence 32, Application US/08686968C
; Patent No. 6221361
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82.4%;
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82.4%;
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                                        2 tttgctagatgctaggt 18
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Best Local Similarity 82.4
Matches 14; Conservative
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Best Local Similarity 82.4
Matches 14; Conservative
   Matches 14; Conservative
                                                                                                                                                                                                           ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-08-686-968C-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-08-478-386A-8
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: primer US-08-686-968C-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 12.2; DB 4; Length 35;
Pred. No. 5.4e+02;
0; Mismatches 3; Indels
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                                                                                                                                                                                                           3; Indels
                                                                                                                                                                        Length
                                                                                                                                                                  Score 12.2; DB 3;
Pred. No. 5.3e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: Recombinant Swinepox Virus
FILE REFERENCE: 39119-H/JML
CURRENT APPLICATION NUMBER: US/08/686,968C
NUMBER OF SEQ ID NOS: 231
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 28
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 12.2; DB 4;
Pred. No. 5.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
TILE APPLICANT: Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
FILE REFERENCE: 39119-H/JML
CURRENT APPLICATION NUMBER: US/08/686,968C
CURRENT FILING DATE: 1996-07-25
NUMBER OF SEQ ID NOS: 231
SOFTWARE: PALENTI VET: 2.1
SEQ ID NO 30
LENGTH: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-08-686-968C-30
; Sequence 30, Application US/08686968C
; Patent No. 6221361
                                                                                                                                                                                                                                                                                                                                                                       Sequence 28, Application US/08686968C Patent No. 6221361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                  Query Match 61.0%;
Best Local Similarity 82.4%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 61.0%;
Best Local Similarity 82.4%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.0%;
82.4%;
                                                                                                                                                                                                                                                                 2 TTGCTTATTGCTAGGTA 18
                                                                                                                                                                                                                                           3 ttgctagatgctaggta 19
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                      TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-033-055A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                        US-08-686-968C-28
                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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Pred. No. 5.5e+02;
0; Mismatches 3; Indels
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OTHER INFORMATION: /note= "Region of homology with
OTHER INFORMATION: target sequence."
                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BIM PC compatible
OPERATING SYSTEM: PC/DOS/MS/DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,597
FILING DATE: 18/AUG/1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                 APPLICANT: Spencer, David M.
APPLICANT: Spencer, David M.
APPLICANT: Wandless, Thomas J.
APPLICANT: Belshaw, Peter
TITLE OF INVENTION: Regulated Apoptosis
CORRESPONDENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARIAD Pharmaceuticals, Inc.
STREET: 26 Landsdowne Street
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: F199, E. Anthony
REGISTRATION UNDRER: 27,195
REFERENCE/DOCKET NUMBER: 2054-108A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEPHONE: (202) 783-6041
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TENGTH: 41 base pairs
TOPOLOGY: 11 noar
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CHER INFORMATION: /note= "A to G."
US-08-292-597-8
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% Sequence 8, Application US/08388653
% Patent No. 5869337
% GENERAL INFORMATION:
% APPLICANT: Crabtree, Gerald R.
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82.4%;
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Best Local Similarity
Matches 14; Conserv
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       APPLICANT: Crabtree, Gerald R.
APPLICANT: Schreiber, Stuart L.
APPLICANT: Spencer, David M.
APPLICANT: Spencer, David M.
APPLICANT: Wandless, Thomas J.
APPLICANT: Wandless, Thomas J.
APPLICANT: Belshaw, Peter
TITLE OF INVENTION: REGILATED TRANSCRIPTION OF TARGETED
TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS
INVERS OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARIAD Pharmaceuticals, Inc.
STRREET: 26 Landsdowne Street
CITY: Cambridge
STRTE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 61.0%; Score 12.2; DB 2; Length 41; Best Local Similarity 82.4%; Pred. No. 5.5e+02; Matches 14; Conservative 0; Mismatches 3; Indels
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OTHER INFORMATION: /note= "Region of homology with OTHER INFORMATION: target sequence."
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LOCATION: 6.11
OTHER INFORMATION: /note= "Xho I restriction site."
                                                                                                                                                                                                                                                                                                                                          COMPRY: USA

ZIP: USA3

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC/DOS/MS/DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATE: 0//JUN/195

FILING DATE: 0//JUN/195

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Figg, E. Anthony

REGISTRATION NUMBER: 2054-114A

TELEPHONE: (202) 783-6040

TELEPHONE: (202) 783-6041

INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:

LENGTH: 41 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPPOLUCE TYPE: CDNA
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CHER INFORMATION: /note= "A to G."
US-08-478-386A-8
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Sequence 8, Application US/08292597

Patent No. S834266

BENERAL INFORMATION:

APPLICANT: Gerald R. Crabtree
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LOCATION: 12..41
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GENERAL INFORMATION:
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APPLICANT: Schreiber, Stuart L.
APPLICANT: Schreiber, Stuart L.
APPLICANT: Schreiber, Stuart L.
APPLICANT: Spencer, David M.
APPLICANT: Spencer, David M.
APPLICANT: David M.
APPLICANT: Westalm M. Peter Trans J.
APPLICANT: Westalm M. Peter Trans J.
APPLICANT: Cambridge C.
APPLICANT: Cambridge C
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Nucleotide sequenc Mutagenic PCR prim Mutagenic PCR prim Reverse primer amp Petunia flower bud CPV VP2 gene PCR p CPV VP2 gene PCR CPV VP1/2 gene PCR CPV VP1/2 gene PCR CPV VP1/2 gene PCR CPV VP1/2 gene PCR CD3 transmembrane Murine signalling Murine signalling Murine signalling Murine signalling Murine signalling Murine signalling PCB primer #3. Uniden PCR primer #3. Uniden PCR primer for amp HPV16 E6-coding re 3/ junction sequen Nucleotide fragmen PCR primer for amp HPV16 E6-coding re 3/ junction sequen Nucleotide fragmen PCR primer for amp HUM IIIB gp160 PCR HIV IIIB gp160 gene amp PKPINV expression Primer C to isolat

12.6 63.0 36 21 AAZ99289 . 12.4 62.0 27 20 AAV99615 12.4 62.0 27 21 AAA48985 12.2 61.0 29 18 AAT5949	12.2 61.0 29 19 AAV44905 12.2 61.0 35 19 AAV26145 12.2 61.0 35 19 AAV26147	12.2 61.0 35 19 AAV26149 12.2 61.0 35 19 AAV26151 12.2 61.0 38 14 AAQ38730 12.2 61.0 38 14 AAQ38730	12.2 61.0 41 19 AAV62947 12.2 61.0 41 20 AAX02031 12.2 61.0 41 21 AAA60480	12.2 61.0 41 21 AAA14290 12.2 61.0 41 21 AA286759 12.2 61.0 41 22 AAF27538	29 12.2 bl.0 41 22 AAC83458 30 12 60.0 26 19 AAC85088 31 12 60.0 27 20 AAC85088	12 00:0 2/ 20 APAZ23623 12 00:0 2/ 20 APAZ05156 . 12 60 2/ 21 10 APAZ67514	34 12 60.0 33 20 AAN05594 35 12 60.0 35 19 AAN34760 35 12 60.0 35 19 AAN34760	30 12 60.0 42 16 38 15 60.0 43 16 39 12 60.0 43 16 39 12 60.0 43 16 39 12 60.0 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16 43 16	c 40 12 00.0 43 18 AAT8525 HIV IIIB 9P160 PCI c 42 12 60.0 43 19 AAV21751 HIV IIIB 9P160 PCI c 43 12 60.0 43 19 AAV21752 HIV IIIB 9P160 9PCI c 43 12 60.0 43 19 AAV21752 HIV 9P160 9PCI c 44 11.8 59.0 20 14 AAQ41648 PRIAV expression d 11 8 69.0 20 14 AAQ41648 PRIAV PCI	ALIGNMENTS	SULT 1 265541	ID AACOSO41 Scandard; DNA; 20 BF. XX XA AC AAC65541;	XX DT 12-FEB-2001 (first entry) xx	DE Human focal adhesion kinase antisense sequence #7.	KW Human; focal adhesion kinase; FAK; signal transduction; cancer; KW embryonic development disorder; angiogenic disorder; wound healing; KW antisense; phosphorothioate; ss. xx	OS Homo sapiens. XX	XX PD 17-OCT-2000.	19-AUG-1999;	FR 19 RUG-1999; 990S-03/73LU. XX PA (ISIS-) ISIS PHARM INC.	XX PI Monia BP, Gaarde WA;	DR WPI; 2001-006141/01.	New antisense compounds for inhibiting focal adhesing expression, especially useful for inhibiting retine expression or for diamonal and treating retines.	neovascutatization, of tot diagnosting and treating e.g. coton
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	nucleic - nucleic search, using sw model	<pre>Run on: October 2, 2001, 16:18:38 ; Search time 876.95 Seconds (without alignments) 14.320 Million cell updates/sec</pre>	Title: US-09-757-1008-9 Perfect score: 20 Sequence: 1 ttttgctaggtat 20	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 730101 seqs, 313950809 residues	Total number of hits satisfying chosen parameters: 854978	Minimum DB seq length: 0 Maximum DB seq length: 50	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries		5: /SIDSB/gcgdata/genesed/geneseqn/MA1984.DAT:* 6: /SIDSB/gcgdata/geneseq/geneseqn/NA1985.DAT:* 7: /SIDSB/gcgdata/geneseq/geneseqn/NA1986.DAT:* 8: /SIDSB/gcgdata/geneseq/geneseqn/NA1986.DAT:*	9: /SIDS8/gcgdata/geneseq/geneseqn/Na1988.DAT:* 10: /SIDS8/gcgdata/geneseq/geneseqn/Na1989.DAT:* 11: /SIDS8/gcgdata/geneseq/geneseqn/Na1999.DAT:* 13: /SIDS8/gcgdata/geneseq/geneseqn/Na1990.DAT:*	12: />Libosygydata/yeneseq/geneseqi.NA1992.bAT:* 13: /SIDS8/gcgdata/geneseq/geneseqn/NA1992.bAT:* 14: /SIDS8/gcgdata/geneseq/geneseqn/NA1993.bAT:*	15: /SIDSB/gcgdatd/yeneseq/geneseqn/NA1994.DAT:* 16: /SIDSB/gcgdatd/yeneseq/geneseqn/NA1995.DAT:* 17: /SIDSB/gcgdata/geneseqn/RA1995.DAT:*		20: /SIDS8/gcgdata/geneseq/geneseqn/NA1999.DAT:* 21: /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:* 22: /SIDS8/gcgdata/geneseq/geneseqn/NA2001.DAT:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	ery tch Length DB ID Descript	20 100.0 20 22 AAC65541 15 75.0 15 22 AAC65561	13.6 69.0 20 AAKG5540 13.8 69.0 20 AAK33269 13.8 60.0 37 37 878 878 878	6 13.6 68.0 31 16 AAT100213 7 13.6 68.0 31 22 AAF70755	2 66.0 27 21 2 66.0 31 21 3 65.0 15 22	12.6 63.0 36 21 AA299288

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Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; anglogenic disorder; wound healing;
                                                                                                                                                                                                                                      Human focal adhesion kinase antisense sequence #6.
                                                                                                                                                                                                                                                                                                            antisense; phosphorothioate; ss.
                    AAC65540 standard; DNA;
     ttgctagatgctagg 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-006141/01.
                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-AUG-1999;
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                                                                                                                                                                                                  12-FEB-2001
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                                                                                                                                                                 AAC65540;
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                                 The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, anglogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; focal adhesion kinase; FAK; signal transduction; cancer;
embryonic development disorder; angiogenic disorder; wound healing;
antisense; phosphorothloate; ss.
                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                    Length 20;
                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human focal adhesion kinase antisense sequence #27.
                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                    DB 22
0.16;
                                                                                                                                                                              Sequence 20 BP; 4 A; 2 C; 5 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 BP; 3 A; 2 C; 5 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                  Score 20;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Column 25; 30pp; English
Claim 3; Column 23; 30pp; English
                                                                                                                                                                                                                                Query Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                       1 ttttgctagatgctaggtat 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaarde WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-006141/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6133031-A.
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99US-0377310.

99US-0377310

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The present invention describes a number of phosphorothicate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated
New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEBP2 alpha A gene expression regulating DNA PCR primer SEQ ID NO:26.
                                                                                                                                                                                             in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in treatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                        22; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEBP2 alpha A gene; expression; regulation; bone disease; osteoporosis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 4 A; 4 C; 5 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                      DB
63;
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                        Score 15;
Pred. No.
                                                                                          Claim 3; Column 23; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                           75.00.
100.08; Pie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
                                                                                                                                                                                                                                                                                                                                                                        75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX33269 standard; DNA; 20
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                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 ctagatgctaggtat
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Gaps

ö

0; Indels

Length 15;

22;

DB 1

75.0%; Score 15; DB 100.0%; Pred. No. 61;

Conservative

Best Local Similarity Matches 15; Conserv

Query Match

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A new method for developing vaccines has been identified, in which a non-naturally occurring molecular scaffold, having a core particle and a covalently attached organiser, is attached to an antigen or antigenic determinant. The scaffold and antigen or antigenic determinant interact to form an ordered and repetitive antigen array. The composition is useful as a vaccine against infectious diseases, to induce immune responses in farm animals and also in the treatment of cancer and allergies. The present sequence is the PCR primer, 9p140CysEcoRI. This primer was used to amplify the coding sequence for the gp140 gene of human immunodeficiency virus (HIV). The PCR product was then used as an antigen in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                     Composition for use as vaccine against infectious diseases and in treatment of cancer and allergies comprises non-naturally occurring molecular scaffold and antigen or antigenic determinant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Family 1; family 2; ligand; thrombin; systematic evolution of ligands by exponential enrichment; SELEX; heparin; selection; region of homology; inhibitor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identification of ligands to basic fibroblast growth factor and thrombin - which can be modified for increased in vivo stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.0%; Score 13.8; DB 21;
88.2%; Pred. No. 2.8e+02;
ive 0; Mismatches 2;
 Ξ
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 36 BP; 11 A; 10 C; 6 G; 9 T; 0 other;
Bachmann
                                                                                                                                                Example 26; Page 77; 102pp; English.
Nieba L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 39; Page 95; 236pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thrombin DNA ligand, clone #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
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94US-0195005.
90US-0536428.
91US-0714131.
93US-0061691.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gold L, Janjic N, Tasset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NEXS-) NEXSTAR PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 tgctagatgctaggtat 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 TGCTAGCTGCTAGGAAT 6
 Hennecke F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-293073/38.
                                    WPI; 2000-412159/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-FEB-1994;
11-JUN-1990;
10-JUN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-AUG-1995.
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Renner WA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT00213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen presentation; vaccine; infectious disease; allergy; cancer; molecular scaffold; immune response; farm animal; organiser; gpl40; immunostimulatory; cytostatic; antiallergy; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes DNA which participates in the regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of expression of PEBP2 alpha A gene. The DNA produces a regulator protein with the activity of promoting bone formation and can serve as promoter for prevention and treatment of bone diseases including osteoporosis. The present sequence represents a PCR primer used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                     DNA regulating expression of PEBP2 alphaA gene to produce regulator protein, useful as promoter for prevention or/and treatment of bone diseases e.g. osteoporosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.0%; Score 13.8; DB 20; Length 20; 88.2%; Pred. No. 2.6e+02; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                              Katsumata T, Nakatsuka M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 6 A; 1 C; 6 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV gp140 gene PCR primer, gp140CysEcoRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Page 39; 118pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CYTO-) CYTOS BIOTECHNOLOGY AG.
                                                                                                                                                                                                                                         (SUMU ) SUMITOMO PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA48327 standard; DNA; 36 BP
                                                                                                                                                              98JP-0114135.
97JP-0254250.
97JP-0299407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus.
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99US-0142788.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 tttgctagatgctaggt 18
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                                                                                                                                                                                                                                                                            4, Harada H,
Tagashira S;
                                                                                                                                                                                                                                                                                                                                  WPI; 1999-243621/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200032227-A2
                                                  W09911787-A1
                                                                                                                           02-SEP-1998;
                                                                                                                                                              08-APR-1998;
02-SEP-1997;
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                                                                                                                                                                                                     15-OCT-1997;
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                                                                                        11-MAR-1999
                                                                                                                                                                                                                                                                              Fujiwara M,
                 Synthetic.
                                                                                                                                                                                                                                                                                                 Ogawa S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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g g

Sequence 31 BP; 5 A; 3 C; 11 G; 12 T; 0 other;

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of ligands to thrombin. These sequences were isolated using the single stranded DNA molecules given in AATO0201 and AATO0226 which comprise a 30N and a 60N variable region, respectively. These ligands were isolated using systematic evolution of ligands by exponential enrichment (SELEX). The selection was conducted in a buffer solution at 37 deg. C. After 12 rounds of selection, no additional improvement in binding was seen. By studying regions of homology between the isolated ligands, a truncated ligand of 38 nucleotides (see AAQ98403-04) was identified which inhibitors of thrombin and are therefore useful in treating thrombin mediated conditions and in studying the structure and binding of
                                                                                                                                                                                                                                                                             ;
0
sequences given in AAT00202-25 and AAT00227-57 represent two groups
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acid ligands to basic fibroblast growth factor that are useful as inhibitors of basic fibroblast growth factors and 2'-amino modified RNA ligands, exhibit increased in vivo stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ligand; basic fibroblast growth factor; bFGF; gene therapy; vascular; atherosclerosis; angioplasty; stability; ss.
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                             68.0%; Score 13.6; DB 16; Length 31; 80.0%; Pred. No. 3.5e+02; 1ve 0; Mismatches 4; Indels (
                                                                                                                                                                                                    Sequence 31 BP; 5 A; 3 C; 11 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 19; Column 57-58; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thrombin high affinity ligand #12.
                                                                                                                                                                                                                                                                                                                                                                                                          AAF70765 standard; DNA; 31 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90US-0536428.
91US-0714131.
92US-0973333.
94US-0195005.
94US-0219012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gold L, Tasset D;
                                                                                                                                                                                                                                                                                                        1 ttttgctagatgctaggtat 20
                                                                                                                                                                                                                                                                                                                         96US-0687421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NEXS-) NEXSTAR PHARM INC.
                                                                                                                                                                                                                                                                           16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-158583/16.
                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF70765;
                                                                                                                                                                         thrombin.
                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                             Matches
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AAF70765
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The present invention relates to a purified and isolated non-naturally occurring DNA ligands to basic flibroblast growth factor (bFGF). The ligands are useful as part of gene therapy treatments and for diagnosing pathogenesis of vascular diseases including intitation and progression of atherosclerosis, acute coronary syndromes, vein graft disease and restenosis following coronary angloplasty. The ligands have improved stability in vivo.

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sample which uses a calibrator, suitable primers and probes, and sample which uses a calibrator, suitable primers and probes, and a nucleic acid polymerase with 5'-3' nuclease activity is described. The method comprises adding a calibrator nucleotide to the sample, the calibrator nucleotide having the same sequence as the target with the exception of one or more regions which in the target hybridize with the probe labeled with a reporter and quencher, or which hybridize with the probe and with 2 or more primers. These regions have a different, randomized nucleotide sequence and a similar Im. Then extracting the calibrator and target nucleotides from the sample. Probes and primers are then added to the extracted sample/calibrator mixture and PCR is performed. Reaction in the presence of the target nucleic acid specific probe permits quantitation of the copy number of the calibrator nucleotide permits quantitation of the calibrator copy the total number of target templates and calibrator copy the total number of target templates and calibrator and submits and primers are the parallely may be mathed may the post of the calibrator of the calibrator copy and the coll number. The reaction in the presence of the calibrator copy and the coll number of target templates and calibrator, allowing may make mathed may and the coll number of target templates and calibrator, allowing may be accepted the calibrator who may make mathed may and the calibrator who may make mathed may and the calibrator properties and calibrator who may make may be accepted the calibrator who may make may and the calibrator who may make may be accepted the calibrator who may be accepted the calibrator who are the call the calibrator who are the call t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quantitative detection of nucleic acids, based on the use of a calibrator, suitable primers and probes, and a nucleic acid polymerase with 5' \cdot 3' nuclease activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   calculation of the percentage of calibrator recovery. The method may be used for the diagnosis of viral and any other pathogenic agents in body fluids, and to monitor safety and/or genetic composition of waters, foods, and plant species used in the alimentary field. The method is used to quantitatively detect the genomic nucleic acid of human herpes virus (HHV)-6, HHV-7, HHV-8 and human immunodeficiency
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection; identification; PCR; polymerase chain reaction; probe; primer; calibrator; diagnosis; pathogen; virus; bacteria; HHV-6; HHV-7; HHV-8; human herpes virus; human immunodeficiency virus; HIV; AIDS; acquired immune deficiency syndrome;
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  Length 31;
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CaMV Calibrator probe sequence used in detection method.
  DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Locatelli G, Lusso P, Malnati M, Salvatori F,
Score 13.6; DB 22
Pred. No. 3.5e+02;
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                                                    Mismatches
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68.0%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                29-AUG-2000 (first entry)
                                                                                                                                      16; Conservative
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  Query Match
Best Local Similarity
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Length 31;

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Sequence 31 BP; 9 A; 8 C; 8 G; 5 T; 1 other;
                                                          Query Match
Best Local Similarity
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                                                                                          Matches
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ID AAZ9
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Contiguous bases chosen from one of 632 fragments (AAA78631 to
AAA7952), where the segment comprises a polymorphic site or an
immediately adjacent base, or the complement of the segment. Also
described are: (1) an allele-specific oligonucleotide that hybridises to
a segment of the novelty; (2) an isolated nucleic acid comprising a
segment of the novelty where the polymorphic site within the sequence is
ccupied by a base other than the reference base indicated in the
specification; and (3) analysing a nucleic acid, comprising obtaining a
nucleic acid from an individual, and determining a base occupying any one
of the polymorphic sites of the novelty. The nucleic acid segments and
method can be used to analyse an individuals nucleic acid segments and
the presence of polymorphisms. The method can also be used to test for a
artian and an and correlate the presence of the phenotype with a
artians and an articulate the presence of the phenotype with a
                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genomic polymorphic nucleic acid segments, allele specific primers and probes, and methods of analysis, useful for e.g. forensics, paternity testing, genetic mapping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        particular polymorphism. The presence of polymorphic sites are useful
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for, e.g. forensics, paternity testing, correlation of polymorphisms with phenotypic traits and for genetic mapping of phenotypic traits.

AAA78631 to AAA79262 represent sequence tags of human genomic DNA fragments containing polymorphic sites. The base occupying the polymorphic sites. The base occupying the
                                                                                                                                                                                                                                                                                                                                                                                                   Human; genomic DNA; polymorphism; genome; allele-specific; primer;
probe; hybridisation; polymorphic site; forensic; paternity testing;
medicine; phenotypic trait; genetic analysis; genetic mapping; ds.
virus (HIV). The method provides an enhanced sensitivity, accuracy, and precision and a reduced measure viability. For specific probe, primer and calibrator sequences used in the method, see GENESEQ records AA293935-293965.
                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                         Human genomic DNA polymorphic site sequence tag SEQ ID NO:384.
                                                                                                                    Score 13.2; DB 21; Length 27;
Pred. No. 5.6e+02;
0; Mismatches 3; Indels (
                                                                       Sequence 27 BP; 5 A; 7 C; 7 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 15; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Warrigton JA;
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                                                                                                                                                                                                                                                                   AAA79014/c
ID AAA79014 standard; DNA; 31 BP.
                                                                                                                  66.0%;
ilarity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0238402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JAN-2000; 2000EP-0250023
                                                                                                                                                                             3 ttgctagatgctaggtat 20
                                                                                                                                                                                              2 tcgctacatgctaggcat 19
                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-500198/45.
                                                                                                                    Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1024200-A2
                                                                                                                                                                                                                                                                                                                                            20-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-2000
                                                                                                                                                                                                                                                                                                              AAA79014;
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                                                                                                                                                                                                                                                   RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a number of phosphorothicate antisense
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothioate; ss.
                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense compounds for inhibiting focal adhesion kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.0%; Score 13; DB 22; Length 15
100.0%; Pred. No. 6.7e+02;
ive 0; Mismatches 0; Indels
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human focal adhesion kinase antisense sequence #26.
66.0%; Score 13.2; DB 21;
75.0%; Pred. No. 5.7e+02;
iive 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15 BP; 4 A; 2 C; 4 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Column 25; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ99288 standard; DNA; 36 BP.
                                                                                                                                                                                                                                                                                                                 BP
                                                                                                               1 ttttgctagatgctaggtat 20
                                                                                                                                               24 TTCTGCTCRATGCTAGAGAT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0377310.
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                                                                                                                                                                                                                                                                                                              AAC65560 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Best Local Similarity 100.
Matches 13; Conservative
                                                          15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
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AAZ99288;

Synthetic.

Key

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The present sequence represents a fragment from a clone of a method for including the 3'-untranslated region of a DNA molecule comprising an open reading frame (ORF). The method comprises providing a DNA molecule having an ORF and a 3'-untranslated region, the DNA having a 5' overhang and a blunt end at the 3' end, and treating the DNA molecule with a 3'-5' exonuclease followed by a single-stranded nuclease to remove the 3'-untranslated region. The products can be used to produce RNA-protein fusion libraries. The fusion libraries can be used for the identification of protein-protein interactions, identification of drug targets, and hybridisation to solid supports to erreate protein of protein molecules may be arranged in spatially defined arrays on the protein chips to carry out large scale screening for protein or compound identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing nucleic acids lacking 3'-untranslated regions to optimise production of fusion proteins, used to produce fusion libraries for identification of protein:protein interactions and drug targets for the production of protein chips:
                                                                                                                                                                                                                                                                                    a
"an unspecified number of bases are present
between these nucleotides"
Nucleotide sequence of a clone from a RNA-protein fusion library.
                                                              RNA-protein fusion; protein-protein interaction; drug target;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Promoter; nuclear encoded plastid RNA polymerase; NEP; rpoB; chloroplast; transgenic plant; maize; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 12.6; DB 21;
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36 BP; 6 A; 9 C; 10 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 14; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV99615 standard; DNA; 27 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.0%;
78.9%;
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PHYL-) PHYLOS INC.
                                                                                               protein chip; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                 WO200009737-A1
                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-FEB-2000
                                                                                                                                                          Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    οy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a fragment from a clone of a mak-protein fusion library comprising KIAA0111. specification describes a method for removing the 3'-untranslated region of a DNA molecule comprising an open reading frame (ORF). The method comprises providing a DNA molecule having an ORF and a 3'-untranslated region, the DNA having a 5' overhang and a blunt end at the 3' end, and treating the DNA molecule with a 3'-5' exonuclease followed by a single-stranded nuclease to remove the 3'-untranslated region. The products can be used for the identification of protein protein interactions, identification of drug targets, and hybridisation to solid supports to create protein chips (or beads). The RNA-protein molecules may be arranged in spatially defined arrays on the protein chips to carry out
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing nucleic acids lacking 3'-untranslated regions to optimise production of fusion proteins, used to produce fusion libraries for identification of protein:protein interactions and drug targets for the production of protein chips
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 a "an unspecified number of bases are present between these nucleotides"
                                                                                                                         Nucleotide sequence of a clone from a RNA-protein fusion library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                    fusion; protein-protein interaction; drug target;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          large scale screening for protein or compound identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.0%; Score 12.6; DB 21; Length 36; 78.9%; Pred. No. 1.2e+03; ive 0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36 BP; 6 A; 9 C; 10 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
18..19
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 14; 52pp; English.
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                                                           (first entry)
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                                                                                                                                                                                        RNA-protein fusio
protein chip; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200009737-A1
                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
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                                                           03-JUL-2000
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Gaps

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Indels

AAZ99289;

AAZ99289 ID AAZ9: XX AC AAZ9: XX DT 03-JI

Query Match

Best Loc Matches

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Length 36;

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The present invention relates to the use of apoptotic genes in the the production of transgenic plants with improved resistance characteristics. The present sequence is the mutagenic PCR primer Bcl2-3. This primer was used with primer Bcl2-5 (AAA48984) to introduce a 5' Ncol site and a 3' Xbal site in the human apoptotic gene bcl-2. Specifically the primer introduced an Ala residue between the Met (position 1) and His (position 2) residues of the native protein. The altered bcl-2 sequence was used in the creation of the final vector used to transform plants. The improved resistance characteristics of the plants helps protect against bacterial, viral and other pathogens. Resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-terminal transport polypeptide; insect pest control; cell cycle; Autographa californica multinucleocapsid nuclear polyhedrosis virus; ACMNPV; occlusion derived virus; ODV; 66 kD envelope protein; ODV-866; membrane protein; intranuclear viral-induced microvesicle; GFP; URF-13; beta-galactosidase; b-gal; green fluorescent protein; marker; primer; polymerase chain reaction; PCR; amplify; ss.
                                                                                                  Transgenic plants with improved resistance characteristics comprising nucleic acids encoding apoptotic proteins \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reverse primer amplifies fragment encoding ODV-E66 residues 1-23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.0%; Score 12.4; DB 21; Length 27; 92.9%; Pred. No. 1.5e+03; ive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated transport polypeptide from AcMNPV - can direct localisation of desired proteins to occlusion derived virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27 BP; 2 A; 5 C; 8 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                             abiotic challenges may also be conferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Summers MD;
                                                                                                                                                              Example 3; Page 58; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 39; 104pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT59549 standard; DNA; 29 BP.
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95US-0000955
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                                                         WPI; 2000-365634/31.
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                   Dickman MB;
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                                                                                                                                                                                                                                                                                                                                                                                    Isolated nuclear-encoded plastid RNA polymerase promoter sequences useful for expressing exogenous protein in plant plastids such as chloroplasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutagenic PCR primer Bcl2-3 targeted to anti-apoptotic gene bcl-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the nucleotide sequence of maize rpoB gene primer rpoB#3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 27 BP; 9 A; 5 C; 6 G; 7 T; 0 other;
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09-JUN-1999;
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AAA48985 RESULT

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The sequences given in AAT59548-49 are primers which were used to amplify the sequence encoding residues 1-23 of Autographa californica multi- nucleacopsis on unclear polyhedrosis virus (AcMNPV) occlusion derived virus (ODV) 66 kD envelope protein (ODV-E66). ODV-E66 is an integral membrane protein of the ODV envelope. In an infected cell outlets, ODV-E66 is present in the intranuclear viral-induced microvesicles and ODV envelope, providing evidence that the microvesicles microvesicles on immediate precursor in the assembly of the ODV envelope. In infected cells, ODV-E66 localises to the ODV envelope. The ampranes of function as an immediate precursor in the assembly of the ODV envelope. CC in infected cells, ODV-E66 localises to the ODV envelope. The amplified microvesicles, membranes of the nuclear envelope. The amplified sequence encodes the N-terminal, target sequence domain of ODV-E66. The target sequence may be used to target beta-galactosidase (b-gal), green carget sequence may be used to target beta-galactosidase (b-gal), green cluorescent protein (GFP) and URF-13 to the membranes of the nuclear correlan proteins to the ODV envelope and intranuclear microvesicles. It can be used for insect pest control, for therapeutic applications, e.g. correlan proteins to the ODV envelope and intranuclear microvesicles. CC foreign proteins to the ODV envelope and intranuclear microvesicles. CC for location of a protein, peptide or derivative into the nuclear correlan marker specific for a disease or abnormality into a cell tissue correct control correct manifesting such abnormalities.
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Sequence 29 BP; 5 A; 3 C; 6 G; 15 T; 0 other;

Gaps ó Score 12.2; DB 18; Length 29; Pred. No. 1.9e+03; 0; Mismatches 3; Indels ( Query Match 61.0%; Best Local Similarity 82.4%; Matches 14; Conservative

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12 12.6 63.0 21 18 AAT72309 13 12.6 63.0 21 19 AAV53849 14 12.6 63.0 21 19 AAV11268 15 12.6 63.0 21 20 AAV70613 16 12.6 63.0 21 21 AAV35647 17 12.6 63.0 21 21 AAV31178	18 12.6 63.0 21 21 20 20 12.6 63.0 21 21 21 20 12.6 63.0 21 21 21 21 22 21 22 22 22 22 22 22 22	22 12.0 63.0 21 22 22 24 12.6 63.0 22 22 22 25 12.6 63.0 37 14 25 12.6 63.0 37 14	12.6 63.0 39 16 12.6 63.0 39 16 12.6 63.0 39 16	29 12.6 63.0 39 20 30 12.6 63.0 39 20 31 12.4 62.0 33 21	32 12.4 62.0 33 21 33 12.4 62.0 33 21	34 12.4 62.0 35 19 35 12.2 61.0 18 13	30 12.2 61.0 36 21 37 12.2 61.0 36 21 38 12.2 61.0 36 21 39 12.2 61.0 42 18	41 12 60.0 17 42 12 60.0 17 43 12 60.0 17 44 12 60.0 24 45 12 60.0 24	ALIGNMENTS	SULT 1 265540	AAC65540 standard; DNA; 20 BP. AAC65540;	12-FEB-2001 (first entry)	Human focal adhesion kinase antisense sequence	Human; focal adhesion kinase; FAK; signal tembryonic development disorder; angiogenic antisense; phosphorothioate; ss.		US0133031-A	19	19-AUG-1999; 99US-0377310.	(ISIS-) ISIS PHARM INC.	Monia BP, Gaarde WA;	WPI; 2001-00	New antisense compounds for inhibiting focal expression, especially useful for inhibiting	neovascularization, or for diagnosing and tre
							···········	v		RES	XX	X	XX DE	K K K K K	X OS	X X	XX PF	XX PR	PA XX	Id	DR XX	PT P	T A XX
4.5 Compugen Ltd.	Search time 876.95 Seconds (without alignments) 14.320 Million cell updates/sec				s: 854978			eqn/Na1980.DaT:* eqn/Na1981.DaT:* eqn/Na1983.DaT:* eqn/Na1983.DaT:*	eqn/NA1984.DAT:* eqn/NA1985.DAT:* eqn/NA1986.DAT:*	eqn/NA1988.DAT:* seqn/NA1989.DAT:* seqn/NA1990.DAT:*	seqn/Na1991.DAT:* seqn/Na1992.DAT:* seqn/Na1993.DAT:*	seqn/NA1994.DAT:* seqn/NA1995.DAT:*	Seqn/NA1997.DAT:* Seqn/NA1997.DAT:*	seqn/NA1999.DAT:* seqn/NA2000.DAT:* seqn/NA2001.DAT:*	ceted by chance to have a of the result being printed,	ore distribution.	:	Description	numen local admest CaMV Calibrator pr Human focal adhesi		rimer Fase	timer for 1- tumour supp	
GenCore version 4.5 Copyright (c) 1993 - 2000 Com nucleic search, using sw model	1, 16:18:37 ;	US-09-757-100B-8 20 1 ctagatgctaggtatctgtc 20	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	730101 seqs, 313950809 residues	hits satisfying chosen parameters	length: 0 length: 50	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	N_Geneseq_0601:*  1: /SIDSB/gcgdata/geneseq/geneseqn/NA1980.DAT 2: /SIDSB/gcgdata/geneseq/geneseqn/NA1981.DAT 3: /SIDSB/gcgdata/geneseq/geneseqn/NA1982.DAT 4: /SIDSB/gcgdata/geneseq/geneseqn/NA1983.DAT	<pre>: /SIDS8/gcgdata/geneseq/geneseqn/NA1984.DAT:* :: /SIDS8/gcgdata/geneseq/geneseqn/NA1985.DAT:*     /SIDS8/gcgdata/geneseq/geneseqn/NA1986.DAT:* : /SIDS8/dcgdata/geneseq/deneseqn/NA1987.DAT:* </pre>	: /SIDS8/gcgdata/geneseg/genese 0: /SIDS8/gcgdata/geneseg/genee 1: /SIDS8/gcgdata/geneseg/genee	<ol> <li>/SIDS8/gcgdata/geneseq/genes</li> <li>/SIDS8/gcgdata/geneseq/genes</li> <li>/SIDS8/gcgdata/geneseq/genes</li> </ol>	5: /SIDS8/gcgdata/geneseq/genes	8: /SIDS8/gcgdata/geneseq/genes 8: /SIDS8/gcgdata/geneseq/genes	0: /SIDS8/gcgdata/geneseq/geneseqn/NA1999.DAT 1: /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT 2: /SIDS8/gcgdata/geneseq/geneseqn/NA2001.DAT 2: /SIDS8/gcgdata/geneseq/geneseqn/NA2001.DAT	No. is the number of results predicted by greater than or equal to the score of the	ved by analysis of the total sc. SUMMARIES	;	Length DB	27 21	20 22	38 13	64.0 27 21 AAA37684 64.0 39 21 AAZ87799	21 16 21 16
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                                      The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      calibrator, suitable primers and probes, and a nucleic acid polymerase with 5'-3' nuclease activity
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                                                                                              in cancer, particularly colon, breast and oral tumours, embryonic development disorders, anglogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection; identification; PCR; polymerase chain reaction; probe; primer; calibrator; diagnosis; pathogen; virus; bacteria; HHV-6; HHV-7; HHV-8; human herpes virus; human immunodeficiency virus; HIV; AIDS; acquired immune deficiency syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mixture and PCR is performed. Reaction in the presence of the target nucleic acid specific probe permits quantitation of the copy number
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                                                                                                                                                                                              Sequence 20 BP; 4 A; 4 C; 5 G; 7 T; 0 other;
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Claim 3; Column 23; 30pp; English.
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Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                  calculation of the percentage of calibrator recovery. The method may be used for the diagnosis of viral and any other pathogenic agents in body fluids, and to monitor safety and/or genetic composition of waters, foods, and plant species used in the alimentary field. The method is used to quantitatively detect the genomic nucleic acid of human herpes virus (HHV)-6, HHV-7, HHV-8 and human immunodeficiency virus (HIV). The method provides an enhanced sensitivity, accuracy, and precision and a reduced measure viability. For specific probe, primer and calibrator sequences used in the method, see GENESEQ records AAL393935-293965.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
of the extracted target nucleic acid. The reaction in the presence of the calibrator nucleotide permits quantitation of the calibrator columber. The reaction in the presence of both permits calculation of the total number of target templates and calibrator, allowing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 27;
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Pred. No. 28;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27 BP; 5 A; 7 C; 7 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 BP; 4 A; 2 C; 4 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Column 25; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antisense; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.0%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0377310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0377310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ctagatgctaggtatctgt 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 ctacatgctaggcatctgt 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC65560 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 79.0
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monia BP, Gaarde WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-006141/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6133031-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC65560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC65560
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The sequences given in AAQ50202-70 are oligonucleotides which were used to illustrate the method of the invention for the mutagenesis of inhibitory/instability signals (INS). Mutation in an INS produced using oligonucelotides such as these, increases the stability and/or utilisation of mRNA without changing its protech coding capacity, or if the sequence is changed, its function is maintained. Other genes encoding such mRNA molecules include growth factor, interferon,
                                              HIV-1; p17gag; inhibition; gag; M1; M2; M3; M4; silent mutation; mRNA vector; p17; point mutation; p17M1234; HLtat cells; gene replacement; inhibitory/instability signal; INS; stability; utilisation; vaccine; interferon; interleukin; fos proto-oncogene protein; growth factor; env; attenuated; AIDS; AIDS-related disease; latent infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interleukin, fos proto-oncogene protein and HIV env and gag gene proteins. Nucleic acid constructs in which INS function has been impeded, can be used as vaccines, esp. against AIDS and AIDS-related diseases by preventing HIV from establishing a latent infection, as is possible using the INS, and thus escaping immune system surveillance. The constructs may also be used in gene therapy for each explacement by homologous recombination with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor tyrosine kinase; vascular endothelial cell growth factors;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eliminating inhibitory-instability regions in mRNA to improve stability and expression - by making multiple point mutations within A-T rich regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR primer 2 for a novel type III RTK gene - the KDR gene.
                 c-fos position 3392-3434 INS mutagenic oligonucleotide.
                                                                                                                                                Human immunodeficiency virus type 1; p24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 13.4; DB 14;
Pred. No. 5.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 43 BP; 9 A; 11 C; 5 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer; tumour; diagnosing; monitoring; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 69; 117pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ28274 standard; cDNA; 38 BP.
                                                                                                                                                                   ong terminal repeat; LTR; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.0%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                           92US-0858747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      See also AAQ50200-02
                                                                                                                                                                                                                                                                                                                                                                                                (USSH ) US SEC DEPT HEALTH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pavlakis GN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 gatgctaggtatctg 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-336919/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                therapy;
                                                                                                                                                                                                                                                                                                                                                           27-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-FEB-1993
                                                                                                                                                                                                                                            WO9320212-A.
                                                                                                                                                                                                                                                                                 14-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                 Felber BK,
                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ28274;
                                                                                                                                                gene
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                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a number of phosphorothioate antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                   Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; anglogenic disorder; wound healing; antisense; phosphorothioate; ss.
                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
       DB 22; Length 15; 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22; Length 20;
                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                   Human focal adhesion kinase antisense sequence #7
                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Sequence 20 BP; 4 A; 2 C; 5 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 75.0%; Score 15; Local Similarity 100.0%; Pred. No. les 15; Conservative 0; Mismatri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Column 23; 30pp; English
                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0377310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0377310.
                                                                                                                                                                                                                      AAC65541 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ50213 standard; DNA; 43
                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antisense sequences, inclutreatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-1994 (first entry)
                                                  Conservative
                                                                                     3 agatgctaggtatct 17
                                                                                                                         1 agatgctaggtatct 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaarde WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-006141/01.
           Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6133031-A.
                                                                                                                                                                                                                                                                                                12-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monia BP,
                                                                                                                                                                                                                                                           AAC65541;
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Indels

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RESULT

Length 43;

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Example 1; Page 11; 26pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gressel J, Eyal Y, Fluhr R;
                                                                                                                                                                                                                                                                                                                                                              64.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               citrus fruit; PCR primer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JAN-2000; 2000WO-IL00038.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99IL-0128193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
AAA37664/c
ID AAA37684 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        18
                                                                                                                                                                                                                                                                                                                                                                                                                           agatgctggggatctg 23
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-289283/26
(SANO ) SANDOZ-ERF
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                    Buehler T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Citrus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA37684;
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                                                                                                                                                                                                                                                                                   This PCR primer is designed from a region of the kinase domain 5' to the kinase insert domain of a consensus sequence of known type III str gene catalytic domains. It is used with AAQ28273 to amplify human endothelial cDNA producting 251 and 420 bp products. Sequencing of the 251bp product revealed a novel sequence containing both primers but with little homology to known tyrosine kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human Fas ligand; hFasL; fusion protein; truncated; T lymphocyte; glycosyl-phosphatidylinositol; GPI; treatment; allograft; xenograft;
                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                 DNA encoding type III receptor tyrosine kinase - useful for
                                                                                                                                                                                                                                                                                                                                                                                            Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Fas signal sequence generating oligonucleotide Fasl.
                                                                                                                                                                                                                                                                                                                                                                                            65.0%; Score 13; DB 13; Length 38
68.4%; Pred. No. 8.1e+02;
ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                              Sequence 38 BP; 5 A; 10 C; 8 G; 10 T; 5 other;
                             Location/Qualifiers
                                                                                                                                                                                                                                                                Claim 16; Fig 2; 101pp; English.
                                                                                                                                                                                                                                            diagnosing the onset of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT97310 standard; DNA; 24 BP
                                                                                                                                                                   (AMCY ) AMERICAN CYANAMID CO.
                                                   /*tag= a
/mod_base= I
                                                                                                                          92WO-US01300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 ctrgcygccaggtctcygt 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fas signal sequence; ss.
                                                                                                                                                                                         Terman BI;
                                                                                                                                                                                                             WPI; 1992-316117/38.
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 13; Conserv
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(SANO ) SANDOZ
                                       modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
           Homo sapiens
                                                                                                                          20-FEB-1992;
                                                                                                                                               22-FEB-1991;
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                                                                                 W09214748-A.
                                                                                                                                                                                         Carrion ME,
                                                                                                      03-SEP-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT97310;
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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RESULT

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This oligonucleotide Fas1 is used for the generation of a Fas signal sequence for post translational modification of a novel human Fas ligand (hFasL) fusion protein. This novel protein comprises of hFasL or a truncated or functionally equivalent variant that retains the Fas truncated to Incorporate inducing properties of hFasL. This is liked to Glycoxyl-Phosphatidyl inositol (GFI) at its C-terminus. DNA encoding hFasL amino acids, a linker sequence and a human Fas signal sequence derived from human CDIG. The fusion protein can be produced by culturing COS cells transformed by the expression vector product. This novel fusion protein can incorporate its lipid tail can be produced. This novel fusion protein can incorporate its lipid tail can be produced. This novel fusion protein can incorporate its lipid tail can coll membranes, and thus present the FasL protein on the cell surface. This can bind to Fas receptor present on other cells, particularly T lymphocytes, and thereby induce their apoptosis. This is useful for preventing or treating tissue or organ allograft or xenograft rejection. This provides a specific treatment for activated T lymphocytes, i.e. only for T lymphocytes that expresses the Fas antigen, which attack the transplanted tissue or organ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-2-rhamnosyl-transferase; hesperidin conversion; orange peel; NHDC; flavone-7-0-glucosidase-2"-0-rhamnosyl-transferase; flavanoid glycoside; sweetener; neohesperidin dlhydrochalcone; grapefruit; pomelo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
Human Fas Ligand fused to carboxy-terminal glycophospholipid - useful for preventing or treating tissue or organ allograft or xenograft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR primer for 1-2-rhamnosyl-transferase cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 12.8; DB 18;
Pred. No. 9.9e+02;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24 BP; 3 A; 5 C; 9 G; 7 T; 0 other;
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Sequences AAZ87797-812
                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting polymorphism associated with cancer pre:disposition - also DNA, vectors and host cells e.g. for gene or protein replacement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An individual can be diagnosed as having a predisposition to cancer by detecting an alteration in the wild type multiple tumour suppressor (MTS) gene, using gene probes which hybridise to the MTSIElbeta gene ORF (amplified using the PCR primers AAT00719-21). The above assay can also be used in the diagnosis and prognosis of melanoma, lymphoma, leukaemia and pancreas, breast and thyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multiple tumour suppressor; MTS1Elbeta; cancer; diagnosis; assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multiple tumour suppressor 1 exon 1 beta gene PCR reverse primer.
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                                                                                                                     Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     predisposition; melanoma; leukaemia; lymphoma; prognosis; pancreas; breast; thyroid; PCR reverse primer; exon 1; ss
                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
may be used for gene therapy and protein therapy. Seq
represent PCR primers for sequencing the TMPRSS2 CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 12.6; DB 16;
Pred. No. 1.2e+03;
                                                                                                                   Score 12.8; DB 21;
Pred. No. 1e+03;
0; Mismatches 2;
                                                         Sequence 39 BP; 9 A; 11 C; 7 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21 BP; 5 A; 3 C; 7 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skolnick MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 10; Page 64; 148pp; English.
                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.0%;
78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-0251938.
94US-0214582.
94US-0215086.
94US-0215087.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kamb A,
                                                                                                                 64.0%;
87.5%;
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                                                                                                                                                                                                                                                                                                                                        AAT00720 standard; cDNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-0227369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctagatgctaggtatctgt 19
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                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                 Query Match 64.0
Best Local Similarity 87.5
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                 20
                                                                                                                                                                                                                                       30 ATGATAGGTATCCGTC 15
                                                                                                                                                                                                 5 atgctaggtatctgtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cannon-Albright LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-344626/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches .15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAR-1994;
18-MAR-1994;
18-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancers, etc
                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09525813-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-SEP-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                             AAT00720;
                                                                                                                                                                                                                                                                                                                     AAT00720
                                                                                                                                                                                                                                                                                                  RESULT
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                                                                                                                                                                                                            to a polynucleotide encoding a polypeptide with flavone-7-0-glucosidase-2"-0-rhamnosyl-transferase catalytic activity (such as 1-2-rhamnosyl-transferase). The enzyme is useful for converting hesperidin from orange peels to the sweetener neohesperidin dihydrochalcone (NHDC), and to provide genetically modified plants of the citrus genus including an antisense or sense (for oc-suppression) construct, or knockout integrated construct, to provide less bitter grapefruits, pomelos and other citrus fruits containing flavanoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The TMPRSS2 polynucleotides and polypeptides can be used in methods for diagnosing and prognosing predisposition to cancer in humans. The polypeptides may also be used in assays to screen for compounds with anti-cancer or therapeutic properties. The polypeptides are also useful for rational drug design. The TMPRSS2 polynucleotides and polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention provides a new tumour suppressor gene, designated TMPRSS2
                                     Polynucleotide encoding a flavone-7-0-glucosidase-2"-0-rhamnosyl-transferase, useful for converting hesperidin from orange peels to the sweetener neohesperidin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumor suppressor TMPRSS2 used for the diagnosis and prognosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour suppressor gene; TMPRSS2; cancer; human; drug design;
gene therapy; protein therapy; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human tumour suppressor TMPRSS2 cDNA sequencing primer 1B.
                                                                                                                                                                             This sequence represents a PCR primer for DNA encoding a 1-2-rhamnosyl-transferase. The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 12.8; DB 21;
Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27 BP; 11 A; 6 C; 5 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tavtigian SV, Teng DHF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 53; 89pp; English.
                                                                                                                                      Example; Page 24; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ87799 standard; DNA; 39 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0091044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MYRI-) MYRIAD GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 14; Conservative
                                                                                                dihydrochalcone (NHDC) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ctagatgctaggtatc 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 CTTGATGCTTGGTATC 12
WPI; 2000-499220/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-170914/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200000605-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                 glycosides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ87799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ87799/c
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RESULT 11 AAQ99928

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Primer; polymerase chain reaction; PCR; amplification; Elbeta; human; multiple; tumour; suppressor; MTS1; cancer; diagnosis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multiple tumour suppressor; MTS; human; cancer; hybridisation; somatic mutation; gene therapy; PCR; primer; amplification; ss.
                                                                                                            Human multiple tumour suppressor gene 1 Elbeta reverse primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human mutant multiple tumour suppressor gene sequences - for production of recombinant mutant polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63.0%; Score 12.6; DB 18; 78.9%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.2e+03;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21 BP; 5 A; 3 C; 7 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cannon-Albright LA, Kamb A, Skolnick MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 10; Columns 87-88; 72pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of PCR primer 13.
 AAT72309 standard; DNA; 21 BP.
                                                                                                                                                                                                                                                                                                                                                 95US-0474177.
94US-0214582.
94US-0215086.
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94US-0227369.
94US-0251938.
95WO-US03537.
                                                                                                                                                                                                                                                                                                                   94US-0214582.
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                                                                      10-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV53849 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 63.0 Best Local Similarity 78.9 Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 ctagaggcgaattatctgt
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                                                                                                                                                                                                                                                                                                                                                                                                        18-MAR-1994;
14-APR-1994;
01-JUN-1994;
17-MAR-1995;
                                                                                                                                                                                                                                                                                                                 18-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                      18-MAR-1994;
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                                                                                                                                                                                                                                                                             29-APR-1997
                                                                                                                                                                                                       Synthetic.
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                                     AAT72309;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The cDNA sequences encoding several multiple tumour suppressor (MTS) polypeptides have been isolated and sequenced, using various sequencing and amplification primers such as the primer represented in this sequence. MTS polypeptide-encoding cDNAs and mutants of these are useful for the diagnosis or prognosis of human cancer. Germ-line mutations of MTS cDNAs can be used for diagnosing predisposition to melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL and cancers of the pancreas, thyrold, ovary, uterus, testis, kidney, stomach and rectum. The wild-type gene is useful for gene therapy and MTS polypeptides may also be used for protein replacement therapy. Also the polypeptides or cells contg. an altered MTS gene are useful for screening for potential cancer therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wild-type multiple tumour suppressor (MTS) gene and mutant sequences - useful in diagnosis, prognosis and therapy of human cancer, e.g. melanoma or leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                     Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia; astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma; gene therapy; chronic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.0%; Score 12.6; DB 16; Length 21; 78.9%; Pred. No. 1.2e+03; 1ve 0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21 BP; 5 A; 3 C; 7 G; 6 T; 0 other;
                                                                                                                                                                                                   Human MTS1E1-beta PCR amplification primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 10; Page 64; 156pp; English.
                                                                                         AAQ99928 standard; cDNA; 21 BP.
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940S-0214581.
940S-0215088.
940S-02259.
940S-0215086.
940S-0215086.
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                                                                                                                                                                   (first entry)
3 ctagaggcgaattatctgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 78.9
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                   W09525429-A1.
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18-MAR-1994;
18-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAR-1994;
14-APR-1994;
18-MAR-1994;
                                                                                                                                                               07-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                       28-SEP-1995
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                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                             AAQ99928;
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Kamb A;

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Gaps

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01-SEP-1998. US5801236-A

Query Match

ð g RESULT 12 AAT72309

Length 21; Indels

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Primers AAV11267-V11269 are used in the isolation of the human multiple tumour suppression protein, MTS1E1-beta. The MTS gene locus is also referred to as the familial melanoma (MLM) gene locus, located on human chromosome 9921. Germ line mutations in MTS genes can be used in the diagnosis of predisposition to cancers, e.g. melanoma, leukaemia, astrocytoma, gliboblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid, ovary, uterus, testis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; multiple tumour suppressor 1 gene; MTS1; cancer; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse multiple tumour suppressor gene segment - useful for primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.0%; Score 12.6; DB 19; Length 21; 78.9%; Pred. No. 1.2e+03; ive 0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                         DNA specific for Multiple Tumour Suppressor 1E1-beta gene useful for the diagnosis of cancers related to MTS1E1-beta mutation(s) and their treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reverse PCR primer used to amplify human MST1E1-beta gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21 BP; 5 A; 3 C; 7 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                   Example 10; Column 87-88; 72pp; English.
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               94US-0214582.
94US-0215086.
94US-0215087.
                                                                    94US-0227369.
94US-0251938.
95WO-US03316.
95US-0487033
                                                                                                                                              (MYRI-) MYRIAD GENETICS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ctagaggcgaattatctgt 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kidney, stomach and rectum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 78.9'
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                                                                                                                                                                                                                      WPI; 1998-250421/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kamb A,
               18-MAR-1994;
18-MAR-1994;
18-MAR-1994;
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07-JUN-1995;
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                                                                      14-APR-1994;
01-JUN-1994;
                                                                                                           17-MAR-1995
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                                                                                                                                                                                   Kamb A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV70613
οy
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                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the nucleotide sequence of a PCR primer used for amplification in the method of the invention involving the use of the multiple tumour suppressor (MTS) gene, to diagnose and treat cancer. The WTS gene is useful in the diagnosis and prognosis of human cancer, e.g. by standard nucleic hybridisation techniques, of patient samples. The mutated sequences are those that are present in somatic mutations of the gene in cancers. The vectors can be used for gene therapy strategies to replace function of mutated protein in patients. These can also be used to construct protein mimetics, also for therapeutic strategies. In addition the expression constructs can also be used for recombinant production of MTS. Recombinant MTS can be used to screen for drugs to be used for cencer therapy, and the protein itself may also be used to restore MTS function in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WTSLE1-beta; multiple tumour suppressor; diagnosis; cancer; germ-line mutation; familial melanoma locus; MLM; predisposition; ss.
                                                                                                                                                                                                                                                                                                             Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.0%; Score 12.6; DB 19; Length 21; 78.9%; Pred. No. 1.2e+03; Live 0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21 BP; 5 A; 3 C; 7 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                           Example 10; Column 87-88; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human MTS1E1-beta PCR primer #2.
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                                                                  94US-0214582.
94US-0215086.
94US-0215087.
94US-0227369.
94US-0251938.
95WO-US03316.
               95US-0480810
                                                  95US-0480810
                                                                                                                                                                                                    (MYRI-) MYRIAD GENETICS INC.
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hes 15; Conserv
                                                                                 18-MAR-1994;
18-MAR-1994;
14-APR-1994;
01-JUN-1994;
17-MAR-1995;
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             07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                        mutation(s)
                                                                    18-MAR-1994
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Best Local Si
Matches 15,
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AAV11268

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Gaps

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PCR primers AAV70612-14 were used to amplify nucleic acid encoding a human multiple tumour suppressor 1E1-beta (MTS1E1-beta) protein. Primers designed from the gene can be used to design primers to detect annormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.
                       Example 11; Column 48; 80pp; English.
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Gaps 0; Query Match 63.0%; Score 12.6; DB 20; Length 21; Best Local Similarity 78.9%; Pred. No. 1.2e+03; Matches 15; Conservative 0; Mismatches 4; Indels (

Sequence 21 BP; 5 A; 3 C; 7 G; 6 T; 0 other;

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Search completed: October 2, 2001, 16:18:38 Job time: 15482 sec

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AAC65559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes new purified and isolated nucleic acids (i) encoding: (i) the A and B chains of a ricin-like toxin (II); and (ii) a heterologous linker, joining the two chains and including a cleavage recognition site for a disease-specific protease (III). Also described are: (I) plasmids or baculovirus transfer vectors that contain (I); and (2) recombinant protein (IV) consisting of the A and B chains of (III) joined by the specified linker. (IV), produced by expression of (I) in host cells, are used to inhibit or kill diseased cells that produce (III), particularly for treating cancers (e.g. leucocyte prodliferation; cancer of ovary, pancreas, breast or prostate; glioma) or infections caused by fungi, parasites (e.g. malaria) or viruses (e.g.
                     The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated
                                                          in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding ricin-like toxin with an interchain linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cleaved by protease - is specific for diseased cells, useful for,
e.g. killing selectively cancer or infected cells
                                                                                                                                                                                                                                                                                                                                                                                                          Ricin-like toxin; cancer; viral infection; parasitic infection; linker; B chain; A chain; protease; fungal infection; malaria; leucocyte proliferation; cytomegalovirus; herpes; hepatitis; rinnovirus; laryngedtracheitis; pollomyelitis; varicella zoster; cystic fibrosis; multiple sclerosis; ds.
                                                                                                                                                                                         ;
0
                                                                                                                                                                Length 20;
                                                                                                                                                                                                                                                                                                                                                                                  Human prostate-specific antigen linker regions of pAP-290.
                                                                                                                                                                                         0; Indels
                                                                                                                                                               Score 20; DB 22;
Pred. No. 0.68;
                                                                                                                           Sequence 20 BP; 1 A; 7 C; 1 G; 11 T; 0 other;
                                                                                                                                                                                           Mismatches
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Claim 3; Column 23; 30pp; English.
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                                                                                                                                                                                                                                                                                                         AAX04289 standard; DNA; 36
                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                  treatment of all of these.
                                                                                                                                                                                                                   1 ttctcccttccgttattctt
                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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cytomegalovirus (CMV), herpes, hepatitis, rhinovirus, laryngeotracheitis, poliomyelitis or varicella zoster), also cystic fibrosis and multiple sclerosis. Alternatively, (I) is used to express (IV) in vivo. (IV) is toxic specifically for (III)-expressing cells and does not depend for specificity on a cell-binding component. When used to treat virus-retrograde cells, transcytosis and cytotoxicity of (IV) are increased by retrograde translocation from endoplasmic reticulum to cytoplasm (which some viruses exploit to avoid immune detection), so selectivity and safety are further improved. (IV) are not toxic until chain A is released and this occurs only in target cells. The present sequence represents a nucleotide sequence from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human focal adhesion kinase antisense sequence #25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15.2; DB 20;
Pred. No. 1.4e+02;
); Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15; DB 22; I
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 36 BP; 5 A; 9 C; 3 G; 19 T; 0 other;
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85.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Best Local Similarity
Matches 17; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               embryonic
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Matches

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AAV49869 RESULT

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Enhanced LM609 grafted antibodies exhibiting selective binding affinity to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of angiogenesis, inflammatory diseases e.g. psoriasis, cancers and osteoporosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to enhanced LM609 grafted antibodies exhibiting selective binding affinity to aphabveta_3 integrin or their functional fragments. The antibodies or their functional fragments can be used in the diagnosis and treatment of aphabveta_3-mediated diseases such as anglogenessis, inflammatory diseases (such as psociasis and chronic articular rheumatism), disorders associated with inappropriate or inopportune invasion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequencing; target specificity; PCR; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vessels (such as diabetic retinopathy, neovascular glaucoma and cancer disorders such as tumours and Kaposi's sarcoma), retinal diseases (such as macular degeneration), restenosis and
                                                                                                                                                                                              LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis; inflammatory; cancer; retina; restenosis; osteoporosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 13.8; DB 22;
Pred. No. 6.5e+02;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 33 BP; 4 A; 13 C; 2 G; 14 T; 0 other;
                                                                                                                                                        DNA encoding mutant VL CDR2 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) APPLIED MOLECULAR EVOLUTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 42; 132pp; English.
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                                        AAF28225 standard; DNA; 33 BP.
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88.2%;
                                                                                                                                                                                                                                                                                                                                                                    23-JUN-2000; 2000WO-US17454.
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                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M13mp18 template sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-050110/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                            grafted
                                                                                                                                                                                                                                                                                            WO200078815-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Μū
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ss; M13mp18;
differential
                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                          24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         osteoporosis
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                                                                                                                  03-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Simi
Matches 15;
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                                                                              AAF28225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huse WD,
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                  AAF28225
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  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody LM609 heavy and light chain variable region. LM609 and the antibody LM609 heavy and light chain variable region. LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psorlasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times
                                                                                                                                                                                                                                                                                                                            Vitaxin; antibody; variable region; heavy chain; light chain; integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis; primer; V-L region; CDR; complementarity determining region; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose
  ;
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  Indels
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                                                                                                                                                                                                                                                                                        LM609 grafted antibody V-L region CDR2 DNA fragment #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 13.8; DB 19;
Pred. No. 6.5e+02;
); Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            greater than that of parent the parent antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 33 BP; 4 A; 13 C; 2 G; 14 T; 0 other;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Pagé 42; 129pp; English.
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0
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0
                                                                                                                                                                        AAV49869 standard; DNA; 33 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.0%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0791391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US01826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         angiogenesis or restenosis
                                                                                                                                                                                                                                                  (first entry)
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                    Huse WD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-437472/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IXSY-) IXSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAW76032.
                                                                                                                                                                                                                                                  02-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9833919-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-1998;
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glaser SM,
                                                                                                                                                                                                                AAV49869;
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셤 ò

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Gaps

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Length 33; Indels

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The invention provides polymorphic fragments of genes associated with hypertension. The nucleic acids including the polymorphic sites can be used as probes or primers for expressing variant proteins. Detection of the polymorphisms is useful in designing prophylactic and therapeutic regimes customized to underlying abnormalities. The polymorphisms can be used for association studies for hypertension, and in hypertension of hypertension, within a gene, they are likely to have a causative role in hypertension. This information can be used to find the precise role of polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. The polymorphisms can be tested for association with other disease e.g. agammaglobulinemia, diabetes inspidus, Lesch-Nyhan syndrome, muscullar dystrophy, wiskort. Aldrich syndrome, Fabrys disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrands disease, tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial colonic polyposis, Ehers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in forensics to identify individuals.
                                                                                                                                                                                                                                                              Novel nucleic acids containing polymorphisms used in the diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marek's disease virus; MDV; vaccine; antisense; therapy; latency; tumor; primer; polymerase chain reaction; PCR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 13.2; DB 21; Length 29;
Pred. No. 1.2e+03;
1; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 29 BP; 11 A; 2 C; 12 G; 3 T; 1 other;
                                                                                                                                                                          Chakravarti A, Haluska MK;
                                                                                                         (AFFY-) AFFYMETRIX INC.
(UYCA-) UNIV CASE WESTERN RESERVE.
                                                                                                                                                                                                                                                                                                                            Claim 1; Page 33; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.0%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
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  99EP-0250150.
                                            98US-0084641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ97859 standard; cDNA; 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-US00052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MDV L1 cDNA primer 1.
                                                                                                                                                                                                                   WPI; 2000-107928/10
                                                                                                                                                                                                                                                                                    hypertension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JAN-1994;
  07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JAN-1995;
                                          07-MAY-1998;
03-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9518860-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ97859;
                                                                                                                                                                             Fan JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ97859/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The target nucleotide sequence was used to demonstrate a method for improving the priming specificity of a non-unique oligonucleotide primer. Preferably the oligonucleotide primer is modified by a radioactive element, a fluorescent moiety or a biotin moiety. The methods are used particularly for the sequencing of target DNA sequences. The methods using the priming specificity of a non-unique oligonucleotide primer by using differential extension of the primer with nucleotide primer by length discrimination against shorter extensions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymorphism; hypertension; agammaglobulinemia; diabetes insipidus; Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome; Fabrys disease; familial hypercholesterolemia; hereditary spherocytosis; polycystic kidney disease; von Willebrands disease; forensic; human; tuberous sclerosis; hereditary hemorrhagica telangiectasia; familial colonic polyposis; osteogenesis imperfecta; porphyria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Improving priming specificity of oligo:nucleotide primers - by using differential extension of the primer with nucleotide subsets and length discrimination against shorter extensions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                     a
"Unspecified amount of nucleotides not given
in specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 13.4; DB 19; Length 46; Pred. No. 1.1e+03; 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphic fragment of hypertension associated gene HAPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 46 BP; 6 A; 19 C; 2 G; 19 T; 0 other;
                                      Location/Qualifiers
20..21
/*tag= a
/note= "Unspecified a
                                                                                                                                                                                                                                                                                                                                                                                           Mugasimangalam RC, Ulanovsky LE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 1; 46pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 67.0%;
Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                              97WO-US17305
                                                                                                                                                                                                                                                                                                        96IL-0119342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ehlers-Danlos syndrome; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAY-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                   (USAT ) US DEPT ENERGY
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-286423/25
Bacteriophage M13.
                                                                                                                                                                          WO9814608-A1
                                                              misc_feature
                                                                                                                                                                                                                                                              30-SEP-1997;
                                                                                                                                                                                                                                                                                                        02-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                   09-APR-1998
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AAA04352/C RESULT

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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FREE/) FREEDMAN R. (LEON/) LEONARD S.
                                                                                              Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polynucleotides
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                 W09920757-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Freedman R,
                                                                                                                                                                                                                                                         15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                    AAX56167;
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                                                                                                                                                                                                     AAX56167,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a mammalian PGI gene and protein, and a set of PGI biallelic markers. The PGI polynucleotide and biallelic markers are used in a hybridisation assay, a sequencing assay, or in an allele-specific amplification assay for determining the identity of a nucleotide at a PGI-related biallelic marker. The methods can be used to detect and to assess the risk of developing cancer or prostate cancer. Barly-stage diagnosis of prostate cancer relies on prostate specific antigen (PSA) dosage. However, the effectiveness of this is limited due to its inability to discriminate between malignant and non-malignant
                                                                                                                                                                                                                                                                                                                                                                                               gene; biallelic marker; PCR primer; PG1-related biallelic marker;
er; prostate cancer; diagnosis; therapy; prostate specific antigen;
                                                  Marek's disease virus protein and its nucleotide sequence - used to protect chickens against Marek's disease and inhibit the establishment of latency and tumour cell development
                                                                                                                                                                                                                Gaps
                                                                                                                The primers given in AAQ97859-60 were used for the PCR amplification of the upstream region of MDV Ll cDNA. The amplified fragment, Q2L1, was cloned into pBluescript KS+ for sequencing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a prostate cancer associated gene and biallelic markers
                                                                                                                                                                                           Length 17;
                                                                                                                                                                                                                                                                                                                                                                           PCR primer for PG1 biallelic markers 4-54-283 and 4-55-95.
                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chumakov I, Cohen
                                                                                                                                                                                         Score 12.8; DB 16;
Pred. No. 1.8e+03;
0; Mismatches 2;
                                                                                                                                                           Sequence 17 BP; 9 A; 2 C; 5 G; 1 T; 0 other;
           Schat KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 354; 385pp; English.
                                                                                            Example 1; Page 11; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blumenfeld M, Bougueleret L,
                                                                                                                                                                                                                                                                                                            AAZ01237 standard; DNA; 18 BP.
                                                                                                                                                                                         64.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-IB02133
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                                                                                                                                                                                                                                                                                                                                                      27-SEP-1999 (first entry)
                                                                                                                                                                                         Query Match 64.0
Best Local Similarity 87.5
Matches 14; Conservative
          Ohashi K,
                                                                                                                                                                                                                                   5 cccttccgttattctt 20
                                                                                                                                                                                                                                              CCCTTCCTTTATTGTT 2
                             WPI; 1995-255063/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-405178/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                derived from it
                                                                                                                                                                                                                                                                                                                                                                                                                      PSA; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEST ) GENSET
          O'Connell PH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9932644-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                  AAZ01237;
                                                                                                                                                                                                                                                                                                                                                                                                             cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of
                                                                                                                                                                                                                                                       17
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The present invention describes an isolated nucleotide sequence (I)
encoding at least a portion of the human alpha-7 neuronal nicotinic
acetylcholine receptor (alpha7-hnAchR). Also described are: (1) a
peptide encoded by (I): (2) a vector comprising (I): (3) a host cell
transformed with a vector of (2): (4) a polynucleotide comprising at
least 15 nucleotides which hybridises under stringent conditions to at
least a portion of (I): (5) a method for detection of a polynucleotide
encoding alpha 7-hnAchR in a biological sample; and (6) a method for
amplification of nucleic acid from a sample suspected of containing
nucleic acid encoding alpha 7-hnAchR. The primers and probes from the
present invention can be used on brain tissue and blood samples of
humans suspected of suffering from schizophrenia, small cell lung
carcinoma, breast cancer and nicotine-dependent illness. This is
particularly useful for diagnosis of schizophrenia. Other illnesses
that can be studied/diagnosed are epilepsy (e.g. juvenile myoclonic
epilepsy) and Prader-Willi and Angelman's syndromes.
affections of the organ. A need exists for both a reliable diagnostic procedure which would enable early-stage diagnosis, and for preventative and curative treatments of the disease. The PGI gene can be used for detection of prostate cancer, and the risk of developing it in the future, and can also be used to determine therapies for the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; alpha-7 nicotinic receptor; neuronal; hybridisation; probe;
alpha-7 neuronal nicotinic acetylcholine receptor; schizophrenia;
small cell lung carcinoma; breast cancer; nicotine-dependent illness;
epilepsy; juvenile myoclonic epilepsy; Prader-Willi syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human alpha-7 neuronal nicotinic acetylcholine receptor and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human alpha-7 nicotinic receptor PCR primer SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 64.0%; Score 12.8; DB 20;
87.5%; Pred. No. 1.8e+03;
ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                           Sequence 18 BP; 6 A; 1 C; 8 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Angelman's syndrome; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 15; Page 64; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US21762.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX56167 standard; DNA; 21
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BP.

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XLIS gene; human; detection; diagnosis; prenatal diagnosis; therapy; lissencephaly; LIS; agyria-pachygyria; subcortical laminar heterotopia; SCLH; cortical dysgenesis; cryptogenic epilepsy; neurological disorder; neurodegenerative disease; Alzheimer's disease; X-linked disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New gene and its gene product expressed in the brain, useful for diagnosing and treating disorders such as lissencephaly and subcortical laminar heterotopia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                     Human XLIS gene fragment PCR primer 6 F.
                                                                                                                                                                                                                                                                                                                genetic counselling; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chelly J, Des Portes V, Kahn A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Page 50; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97EP-0402811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97EP-0402811
2 tttcccatccgttatccct 20
                                                                                                                                                                 (first entry)
                                                                                       AAX36892 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-290318/25.
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-NOV-1997;
                                                                                                                                                             14-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-1999.
                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                           AAX36892;
                                                     12
                                                                        AAX36892
                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; hoclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer; bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        These ORFs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ORFs) of the genome of Childran trachomatis (see AA201425). These ORFs encode polypeptides (see AA216754 *137949) which can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, barholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primers AA201426-Z06209 were used to amplify open reading frames
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                                                                        Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
                                                                                                                                                                                                                                                                                                                                                                                    PCR primer used to amplify an ORF of Chlamydia trachomatis.
                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.0%; Score 12.6; DB 20; 78.9%; Pred. No. 2.3e+03; ive 0; Mismatches 4;
                                                                    Score 12.8; DB 20;
Pred. No. 1.9e+03;
0; Mismatches 2;
               BP; 9 A; 3 C; 8 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 BP; 2 A; 8 C; 2 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 1829; 1755pp; English.
                                                                                                                                                                                                                                                                        AAZ06154 standard; DNA; 20 BP.
                                                                  Ouery Match 64.0%;
Best Local Similarity 87.5%;
Matches 14; Conservative
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97FR-0016034.
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Best Local Similarity 78.99
Matches 15; Conservative
                                                                                                                                            2 tctcccttccgttatt 17
                                                                                                                                                                              18 TCTCCCTTGCGTTCTT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydía trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-371125/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09928475-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-NOV-1998;
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17-DEC-1997;
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               Sequence 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                              AAZ06154;
                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                         AAZ06154
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Pinard J;

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This sequence is a primer for the human XIIS gene of the invention.

The XLIS fragments may be used to detect abnormalities in the expression of the XLIS gene transcripts or to compare their sequence with that of the XLIS transcripts from patients for in vitro especially prenatal diagnosis of lissencephaly (LIS) (or agyria-pachygyria), subcortical annuar heterotopia (SCLH), cortical dysgenesis, cryptogenic epilepsies or neurodegenerative diseases such as Alzaheimer's disease. These disorders mainly affect females as the XLIS gene is X-linked. The XLIS fragments may also be used to administer to patients to prevent or treat the above disorders and may be used to administer to patients to prevent or treat the above disorders and may be used as a tool in genetic counselling.

CIIS gene from a sample for comparison to normal samples in the in vitro diagnosis regime. This may also be performed by amplifying XLIS cDNA from the mRNA in the sample. Antibodies to XLIS may be used to detect XLIS in a biological sample. XLIS may also be administered to patients to prevent or treat the above disorders. They may also be administered to patients to prevent or treat the above neurological disorders. In addition XLIS may be used as a marker of neuronal cells at m early stage of development, its class as a marker of neuronal cells at m early stage of development is a leads to development of the fortical region of the brain and of the labore labore as a marker of the cortical region of the brain and of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pathogenesis of the group of neuronal disorders mentioned above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 12.6; DB 20;
Pred. No. 2.3e+03;
); Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 1 A; 7 C; 0 G; 12 T; 0 other;
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0
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Best Local Similarity 78.99
Matches 15; Conservative
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Gaps

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Indels

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Synthetic.

AAZ30696;

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The sequences given in AAT42898-901 are single stranded (ss) circular oligonucleotides and their targets, which are used in the inhibition of the proliferation of myeloid leukaemia cells. These oligos are specifically targetted to a region in the bcr3/abl2 gene 385 conceptions by the bcr3/abl2 gene 385 circular oligonucleotides comprise a parallel binding (P) domain. The P and AP domains have sufficient complementarity to bind detectably to 1 strand of a defined nucleic card target. The P domain is capable of binding in a parallel manner to the target. The AP domain is capable of binding in an anti-parallel manner to the target and the ends of the P and AP domains are separated by the loop domains. The sc circular oligonucleotides can be used to regulate the synthesis of DNA, RNA or protein (pref. by DNA replication, DNA reverse transcription, RNA splicing, RNA polyadenylation, RNA cranslocation or protein (ranslocation) by binding a target sequence in the template. They can also be used to deliver a drug to a specific cell type by administering a drug covalently bound to them (i.e. to requiate the biosynthesis of DNA, RNA or protein in a targetted mammalian tumour cell in vivo, without substantially altering the blosynthesis of the DNA). They can also be used to detect a target on ucleic acid by detecting an oligonucleotide-target complex. The circular oligonucleotide can bind both single and double stranded to target nucleic acids, and has enhanced stability, compared to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single stranded circular oligo:nucleotide comprising parallel and anti-parallel binding domain - used to regulate biosynthesis of DNA, RNA or protein in targetted mammalian tumour cell in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12.6; DB 17; Length 34; Pred. No. 2.5e+03; 0; Mismatches 4; Indels C
                                                                                                                                                       /*tag= c
/note= "forms anti-parallel binding domain"
                                                                                                         "forms parallel binding domain"
                            a
"forms 5' > 3' bond with C34"
                                                                                                                                                                                                                /*tag= d
/note= "forms 3' > 5' bond with Tl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 34 BP; 1 A; 18 C; 1 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RESE ) RESEARCH CORP TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 11; Page 135; 195pp; English.
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78.9%;
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Best Local Similarity 78.9
Matches 15; Conservative
                                                                                     *tag=
                        /*tag=
                                                /note=
                                                                                                                               18..29
/*tag=
                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-455262/45.
                                                                                                                                                                                                                                                                                                                                                               21-MAR-1996;
      misc_feature
                                                                 misc_binding
                                                                                                                               misc_binding
                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                           WO9630384-A1
                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-1995;
                                                                                                                                                                                                                                                                                                                       03-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KOOl ET;
    ö
                                                                                                                                                                                                                                                                                               Promoter; 40s ribosomal protein S28; genetic engineering; amplification; heterologous protein; gene expression; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This primer was used to PCR amplify the promoter sequence from the 40S ribosomal protein S28 gene (AAZ30685) from Aspergillus oryzae. The invention relates to novel gene promoters (AAZ30680-Z30685) isolated from Aspergillus oryzae which can be used in genetic engineering to express heterologous proteins in Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A new promoter derived from an Aspergillus genus microbe – useful for
producing exotic proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 24;
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    A. oryzae 40S ribosome protein S28 gene promoter primer.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.0%; Score 12.6; DB 20; 78.9%; Pred. No. 2.4e+03; iive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24 BP; 9 A; 6 C; 8 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 7; Page 5; 11pp; Japanese.
                                                                                                                          AAZ30696 standard; DNA; 24 BP
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Best Local Similarity 78.9%
Matches 15; Conservative
2 ttatccttcctttctct
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                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-1998;
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Gaps

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7 ttctcccctcccctcttct 25

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single stranded; circular; target sequence; parallel; detection; binding domain; anti-parallel; loop domain; complementarity; ss; synthesis; regulation; drug delivery; biosynthesis; tumour cell.

Location/Qualifiers

Synthetic.

Key

AAT42899;

RESULT 14

ò a AAT42899

RESULT 15 AAV50562

AAV50562 standard; DNA; 41 BP

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This DNA sequence is a region of a Brassica napus or Brassica oleracea genome which contains a polymorphic marker. This sequence can be used in the construction of allele-specific primers and probes for amplification or hybridisation, e.g. to determine common or disparate ancestry between 2 or more plants, to monitor the genetic contribution of an ancestral plant, to trace the progeny of proprietary plants, in certification of a hybrid plant or to identify the progeny of a back-crossed plant with an ancestral plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassica species allele-specific oligonucleotide probes and primers - useful for plant breeding
                                                                                                               Polymorphic marker; allele-specific; primer; probe; amplification; hybridisation; plant; hybrid certification; genetic contribution; progeny; back-cross; hybrid; ancestry; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.0%; Score 12.6; DB 19; Length 41; 78.9%; Pred. No. 2.5e+03; Live 0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sapolsky RJ;
                                                                                     Brassica sp. polymorphic marker N2/10B8/N3-2A DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 41 BP; 8 A; 11 C; 3 G; 19 T; 0 other;
                                                                                                                                                                                                                                /*tag= a
/replace= "c"
/note= "polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Landry BS, Lemieux B, Murigneux A,
                                                                                                                                                                                         Location/Qualifiers
21
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                                                                                                                                                                                                                                                                                                                                                 97WO-US21782
                                                                                                                                                                                                                                                                                                                                                                            97US-0813507.
96US-0032069.
                                                         (first entry)
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Best Local Similarity 78.9
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-333252/29
                                                         21-DEC-1998
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02-DEC-1996;
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                                                                                                                                                                          Brassica sp.
                                                                                                                                                                                                        Key
variation
                           AAV50562;
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Gaps

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Search completed: October 2, 2001, 16:18:37 Job time: 15481 sec

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APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SSQ ID NO 26
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                            US-09-377-310-6
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LENGTH: 20
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Sequence 6, Appli
Sequence 13, Appl
Sequence 17, Appl
Sequence 4, Appli
Patent No. 544743
Patent No. 5519127
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Sequence 1, Appli
Sequence 148, App
Sequence 148, App
Sequence 148, Appl
Sequence 148, Appl
Sequence 7, Appli
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9.071 Million cell updates/sec
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                                                                       Search time 417.38 Seconds
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Sequence 1,
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Sequence 12,
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-288-405A-3
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US-08-700-186-15
US-08-914-981-12
US-08-914-981-12
US-08-116-115-12
US-08-116-113-13-14
US-08-748-415-1
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US-08-748-415-1
US-08-748-415-1
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US-08-303-275-36
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and is derived by
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Sequence
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APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ESPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
SUFTWARE: Patentin Ver: 2.0
SEQ ID NO 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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PCT-US94-0259-49
US-08-26-56
US-08-036-38-38
US-08-171-89-396
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US-08-171-89-396
US-08-173-396-396
US-08-475-228A-396
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US-08-473-12388-396
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US-08-473-998-118
US-08-493-352A-2
US-07-979-966A-15
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100.0%; Pred. No. 0.37;
ive 0; Mismatches 0
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; OTHER INFORMATION: antisense sequence
US-09-377-310-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-09-377-310-26
Sequence 26, Application US/09377310B
; Patent No. 6133031
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09377310B; Patent No. 6133031; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ilarity 100.0%;
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FEATURE:

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,312
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVET P.
REGISTRATION NUMBER: 28,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.0%; Score 13.6; DB 4;
80.0%; Pred. No. 4e+02;
tive 0; Mismatches 4;
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Sequence 12, Application US/08700186

Patent No. 5780266

GENERAL INFORMATION:
APPLICANT: Dillon, Patrick
APPLICANT: Vockley, Joseph
TITLE OF INVENTION: ARGINASE II
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                               GENERAL INFORMATION:
APPLICANT. CHANG, Lung-Ji
TITLE OF INVENTION: LENTIVIRAL VECTORS
NUMBER OF SEQUENCES: 20
CORRESPONDINCE ADDRESS:
ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = ""DNA""

US-08-935-312-15
                                                                          Sequence 15, Application US/08935312 Patent No. 6207455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: CH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 GAAAGAGCAGAAGACAGTGA 23
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ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 gaaactgcagaaggcactga
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LENGTH: 42 base pairs
TYPE: nucleic acid
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Best Local Similarity 80.0°
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-737-3528 INFORMATION FOR SEQ ID NO:
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CITY: Washington
STATE: D.C.
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US-08-288-405A-3/C
Sequence 3, Application US/08288405A
Patent No. 5559009
GENERAL INFORMATION:
APPLICANT: Chandy, Kanlanthara G.
APPLICANT: Chandy, Grischa
APPLICANT: Chandy, Grischa
TITLE OF INVENTION: A No. 5559009el Voltage-Gated Potassium Channel
TITLE OF INVENTION: Gene
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                                                                                           75.0%; Score 15; DB 3; Length 15; 100.0%; Pred. No. 76; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,
ADDRESSEE: Attn: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,405A
FILING DATE: 10-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,431
FILING DATE: 04-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 13.8; DB 1;
Pred. No. 3e+02;
0; Mismatches 2;
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; OTHER INFORMATION: antisense sequence US-09-377-310-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111-4187
COMPUTER READABLE FORM:
COMPUTER: TELOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-591
TELECOMMULICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Attn: Walter I
STREET: 4 Embarcadero Cel
CITY: San Francisco
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 88.2
Matches 15; Conservative
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                                                                                           Query Match 75.0
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 GGAACTGCAGAAGGGAC 1
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; LOCATION:
US-08-288-405A-3
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Gaps

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Indels

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Patent No. 5372929
GENERAL INFORMATION:
APPLICANT: Cimino, George C.
APPLICANT: Lin, Lilly
TITLE OF INVENTION: MATHOD FOR MEASURING THE INACTIVATION OF TITLE OF INVENTION: PATHOGENS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Ferry Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.0%; Score 13.4; DB 3; Length 43; 93.3%; Pred. No. 5e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                         67.0%; Score 13.4; DB 2; Length 43; ilarity 93.3%; Pred. No. 5e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-116-115-12/C
Sequence 12, Application US/09116115D
Patent No. 604318
GENERAL INFORMATION:
APPLICANT: DILLON, PATRICK J.
TITLE OF INVENTION: ARGINASE II
FILE REFERENCE: ATG-50004-3/D1
CURRENT APPLICATION NUMBER: US/09/116,115D
CURRENT APPLICATION NUMBER: US/09/116,115D
CURRENT APPLICATION NUMBER: US/09/116,115D
GENELIER FILING DATE: 1997-08-20
EARLIER PELLING DATE: 1997-08-20
EARLIER FILING DATE: 1996-08-20
EARLIER FILING DATE: 1966-08-30
EARLIER FILING DATE: 1966-08-30
EARLIER FILING DATE: 1966-08-30
SEARLIER FILING DATE: 1966-08-30
NUMBER OF SEQ ID NOS: 17
SEQUEN NO 12
                                              12:
                   TELEX: 846169
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
  610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                               4 actgcagaaggcact 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-116-115-12
                                                                                                                                   STRANGE TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                              ANTI-SENSE: NO FRAGMENT TYPE: CORIGINAL SOURCE: US-08-914-981-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-825-959-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 13.4; D
Pred. No. 5e+0
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRILIG DATE: 20-AUGUST-1996
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: ATG50004-3
TELECOMUNICATION INFORMATION:
TELECHONE: 610-407-0700
                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Han, william T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG50004-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEPRAX: 610-270-5090
                                   APPLICATION NUMBER: US/08/700,186 FILING DATE: CLASSIFICATION: 435 CLASSIFICATION DATA: APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/914,981
FILING DATE: 20-AUGUST-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-914-981-12/c

Sequence 12, Application US/08914981

Fatent No. 5912159

GENERAL INFORMATION:
APPLICANT: Dillon, Patrick
APPLICANT: Dillon, Patrick
APPLICANT: OCCHEV, JOSEPH
TITLE OF INVENTION: ARCINASE II
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSE:
ADDRESSEE: RATHER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 67.0%;
Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                   CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 actgcagaaggcact 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 ACTGCAGAAGGCAAT 2
                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: CDN
                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-700-186-12
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NAME: Evans, Barry
REGISTATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3580
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-333
TELEFAX: (212) 840-712
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: APPLICATION NUMBER: US/07/841,648 FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/250,934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: APPLICATION NUMBER: US/08/101,274
REFERENCE/DOCKET NUMBER: STER
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 603-9071
TELERAX: (510) 603-9099
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-131-324-13
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 3 aactgcagaaggcactga 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AACTGCAGAAGGCTAGGA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-08-377-495-1
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Patent No. 5565320
GENERAL INFORMATION:
APPLICANT: Cimino, George C.
APPLICANT: Lin, Lily
TITLE OF INVENTION: COMPOUNDS FOR THE PHOTODECONTAMINATION
TITLE OF INVENTION: OF PATHOGENS IN BLOOD
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steritech, Inc.
STREET: 2525 Stanwell Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.0%; Score 13.2; DB 1; Length 27; 83.3%; Pred. No. 5.7e+02; ive 0; Mismatches 3; Indels
                                                                                   COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TIBM PC compatible
COMPUTER: TIBM PC compatible
COMPUTER: TIBM PC compatible
COMPUTER: TIBM PC compatible
COMPUTER: PACHTION DATA:
APPLICATION NUMBER: US/07/825,959
FILING DATE: 19920127
CLASSIFICATION NUMBER: US/07/825,959
FILING DATE: 19920127
AMME: Weseman, James C
REGISTRATION NUMBER: 30,507
REGISTRATION NUMBER: 30,507
RELEFANC (415) 433-4150
TELEFAN: (415) 433-416
TELEFAN: (415) 433-416
TELEFAN: (415) 433-416
TELEFAN: (415) 433-416
TELEFAN: CARACTERISTICS:
LENGTH: 27 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIREET: 2.23 SCHIWELL DILVE
CITY: CONCORD
STATE: California
CONTRY: United States of America
2.1P: 945.20
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN RAPEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/131,324
FILING DATE: 28-210-1993
CLASSIFICATION NUMBER: US/08/131,324
FILING DATE: 27-3AN-1993
ATACHION NUMBER: US 07/825,959
FILING DATE: 27-3AN-1992
ATACHION NUMBER: US 07/825,959
FILING DATE: 27-3AN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Carroll, Peter G. REGISTRATION NUMBER: 32,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MoLECULE TYPE: DNA (genomic) FRAGMENT TYPE: internal US-07-825-959-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 aactgcagaaggcactga 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 66.0
Best Local Similarity 83.3
Matches 15; Conservative
  San Francisco
                          California
: USA
                                                                         94111
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Gaps
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Patent No. 5631137
GENERAL INFORMATION:
APPLICANT: Martin, Mark T.
APPLICANT: Smith, Rodger G.
APPLICANT: Darsley, Michael J.
APPLICANT: Blackburn, Gary F.
TITLE OF INVENTION: REACTION BASED SCREENING FOR EXPRESSION TITLE OF INVENTION: OF AND CONCENTRATION OF CATALYTIC MOIETIES NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                         .;
0
66.0%; Score 13.2; DB 1; Length 27; 83.3%; Pred. No. 5.7e+02; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States
ZIP: 10036
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN RELEASE #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/377,495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
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APPLICANT: Marth, Mark T.
APPLICANT: Smith, Rodger G.
APPLICANT: Sinth, Rodger G.
APPLICANT: Sinpsson, David
APPLICANT: Blackburn, Gary F.
TITLE OF INVENTION: REACTION-BASED SCREENING FOR EXPRESSION
TITLE OF INVENTION: OF AND CONCENTRATION OF CATALYTIC MOIETIES
NUMBER OF SEQUENCES: 4
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Pred. No. 8.6e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               370068-3580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/377,495
FILLING DATE:
RPLICATION NUMBER: US/08/250,934
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/07/841,648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/747,654
FILING DATE: 13*NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/101,274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-235-353-1
; Sequence 1, Application US/09235353
; Patent No. 6177270
; GENERAL INFORMATION:
APPLICANT: Mark T.
                                                                                                      ; Sequence 1, Application US/08747654; Patent No. 6121007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 37,
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 22 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 gaaactgcagaaggca 16
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    5 GAAACTGCAGGAGTCA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 14; Conserv
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                                                                                                                                             GENERAL INFORMATION:
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CITY: New York
STATE: New York
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                                                               RESULT 12
US-08-747-654-1
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APPLICANT: Smith, Rodger G.
APPLICANT: Smith, Rodger G.
APPLICANT: Darsley, Michael J.
APPLICANT: Darsley, Michael J.
APPLICANT: Blackburn, Gary F.
TITLE OF INVENTION: REACTION-BASED SCREENING FOR EXPRESSION
TITLE OF INVENTION: OF AND CONCENTRATION OF CATALYTIC MOIETIES
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                                                            Length 22;
                                                          Score 12.8; DB 1; Length 2
Pred. No. 8.6e+02;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PPC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,415
FILING DATE: 13-NOV-1996
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/377,495
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Curtis, Morris & Safford, P.C. STREET: 530 Fifth Avenue
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NAME: Evans, Barry
REGISSPRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3580
TELECOMMUNICATION INFORMATION:
TELEPRA: (212) 840-3333
TELEPRA: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/250,934 FILING DATE:
APPLICATION NUMBER: US/08/101,274
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APPLICATION NUMBER: US/07/841,648
FILING DATE:
                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08748415
Patent No. 5891648
GENERAL INFORMATION:
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                                                            64.0%;
87.5%;
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: United States
                                                                                                      14; Conservative
                                                                                                                                                                     5 GAACTGCAGGAGTCA 20
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STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
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                                                          Query Match
Best Local Similarity
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STATE: New YOR
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US-08-748-415-1
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US-08-377-495-1
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Pred. No. 1.1e+03;
); Mismatches 4; Indels
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21P: 10036
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,483
FILING DATE: 12-AUG-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pacletti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                           Score 12.8; DB 4;
Pred. No. 9.2e+02;
); Mismatches 2;
                                                                                 CURRENT FILING DATE: 1999-01-15
EARLIER APPLICATION NUMBER: PCT/FR97/01316
EARLIER FILING DATE: 1997-07-15
EARLIER PLING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 18
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 35
TYPE: DNA
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REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Curtis, Morris & Safford ADDRESSEE: C/O William S. Frommer STREET: 530 Fifth Avenue CITY: New York STATE: NY
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APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-WAR-1992
ATTORNEY/AGENT INFORMATION:
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US-08-105-483-148
; Sequence 148, Application US/08105483
; Patent No. 5494807
; GENERAL INFORMATION:
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US-09-232-477-1
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87.5%;
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TELEFAX: (212) 840-0712
INFORMATION FOR SEC ID NO: 148
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 87.5
Matches 14; Conservative
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STRANDEDNESS: single
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GENERAL INFORMATION:
APPLICANT: AUDONNET, Jean-Christophe
APPLICANT: BOUGHARDON, Annabelle
APPLICANT: BOUGHER, Michel
TILLE OF INVENTION: POLYNCLEOTIDE VACCINE FORMULA AGAINST CANINE
TITLE OF INVENTION: PATHOLOGIES, IN PARTICULAR RESPIRATORY AND DIGESTIVE
TITLE OF INVENTION: PATHOLOGIES
APPLICANT: Smith, Rodger G.
APPLICANT: Darsley, Michael J.
APPLICANT: Simpson, David B.
TITLE OF INVENTION: REACTION-BASED SCREENING FOR EXPRESSION
TITLE OF INVENTION: OF AND CONCENTRATION OF CATALYTIC MOIETIES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSED: Curtis, Morris & Safford, P.C.
STREET: S30 Fifth Avenue
CITY: New York
STATE: New York
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MEDIUM TYPE: Floppy disk
COMPUTER: TBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREWT APPLICATION DATA:
FILLING DATE:
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Pred. No. 8.6e+02;
); Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REFERENCE/DOCKET NUMBER: 370068-3580
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/232,477
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APPLICATION NUMBER: 08/748,415
FILING DATE: 13-NOV-1996
APPLICATION NUMBER: US/08/37,495
FILING DATE:
APPLICATION NUMBER: US/08/250,934
FILING DATE:
APPLICATION NUMBER: US/08/101,274
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; Sequence 1, Application US/09232477
; Patent No. 6228846
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TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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87.5%;
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: United States
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Best Local Similarity 87.5
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                10036
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Search completed: October 2, 2001, 16:03:46 Job time: 14590 sec

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Fatent No. 6133031
GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase; TITLE OF INVENTION: Expression; FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 20
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APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT APPLICATION NUMBER: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                             Sequence
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PCT-US95-03032-7

US-08-039-580B-11

US-08-399-580B-11

US-08-413-338A-16

US-08-413-338A-16

US-08-442-144A-91

US-08-442-144A-91

US-08-570-155-8

PCT-US95-02861-8

US-08-509-797-21

US-08-669-685-21

US-08-689-685-21

US-08-689-685-21

US-08-689-685-21

US-08-689-685-21

US-08-689-688-21
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; Patent No. 6133031
; GENERAL INFORMATION:
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Best Local Similarity
Matches 20; Conserv
   US-09-377-310-24
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 SEQ ID NO 24
LENGTH: 15
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                                                                                                           Search time 417.38 Seconds (without alignments) 9.071 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-280-799-185
PCT-US92-02977-4
                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-517-584A-22
US-09-180-437-48
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                                                                                                             2001, 16:03:44
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Listing first 45 summaries
                                                                               OM nucleic - nucleic search, using sw model
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Match Length
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length: 50
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Best Local Similarity 83.3
Matches 15; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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US-08-434-474-19
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Pred. No. 4e+02;
0; Mismatches 3; Indels
                                                                                          Score 15; DB 3; Length 15;
Pred. No. 54;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                       Sequence 19, Application US/08250849;
Patent No. 5567583;
GRNERAL INFORMATION:
APPLICANT: Chang-Ning J. Wang and Kai-APPLICANT: Usan Wu
TITLE OF INVENTION: NUCLEIC ACID
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: 125 Franklin Street
CONTY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.

ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,849
FILING DATE: 05/26/94
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 07/808,463
FILING DATE: December 16, 1991
ATPORNEY AGENT INFORMATION:
NAME: Y. ROCKY TSAO
RECISTRATION NUMBER: 34,053
REFERENCE/DOCKET NUMBER: 06498/002001
             ; OTHER INFORMATION: antisense sequence US-09-377-310-24
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Patent No. 5712386
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TELECOMMUNICATION INFORMATION:
                                                                                          Query Match 75.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative 0
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TELEFAX: (617) 542-8906
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Best Local Similarity 83.3
Matches 15; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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US-08-250-849-19
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FEATURE:
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TITLE OF INVESTION: WEIGHT AT ARKGET

TITLE OF INVESTION: WEIGHT AT ARKGET

TITLE OF INVESTION: WEIGHT AT ARKGET

TOTAL OF INVESTION: WINCERT ACID

CORRESCENCES: 21

CORRESCENCES: 21

CORRESCENCES: 21

CORRESCENCES: 21

CORRESCENCES: 21

CORRESCENCES: 22

CORRESCENCES: 21

CORRESCENCES: 22

CORPETER: 1840 FS/2 Model 502 or 555X

COMPUTER: 1840 FS/2 MODEL 504

COMPUTER: 1
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Gaps

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GENERAL INFORMATION:
APPLICANT: JARVIS, THALE
APPLICANT: ACRAIGEN, JAMES A.
APPLICANT: MCSWIGGEN, JAMES A.
TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF C-FOS
TITLE OF INVENTION OR CONDITIONS RELATED TO LEVELS OF C-FOS
TITLE OF INVENTION OF CONDITIONS RELATED TO LEVELS OF C-FOS
CURRENT FILLING DATE: 1997-12-24
EARLIER APPLICATION NUMBER: 60/037,658
EARLIER APPLICATION NUMBER: 60/037,658
EARLIER PILING DATE: 1997-01-23
EARLIER PILING DATE: 1995-01-13
EARLIER PILING DATE: 1995-01-13
EARLIER PILING DATE: 1994-05-18
NUMBER OF SEQ ID NOS: 375
SEQ ID NOS: 375
SED ID NO ESC ID NOS: 375
SED ID NO ESC ID NOS: 375
  ; OTHER INFORMATION: Description of Artificial Sequence:other nucleic; OTHER INFORMATION: acid, synthetic DNA US-09-180-437-53
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,077
                                                                                                             Score 12.8; DB 4;
Pred. No. 6.1e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.0%; Score 12.2; DB 3;
82.4%; Pred. No. 1.2e+03;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wood, Patricia C
APPLICANT: Quirk, Alan V
TITLE OF INVENTION: Yeast Strains
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Centeon LLC
                                                                                                                                                                                                                                                                                                                                                  ; Sequence 6, Application US/08998099A; Patent No. 6103890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 4, Application US/08750077; Patent No. 5783423; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1020 First Avenue CITY: King of Prussia
                                                                                                               64.0%;
87.5%;
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                                                                                                             Query Match 64.0
Best Local Similarity 87.5
Matches 14; Conservative
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Best Local Similarity 82.4
Matches 14; Conservative
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COMPUTER READABLE FORM:
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; ORGANISM: Homo sapiens
US-08-998-099-6
                                                                                                                                                                                                                                                                                                                              US-08-998-099-6/c
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US-08-750-077-4
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                                                                                        Length 20;
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Pred. No. 6.1e+02;
0; Mismatches 2; Indels
                                                                                                                                 Indels
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APPLICANT: FURUSARO, Shioji
APPLICANT: MORISAWA, Yoshifumi
APPLICANT: KUSUYAMA, Takeshi
TITLE OF INVENTION: Antisense Compounds to CD14
FILE REFERENCE: 1110-209P
CURRENT APPLICATION NUMBER: US/09/180,437
CURRENT FILING DATE: 1998-11-06
EARLIER FILING DATE: 1998-03-09
EARLIER FILING DATE: 1998-03-09
EARLIER FILING DATE: 1997-03-07
NUMBER OF SEQ ID NOS: 289
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 52
LENGTH: 20
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APPLICANT: FUNCISARO, Shioji
APPLICANT: MOSISAMA, Takeshi
TITLE OF INVENTION: Antisense Compounds to CD14
FILE REFERENCE: 1110-209P
CURRENT APPLICATION NUMBER: US/09/180,437
CURRENT FILING DATE: 1998-11-06
EARLIER APPLICATION NUMBER: PCT/JD98/00953
EARLIER PILING DATE: 1998-03-09
EARLIER FILING DATE: 1997-03-07
NUMBER OF SEQ ID NOS: 289
SOFTWARE: PATENTIN VET: 2.0
                                                                                      Score 12.8; DB 4;
Pred. No. 6.1e+02;
                                                                                                                               0; Mismatches
; OTHER INFORMATION: acid, synthetic DNA US-09-180-437-51
                                                                                                                                                                                                                                                                                                                         Sequence 52, Application US/09180437 Patent No. 6251873
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                                                                                      64.0%;
87.5%;
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Best Local Similarity 87.5%;
Matches 14; Conservative
                                                                                                        Best Local Similarity 87.8
Matches 14; Conservative
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                                                                                      Query Match
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Gaps

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COUNTRY: Canada
ZIP: M5G 1R7
           GENERAL INFORMATION:
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                               APPLICANT:
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PREARL NO. 6007990
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Levine, Robert A.
APPLICANT: Wardlaw, Stephen C.
TITLE OF INVENTION: Detection and Quantification of One or
TITLE OF INVENTION: More Nucleotide Sequence Target Analytes in a Sample Using
PREARL NO. 6007990
PITLE OF INVENTION: Spatially Localized Target Analyte Replication
FILE REFERENCE: UFB-001
CURRENT APPLICATION NUMBER: US/08/841,267C
CURRENT PILIG DATE: 1997-04-29
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 15
SEQ ID NO 15
LENGTH: 40
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LOCATION: 1..38
OTHER INFORMATION: /note= "Oligonucleotide for PCR
OTHER INFORMATION: amplification of the 3' end of the Hspl50 gene."
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Pred. No. 1.2e+03;
0; Mismatches 3; Indels
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411356.0
FILLING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/01317
FILING DATE: 07-JUN-1995
ATORNEY/AGRAT INFORMATION:
TELEPHONE: (610) 878 4073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 878 421
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 DASSE PAIRS
TELENGTH: 38 DASSE PAIRS
TELENGTH: 38 DASSE PAIRS
TENGTH: 38 DASSE PAIRS
TYPE: nucleic acid
STRANDEDNESS: Single
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US-08-472-171-46
: Sequence 46, Application US/08472171
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82.4%;
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Best Local Similarity 82.4
Matches 14; Conservative
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Best Local Similarity 82.4
Matches 14; Conservative
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: virus HBV
US-08-841-267-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-841-267-15
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Sequence 46, Application US/08894526

Patent No. 594248

GENERAL INFORMATION:
APPLICANT: Locosmore, Sheena M
APPLICANT: Zealey, Gavin R
APPLICANT: Zealey, Gavin R
TITLE OF INVENTION: EXPRESSION OF GENE PRODUCTS FROM
TITLE OF INVENTION: GENETICALLY MANIPULATED STRAINS OF BORDETELLA
NUMBER OF SEQUENCES: 57
CORRESPONDENCES 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
              APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Lealey, Gavin R.
TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
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                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,171
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/393,334
FILING DATE: 23-FEB-1995
ATPORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I:
NAME: Stewart, Michael I:
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-507 MIS:vg
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Pred. No. 1.2e+03;
0; Mismatches 3;
                                                                                                                                    NUMBER OF SEQUENCES: 56
CORRESPONDENCE S.S.
ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, Suite 701
STRATE: Toronto
STRATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
MSG 1R7
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Loosmore, Sheena M.
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82.4%;
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TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 4
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LENGTH: 50 base pairs
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STRANDEDNESS: single
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Gaps
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APPLICANT: Yacoob, Reza K.
APPLICANT: Yacoob, Reza K.
APPLICANT: Yacoob, Reza K.
APPLICANT: Yacoob, Gavin R.
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Expression Of Gene Products From
TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
CITY: Toronto
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Pred. No. 1.2e+03;
0; Mismatches 3; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/374,597
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Pred. No. 1.2e+03;
0; Mismatches 3;
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/393,334
APPLICATION NUMBER: 08/393,334
FILING DATE: FEBRUARY 23, 1995
CLASSIFICATION:
NAME: STEWATION:
NAME: SLEWATI, MIChael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038-964
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 146-595-1155
TELECOMMUNICATION 16-595-1155
TELECOMMUNICATION 16-595-1163
TELEEXX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 46, Application US/09374597; Patent No. 6140082; GENERAL INFORMATION:
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82.4%;
                     TELEFAX: 416-595-1163
TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 46
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 82.4%;
Matches 14; Conservative
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LENGTH: 50 base pairs
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Best Local Similarity 82.4
Matches 14; Conservative
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US-09-374-597-46
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ZIP: M5G 1R7
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  TELEPHONE:
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US-09-013-047-46
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APPLICANT: Locance, Sheena M.
APPLICANT: Zealey, Gavin R.
APPLICANT: Zealey, Gavin R.
APPLICANT: AICHIN, Michel H.
TITLE OF INVENTION: Expression Of Gene Products From
TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
NUMBER OF SOUBNCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
CITY: Toronto
STATE: Ontario
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       COMPUTER REALMABLE FURM:
MEDDIUM TYPE: FIDOPP disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,526
FILING DATE: 01-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 1038-724 MIS:jb
TELECOMMUNICATION NUMBER: 1038-724 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPAX: (416) 595-1163
INFORMATION FOR SED ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,047
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12.2; DB 2;
Pred. No. 1.2e+03;
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REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-507 MIS:vg
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,171
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 46, Application US/09013047 Patent No. 5998168 GENERAL INFORMATION:
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82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 23-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 61.0°
Best Local Similarity 82.4°
Matches 14; Conservative
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-894-526-46
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Query Match 60.0%; Score 12; DB 1; Length 20; Best Local Similarity 75.0%; Pred. No. 1.5e+03; Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps

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Search completed: October 2, 2001, 16:03:45 Job time: 14589 sec

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c-fos target D3 ribozyme

Human IL4Ralpha ge

Primer #60.

Cyclin D3

Polymorphic fragme

NANBH PCR primer P Primer for amplify Primer for HBV pX Complementary stra Allele-specific PC Probe for alkaline Alkaline protease Human clone cg4492 Human GPC4 exon 2

HGF nucleic acid l Integrin alpha 6 s Oligo #5 for site-

Human PRO1434 (UNQ Forward primer for PCR primer 34387.t

Phanerochaete sord nodosus proteas

PCR primer for C. PRO240 probe #2.

Bacillus lichenifo Nucleotide sequenc Permutein linker e

Porphorymonas ging Oligonucleotide Kb HIF-lalpha gene am TnI gene forward p

Human troponin I f Human troponin I g Mouse CGRP recepto

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New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human focal adhesion kinase antisense sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV32360
AAX25907
                                          AAF69762
AAA04651
AAQ25255
AAT07272
AAV08311
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AAA51273
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AAA60931
AAZ43239
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AAT30041
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AAV07603
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AAT34327
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AAZ00590
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AAA21515
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AAX91843
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                AAA84390
                               AAF74126
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 99US-0377310.
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 (ISIS-) ISIS PHARM INC
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 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-AUG-1999;
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Monia BP,
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 RESULT
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Human gene single
Mass spectrometric
Oligonucleotide SC
Nucleotide Sequenc
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Human AML-1 limiti
Human leukaemia br
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Human focal adhesi
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14.320 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                    **Sinssy_godata/geneseq_geneseq_n/Nal980.DAT:*

**Sinssy_godata/geneseq_geneseq_n/Nal981.DAT:*

**Sinssy_godata/geneseq_geneseq_n/Nal981.DAT:*

**Sinssy_godata/geneseq_geneseq_n/Nal981.DAT:*

**Sinssy_godata/geneseq_geneseq_n/Nal981.DAT:*

**Sinssy_godata/geneseq_geneseq_n/Nal981.DAT:*

**Sinssy_godata/geneseq_geneseq_n/Nal981.DAT:*

**Sinssy_godata/geneseq_geneseq_n/Nal981.DAT:*

**Sinssy_godata/geneseq_geneseq_n/Nal981.DAT:*

**Sinssy_godata/geneseq_geneseq_n/Nal981.DAT:*

**Sinssy_godata/geneseq_geneseq_n/Nal991.DAT:*

**Sinssy_godata/geneseq_geneseq_n/Nal991.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS8/gcgdata/geneseq/geneseqn/NA2001.DAT:*
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                             730101 seqs, 313950809 residues
                                                                                                    •-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                 2001, 16:18:33
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                                                                       OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT87270
AAT87201
AAT09720
AAV09351
AAF95308
AAZ436074
AAV36074
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AAC65556
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 50
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Perfect score:
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AAT87270 standard; RNA; 40 BP.
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                                                          The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, anglogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in cancer, particularly colon, breast and oral tumours, embryonic development disorders, anglogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothloate; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 20; 0.66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human focal adhesion kinase antisense sequence #22.
                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 5 A; 5 C; 9 G; 1 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 20; 100.0%; Pred. No.
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Claim 3; Column 23; 30pp; English.
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of SEREX (Systematic Evolution of Ligands obtained after 17 rounds of SEREX (Systematic Evolution of Ligands by Exponential enrichment). The Sequences were analysed for conserved sequences and aligned by this criterion. The 2'F sequences fell into a single group with 12 orphan sequences. 2'NH2 sequences fell into 2 distinct groups. Group 1 were shown to bind to Lize and were identified by the presence of a direct repeat of the sequence GGAGG. A single orphan 2'NH2 sequence was also found. The 2'F/NH2 sequences fell into 3 groups, of which one group bound to nitrocellulose filters. Nucleic acid (NA) ligands to a cytokine can be identified using SELEX. A candidate mixture of NA's are contacted with a cytokine where the NA's having an increased affinity to the cytokine relative to the candidate mixture may be partitioned from the cytokine relative to the candidate mixture may be partitioned from the cytokine relative to the candidate mixture may be partitioned from the cytokine relative of NA's with increased affinity are amplified to yield a mixture of NA's enriched for the NA sequences and relatively higher affinity and selectivity for binding to the cytokine. The NA is a considered or the cytokine where the NA's enriched for the NA sequences and relatively higher affinity and selectivity for binding to the cytokine. The NA is a considered to the cytokine where the NA is a considered and relatively higher affinity and selectivity for binding to the cytokine. The NA is a considered to the cytokine in the NA is a considered to the cytokine. The NA is a considered to the cytokine to the cytokine. The NA is a considered to the cytokine to the cytokine.
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                                                                                                                                                            high affinity ligand; cytokine; interferon-gamma; IFN-gamma; RANTES; interleukin-4; LL-4; tumour necrosis factor-alpha; TNF-alpha; Systematic Evolution of Ligands by Exponential enrichment; SELEX; diagnosis; inflammatory response; septic shock; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/note= "all U's are 2'-NH2 modified and all C's are
2'-F modified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SELEX
                                                                                                                IL-4 2'F/NH2 RNA ligand, nitrocellulose filter binding clone #21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identification of nucleic acid ligands that bind cytokine(s) partitioning the ligands from a nucleic acid mixture, using ?
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                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gold L, Jayasena S, Pagratis N,
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                                                                    16-NOV-1997 (first entry)
                                                                                                                                                                                                                                                              graft-vs-host reaction; ss
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/*tag=
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modified_base
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Gaps

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0; Indels

0; Mismatches

Conservative

Best Local Similarity Matches 15; Conserve

Query Match

75.0%; Score 15; DB 22; Length 15; 100.0%; Pred. No. 1.6e+02;

to prevent or treat diseases or medical conditions in human patients, e.g. associated with excessive cytokine production such as inflammatory responses mediated by IFN-agamma or interleukin-4, septic shock, arthritis or graft-vs-host reactions mediated by tumour necrosis

Sequence 40 BP; 12 A; 5 C; 18 G; 5 U; 0 other;

factor-alpha

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AAT87178-276 are interleukin (IL)-4 RNA ligands obtained after 17 rounds of SELEX (Systematic Evolution of Ligands by Exponential enrichment). The sequences were analysed for conserved sequences and aligned by this criterion. The 2'F sequences fell into a single group with 12 orphan sequences. 2'NH2 sequences fell into 2 distinct groups. Group were shown to bind to introcellulose filters and were identified by the presence of a direct repeat of the sequence GGAGG. A single orphan 2'NH2 sequence was also found. The 2'F/NH2 sequences fell into 3 groups, of which one group found. The 2'F/NH2 sequences fell into 3 groups, of which one group can be identified using SELEX. A candidate mixture of NA's are contacted with a cytokine where the NA's having an increased affinity to the cytokine relative to the candidate mixture may be partitioned from the cytokine relative to the candidate mixture may be partitioned from the rest of the mixture. The NA's with increased affinity are amplified to yield a mixture of NA's enriched for the NA's equences and relatively higher affinity and selectivity for binding to the cytokine. The NA ligands are useful in diagnostic and therapeutic applications especially
                                                                                       ö
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                             high affinity ligand; cytokine; interferon-gamma; IFN-gamma; RANTES;
                                                                                                                                                                                                                                                                                                                                                                                                            interleukin-4; IL-4; tumour necrosis factor-alpha; TNF-alpha;
Systematic Evolution of Ligands by Exponential enrichment; SELEX;
diagnosis; inflammatory response; septic shock; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identification of nucleic acid ligands that bind cytokine(s) - by
partitioning the ligands from a nucleic acid mixture, using SELEX
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0
                                                    Length 40;
                                                                                       Indels
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/note= "all pyrimidines are 2'-F"
                                                Score 14.2; DB 18;
Pred. No. 4.1e+02;
1; Mismatches 3;
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Sequence 40 BP; 12 A; 5 C; 18 G; 5 U; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Page 65; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pagratis N,
                                                                                                                                                                                                                                                AAT87201 standard; RNA; 40 BP
                                                  71.0%;
78.9%;
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                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                     Conservative
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                                                Query Match
Best Local Similarity
Matches 15; Conserv
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                                     Gaps
                                                                                                                                                                                                                                                                                                       Polymerase chain reaction; amplification; non-specific priming; blocking oligonucleotide; donor; acceptor; fluorophore; energy transfer; ligation; AML-1; acute myeloid leukaemia; breakpoint related sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amplification process could be monitored using either a primer:
blocking oligonucleotide duplex or a universal detection duplex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting target nucleic acid by amplification - with primer-blocking oligo:nucleotide duplex(es) labelled with donor and acceptor fluorophore(s), to reduce non-specific priming
 Length 40;
                                                                                                                                                                                                                                                                            Human AML-1 limiting primer, for asymmetric amplification.
                                 Indels
71.0%; Score 14.2; DB 18; 78.9%; Pred. No. 4.1e+02; ive 1; Mismatches 3;
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                                                                                            5 gcgccaugaagcaaaggga 23
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                                   Conservative
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Query Match
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Matches 15; Conserv
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66.0%; Score 13.2; DB 17; Length 21;

Query Match

Sequence 21 BP; 2 A; 6 C; 11 G; 2 T; 0 other;

BP.

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energy transfer; polymerase; primer; acute myeloid leukaemia; AML-1; ss.
                                                                                                                                               Target; DNA duplex; donor; acceptor; fluorescent label; fluorophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kits for detecting target nucleic acids - and DNA duplexes with donor and acceptor fluorescent labels
                                                                                                               Limiting primer used for detecting target nucleic acid AML-1.
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                AAV09361 standard; DNA; 21
                                                                               15-MAY-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                       26-MAY-1994;
16-DEC-1991;
04-MAY-1995;
                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                           04-MAY-1995;
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                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang CJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       In an example to demonstrate the application of a detection duplex the monitor the asymmetric amplification of target nucleic acids, the monitor the asymmetric amplification of target nucleic acids, the human acute myeloid leukaemia breakpoint related sequence (AMP-1), and the human x chromsome specific ameloginen (AMG-X) were used as amplification targets. The sequences of the primers used for AML-1 and AMG-X respectively were AMT4549 and AAT45480, the duplex comprised AAT45481 and AAT45482 and the sequences of excess and limiting primers for AML-1 and AMG-X respectively were AAT45483 and AAT454848. The respectively were AAT45483 and AAT45484 and AAT45485 and AAT45486. Male human genomic DNA sequences were asymmetrically amplified with excess primer for compiled from detection at cycle 30 demonstrated the quantitative resolution and detection sensitivity by the duplex. The decrease in fluorescence intensity reflected the initial target doses.
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid detection by amplification - in presence of primer-complementary oligo:nucleotide to block non-specific priming
                                                                                                                                                                                                                                                                                                      Detection duplex, asymmetric amplification; human; acute; myeloid; leukaemla; breakpoint; related sequence; AMP-1; X chromosome; specific ameloginen; AMG-X; primer; excess; limiting; ss.
                               ö
                                                                                                                                                                                                                                                                        Human leukaemia breakpoint related sequence, limiting primer.
                               Indels
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21 BP; 2 A; 6 C; 11 G; 2 T; 0 other;
                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Column 12; 17pp; English
                                                                                                                                                                              BP.
             83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-0808463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94US-0250849
91US-0808463
                                                                                                                                                                           AAT45484 standard; DNA; 21
                                                             2 gcgccgtgaagcgaaggc 19
                                                                                             1 gcggcgtgaagcggcggc 18
                                                                                                                                                                                                                                          (first entry)
              Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BIOT-) BIOTRONICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-010704/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wu K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAY-1994;
16-DEC-1991;
                                                                                                                                                                                                                                          02-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                   US5567583-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                          AAT45484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang CJ,
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94US-0250849. 91US-0808463. 95US-0434474.

Wu K;

95US-0434474

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This is a limiting primer used in a kit for detecting a target nucleic acid of human acute myeloid leukaemia breakpoint related sequence (and of human acute myeloid leukaemia breakpoint related sequence (capalle of acting as a primer, with or without a segment noncontiguous to its priming sequence, for use with a polymerase in the amplification of a target nucleic acid, a second oligonucleotide which is hybridised, via the first oligonucleotide, the second oligonucleotide pairings, with the first oligonucleotide, the second oligonucleotide pairings, with the first oligonucleotide, the second oligonucleotide and a second fluorophore covalently attached to the first oligonucleotide, with one of the two fluorophores of being a donor fluorophore and the other being an acceptor fluorophore covalently attached to the second oligonucleotide, with one of the two fluorophores of that when the two fluorophores are in close proximity resonance energy transfer between them is allowed. Each of the first oligonucleotide contains 10-50 nucleotides. Another kit claimed comprises a first and second primer both optionally having a tespectively, which are used with a polymerase for the amplification of the target nucleic acid and an oligonucleotide which is incapable of acting as a primer for the polymerase for the amplification of the first primer. Each of the first oligonucleotide contains 10-50 nucleotide being incapable of acting as a primer for the polymerase on that is incapable of acting as a primer for the polymerase and has at least 5 consecutive nucleotides contains 10-50 nucleotide being incapable of target nucleic acid comprises a first oligonucleotide being incapable of acting as a primer for the polymerase and has at least 5 consecutive nucleotides of the first oligonucleotide soft and containing 10-50 nucleotides with a second plinaer and the first oligonucleotide soft acting as a primer for use with a polymerase of the manual and polymerase of hybridizing, via at least 5 consecutive fluorophore covalently attached
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleotides, and the first and second fluorophores, one of which is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proximity when the first oligonucleotide hybridises to the second oligonucleotide to allow resonance energy transfer between them. The kits are used in homogeneous assays in which the target nucleic acid sequence is amplified and the amplified target is detected without
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Gaps

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66.0%; Score 13.2; DB 18; Length 21; 83.3%; Pred. No. 1.2e+03; Live 0; Mismatches 3; Indels (

1 gcggcgtgaagcggcggc 18

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RESULT AAV09361

2 gcgccgtgaagcgaaggc 19

Conservative

Query Match Best Local Similarity Matches 15; Conserv

Gaps

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Length 21;

Score 12.8; DB 22; Pred. No. 1.9e+03; 0; Mismatches 2;

64.0%; 87.5%;

Conservative

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Similarity
                                           Query Match
Best Local S
Matches 14,
                                                                                                                                                                                                                                                                                                                                    AAZ43694;
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Matches
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                                                                                                                                                                                                                                              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensics, paternity testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of the human gene SNPS shown in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism; pulmonary embolism; paternity test; ds.
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McCarthy JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
replace(11,A)
/*tag= a /*tag= a /standard_name= "single nucleotide polymorphism"
                                                                                                                                                      ;
0
                                                                                                            Length 21;
                                                                                                                                                      Indels
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                                                                                                          Score 13.2; DB 19;
Pred. No. 1.2e+03;
); Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human gene single nucleotide polymorphism #69.
                                       Sequence 21 BP; 2 A; 6 C; 11 G; 2 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21 BP; 7 A; 5 C; 5 G; 4 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Examples; Page 51; 242pp; English.
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                                                                                                                                                                                                                                                                                                                                                        BP.
conducting a separation step.
                                                                                                     66.0%;
ilarity 83.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0153357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0220947.
2000US-0225724.
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                                                                                                                                                                                                                                                                                                                                                      AAF95308 standard; DNA; 21
                                                                                                                                                                                                2 gcgccgtgaagcgaaggc 19
                                                                                                                                                                                                                                         1 geggegtgaageggegge 18
                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gargill M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-226749/23.
                                                                                                          Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-2000;
16-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                  AAF95308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Variation
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                                                                                                                                                                                                                                                                                                                                 AAF95308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified amplification products by mass spectrometry and assigning the masses to wild type or mutant. AAZ43691-Z43717 represent primers used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 known genetic mutations, using modified nucleoside triphosphates to improve the performance. The method compiless: (1) amplifying a DNA sequence by polymerase chain reaction (PCR) using primers selected to amplify a sequence containing the mutation; (2) adding a particular set of modified nucleoside triphosphates (NTPS) to effect innited extension of already present or newly added primers, where: (a) the extension reaction stops at the next occurrence of a particular base in the DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 strand being copied; (b) the extension reaction proceeds up to or past the mutation site, so that wild-type amplification products will have a different molecular weight from mutant amplification products; and (c) the modification of the NTPs results in stabilization of the DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a method for mass-spectrometric analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer; mass-spectrometry; genetic mutation; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mass-spectrometric analysis of known gene mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mass spectrometric mutation analysis primer 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 33 BP; 6 A; 11 C; 11 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BRUK-) BRUKER DALTONIK GMBH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98DE-1024280.
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                                                                                                                                                                                                                                                        AAZ43694 standard; DNA; 33
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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5 ccgtgaagcgaaggca 20
                                                                  ccgtgaagcgaatgaa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Page 8; 16pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-073581/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DE19824280-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                            23-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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Bergstrom DE;

99US-0125251.

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Coupled polymerase chain reaction-restriction endonuclease digestion-ligase detection reaction to identify low abundance sequences differing by single-base changes, insertion or deletion from high
                                                                                                                                                                                                                                                                                                                      abundance sequence in target sequences
                                                                                                                                                                                                         Barany F, Day JP, Hammer RP,
                                                                                                                                        (CORR ) CORNELL RES FOUND INC (LOUU ) UNIV LOUISIANA STATE. (PURD ) PURDUE RES FOUND.
                                                                           17-MAR-2000; 2000WO-US07133.
                                                                                                                                                                                                                                      WPI; 2000-638269/61.
               WO200056929-A2
                                                                                                          19-MAR-1999;
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                                             28-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The specification describes a new regulatory sequence for Trichoderma Villed detaived cellulase cbhl gene and the establishment of a system for mass producing cellulase in moulds such as T. viride. As the regulatory sequence of cbhl genes originating in T. viride can highly express objective proteins, proteins such as cellulase can be expressed. An expression vector containing the regulatory sequence and Hunicola insolens derived endo-glucanase NCE4 DNA was produced, and used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coupled polymerase chain reaction; PCR; ligase detection reaction; LDR; restriction endonuclease digestion; RED; infectious disease; cancer; waste water purification; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotides AAV36074-75 are used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence for Trichoderma viride derived cellulase cbhl producing Humicola insolens derived endo-glucanase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.0%; Score 12.6; DB 19; Length 36; 78.9%; Pred. No. 2.4e+03; ive 0; Mismatches 4; Indels
                                                                                                                                                                                       Regulatory sequence; cellulase cbhl gene; mass production;
Humicola insolens; endo-glucanase NCE4; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                Watanabe
                                                                                                                                                       Oligonucleotide SCE3-Stu of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36 BP; 4 A; 11 C; 12 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of a synthetic duplex DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                Sumida N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endo-glucanase at 15 grams per litre.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 11; Page 29; 92pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                Moriya T, Murakami T,
                                                                                                                                                                                                                                                                                                                                                                                               (MEIJ ) MEIJI SEIKA KAISHA LTD.
                                                            AAV36074 standard; DNA; 36 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA96608 standard; DNA; 50 BP
                                                                                                                                                                                                                                                                                                                                   97WO-JP03268.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-250959/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                    WO9811239-A1
                                                                                                                                                                                                                                                                                                                                 16-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                 13-SEP-1996;
                                                                                                                        02-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Regulatory
                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                               Aoyagi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                          AAV36074;
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                            RESULT 10
AAV36074/C
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The specification describes the use of coupled polymerase chain reaction (PCR), restriction endonuclease digestion (RED) and ligase detection reaction (LDR) to identify one or more low abundance sequences differing by one or more single base changes, inserts or deletions, from a high abundance sequence, in several target nucleotide sequences. The method involves 3 PCR reaction phases, a RED phase and an LDR phase. The method is used to identify one or more low abundance sequences. The method is also useful for detecting a wide variety of infectious diseases caused by acterial, viral, viral, parasite and fungal infectious agent. Cancers can also be detected by this method. The method is also used for detection, identification and monitoring of pathogenic and indigenous municipal waste water purification system and water reservoirs or in polluted areas undergoing bioremediation and to detect plasmids containing genes that can metabolise xenoblotics, to monitor specific target microorganisms in population dynamic studies, or either to detect, identify, or monitor specific target microorganisms in the environment and in industrial plants. The present sequence represents a synthetic duplex DNA template, used in
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cancer; oncogene; leukaemia; neuroblastoma; diagnosis; genetic drift;
mutation; diseased cell; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human c-fos target sequence nucleotide position 97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 12.6; DB 21;
Pred. No. 2.4e+03;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 50 BP; 11 A; 18 C; 12 G; 9 T; 0 other;
Example 7; Fig 6A; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the course of the invention,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV95266/c
ID AAV95266 standard; RNA; 17
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Best Local Similarity 78.9
Matches 15; Conservative
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Sequence 20 BP; 2 A; 8 C; 3 G; 7 T; 0 other;
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                                                                                                                                                                                                            gccgtgaagcgaaggca 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression of the protein
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duda A,
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                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               WO200109161-A1.
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JUL-1999;
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                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                            Primer #60.
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# # X & X O O O O O O O O X & Q
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                                                                                                                                                                                      The present invention describes an enzymatic nucleic acid molecule which specifically cleaves RNA derived from a c-fos gene. AAV95401 to AAV95540 and AAV95541 to AAV95584 represent hammerhead ribozymes and hairpin
                                                                                                                                                                                                                  ribozymes, respectively, which specifically cleave human c-fos. AAV95261 to AAV95400 and AAV95385 to AAV95628 represent human c-fos target sequences. The enzymatic nucleic acid molecules can be used for treating cancer associated with elevated levels of c-fos oncogene, especially leukaemias, neuroblastomas and lung, breast and colon cancers. The ribozymes may also be used as diagnostic tools to examine genetic drift and mutations within diseased cells, or to detect the presence of c-fos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                           Enzymatic nucleic acid molecules which specifically cleave RNA derived from a c-fos gene - useful for treating conditions related to levels of c-fos, especially cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hammerhead; gene therapy; vasotropic;
                                                                                                                                                                                                                                                                                                                                          Score 12.2; DB 19;
Pred. No. 3.6e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                            Sequence 17 BP; 2 A; 8 C; 3 G; 4 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Robbins JM;
                                                                                       DT;
                                                                                       McSwiggen JA, Stinchcomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyclin D3 ribozyme binding site #1.
                                                                                                                                                                    English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                          61.0%;
82.4%;
                            98WO-US01017
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                                              97US-0037658
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                                                                  (RIBO-) RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 82.4
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   17 GGCGCTGTGAAGCAGAG 1
                                                                                                                                                                   Claim 2; Page 50; 72pp;
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                                                                                                          WPI; 1998-427942/36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-412314/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribozyme; hairpin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              restenosis; ss.
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                                                                                                                                                                                                                                                                                          RNA in a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-DEC-1999;
                            20-JAN-1998;
                                               23-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-DEC-1998;
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         30-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tritz R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia
                                                                                       Jarvis
                                                                                                                                                                                                                                                                                                                                                                                                                                  13
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The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.

Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention is used in producing a recombinant organism that can be used to express SLG6A4 for protein structure analysis and binding studies. A composition comprising a genotyping oligonucleotide is used to detect a polymorphism in the SLG6A4 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide comprising a polymorphic variant for the solute carrier family 6 neurotransmitter transporter, serotonin member 4 gene for identifying drugs for treating disorders related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a polymorphic variant of a reference sequence for the solute carrier family 6 neurotransmitter transporter, serotonin member 4 (SLC6A4) gene or a fragment of it
RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1, PCNA and Cyclin B1 ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sectonin 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or a sequence complementary to the first sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 12.2; DB 21;
Pred. No. 3.6e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19 BP; 3 A; 4 C; 7 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                 English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 37; 152pp; English.
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                                                                                                          Disclosure; Page 76; 109pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.0%;
82.4%;
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ID AAF74126 standard; DNA; 20
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                                   Gaps
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                                                                                                                                                                                                                                                                                                                               Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha; allergic disease; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide useful for the identification of therapeutics in allergic diseases is new -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 12.2; DB 22; Length 22; Pred. No. 3.7e+03; 0; Mismatches 3; Indels (
Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
Windemuth AK;
                                   Indels
 DB 22;
Score 12.2; DB 22;
Pred. No. 3.6e+03;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                               Human IL4Ralpha gene PCR primer #98.
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                                                                                                                                                                                          AAF69762 standard; DNA; 22 BP.
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82.4%;
Query Match 61.0%;
Best Local Similarity 82.4%;
Matches 14; Conservative
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                                                                    4 gccgtgaagcgaaggca 20
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Best Local Similarity 82.4
Matches 14; Conservative
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AAF69762
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PCR primer used to
M. tuberculosis 16
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PCR primer for the
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Yeast acyltransfer
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Chicken IgG light
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smegmatis 16S r
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PCR primer for DNA
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Mycobacteria 16S 1
                                                 PCR primer for t
Primer murF2. S
PCR primer used
                                                                                      Primer murF4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human focal adhesion kinase antisense sequence #1.
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                                                            AAT63364
AAX86099
AAT63369
AAX86104
                                    AAA29338
AAZ10873
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AAT92997
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  99US-0377310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC65535 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monia BP, Gaarde WA;
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 Homo sapiens
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AAC65535;
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PCR primer for DNA
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Primer for ribonuc
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PCR primer used to
Polymorphic fragme
3' PCR primer used
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                                                                                               (without alignments)
14.320 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AAC83406
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The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, anglogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; focal adhesion kinase; FAK; signal transduction; cancer;
embryonic development disorder; angiogenic disorder; wound healing;
antisense; phosphorothioate; ss.
                                                                                                                                                                                                                            DB 22; Length 20;
                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human focal adhesion kinase antisense sequence #21
                                                                                                                                                                                                                            100.0%; Score 20; DB 22
100.0%; Pred. No. 0.55;
                                                                                                                                                                         Sequence 20 BP; 2 A; 7 C; 8 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 BP; 2 A; 4 C; 7 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                Mismatches
Claim 3; Column 23; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Column 25; 30pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                        AAC65555 standard; DNA; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                      treatment of all of these.
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treatment of all of these.
                                                                                                                                                                                                                                                             20; Conservative
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Best Local Similarity
Matches 20; Conserv
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Acyl-CoA:cholesterol acyltransferase; ACAT; ACAT-like protein; sterol; ester; triacylglycerol; fatty acyl-CoA; lipid composition; plant cell; diacylglycerol acyltransferase; DAGAT; triglyceride; cancer; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a translational reporter vector selected from p2luc and p2luci. The vectors have a polylinker interposed between a renilla luciferase gene and a firefly luciferase gene, which are out-of-frame with respect to each other but are co-expressed upon recoding. The translational reporter vector is useful for assaying translational recoding in vitro or in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Translational reporter vector for quantification of translation recoding in vivo and in vitro, comprises renilla luciferase gene, polylinker for insertion of selected DNA and an out-of-frame firefly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 31;
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                                                                                                                                                                                                         Translational reporter vector; renilla luciferase; translational recoding; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primer used to amplify the rat ACAT-like gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.0%; Score 13.8; DB 22;
88.2%; Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31 BP; 4 A; 10 C; 9 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  Gesteland RF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Column 33; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                            AAC83406 standard; DNA; 31 BP.
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                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2000 (first entry)
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              geggeteacagtgg 17
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                                                                                                                                                                               Oligonucleotide sfAZ2
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Best Local Similarity
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Length 15;

75.0%; Score 15; DB 22; I ilarity, 100.0%; Pred. No. 1.5e+02; Conservative 0; Mismatches 0;

Query Match Best Local Similarity Matches 15; Conserv

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WPI; 2000-107928/10.
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                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         per primers AA245392-93 were used to amplify rat acyl-CoA:cholesterol acyltransferase (ACAT)-like gene. The ACAT-like protein is active in the formation of a sterol, ester and/or triacylylycerol from a fatty acyl-CoA and sterol and/or diacylglycerol substrate. The DNA can be used for modifying the lipid composition of plant cells. The ACAT-like protein has diacylglycerol acyltransferase (DAGAT) activity, and so the synthesis of triglycerides can be suppressed or increased using the DNA. The protein can be used to produce plant oils with a modified triglyceride content. The products can also be used to identify antagonists and agonists of badAT activity. Such agonists and antagonists are particularly useful in treating or ameliorating diseases associated with DACAT activity, including concentration or PKC activity, including cancer, diabetes, concentration or PKC activity, including cancer, diabetes, cardiopulmonary diseases e.g. heart failure, atherosclerosis, adisorders, obesity, diseases associated with abnormal lipid metabolism, and diseases associated with abnormal fat absorption,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotides used for modifying plant oil composition and for developing products for treating e.g. cancer, diabetes, cardiopulmonary disease or metabolic disorders
cardiopulmonary disease; heart failure; atherosclerosis; adipocytosis; leukaemia; skin carcinoma; fibroblastoma; metabolic disorder; obesity; abnormal lipid metabolism; abnormal fat absorption; lipoprotein secretion; adipogenesis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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80.0%; Pred. No. 7.2e+02;
ive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 41 BP; 7 A; 13 C; 19 G; 2 T; 0 other;
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98US-0108389
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Best Local Similarity 80.0
Matches 16; Conservative
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12-NOV-1998;
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                                                                                                                                        Rattus sp.
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The invention provides polymorphic fragments of genes associated with hypertension. The nucleic acids including the polymorphic sites can be used as probes or primers for expressing variant proteins. Detection of the polymorphisms is useful in designing prophylactic and therapeutic regimes customized to underlying abnormalities. The polymorphisms can be used for association studies for hypertension, and in hypertension within a gene, they are likely to have a causative role in hypertension. This information can be used to find the precise role of a polymorphism in the disease. The polymorphisms can be tested for association with other disease. The polymorphisms can be tested for association with other diseases e.g. agammaglobulinemia, diabetes insipilus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabrys disease, familial hypercholestenolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrands disease, tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial colonic polyposis, Enhars-Danlos syndrome, osteogenesis imperfecta, and content intentitent porphyria. The polymorphic forms can also be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
Fabrys disease, familial hypercholesterolemia; hereditary spherocytosis; polycystic kidney disease; von Willebrands disease; forensic; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids containing polymorphisms used in the diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Retroviral vector; gene delivery vehicle; expression; PCR primer; non-immunogenic selectable marker; gene therapy; activation;
                                     polycystic kidney disease; form Willebrands disease; forenic; tuberous sclerosis; hereditary hemorrhagica telangiectasia; familial colonic polyposis; osteogenesis imperfecta; porphyria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.0%; Score 13.2; DB 21; Length 29; 75.0%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3' PCR primer used to amplify human furin cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 29 BP; 6 A; 5 C; 13 G; 4 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haluska MK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYCA-) UNIV CASE WESTERN RESERVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 forensics to identify individuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 33; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV42721 standard; DNA; 31 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99EP-0250150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0084641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0304232
                                                                                                                                                                    Ehlers-Danlos syndrome; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 cagcgrgcagacagtggttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 75.09
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ccgcgggctcacagtggtcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an JB, Chakravarti A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AFFY-) AFFYMETRIX INC
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membrane

Van Eenennaam A;

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The invention relates to nucleic acids encoding novel plant
acyltransferase-like proteins (AAA37343-A37445) which comprise one of
acyltransferase motifs (AAA9344-Y99481). Acyltransferases
conserved acyltransferase motifs (AAY9944-Y99481). Acyltransferases
catalyse the transfer of acyl groups from an open avriety of
substrates such as glycerides, sterols, stanols and phosphatides.
Characteristics of the plant. For example, cold-hardened plants have
different lipid concentrations in the cell membrane compared to
non-hardened plants, which makes the membrane more fluid and the plant
mon-hardened plants, which makes the membrane sequences of the
invention can be used as probes or for expressing acyltransferase-like
proteins in host cells e.g., for recombinant protein production. They
may be expressed in plant cells to alter the lipid composition of the
primers used in an exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNAs (AAA37331-A37342) for cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prenyltransferase; ATPT1; ATPT2; ATPT4; ATPT4; ATPT5; ATPT6; ATPT7; ATPF8 ATPT9; ATPT8 ATPT1; ATPT12; tocopherol; homogentisic acid; phytylpyrophosphate; 2-methyl-6phytylbenzoquinol; antioxidant; nutritional supplement; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCR primer for DNA encoding a prenyltransferase designated ATPT8.
                                                                                                                                                                   Novel acyltransferase related proteins useful for altering fluidity in plant cells e.g. to induce chill tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weiss JD, Post-Beittenmiller D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 13.2; DB 21;
Pred. No. 1.1e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    into plant and baculovirus expression constructs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 39 BP; 11 A; 9 C; 12 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana acyltransferase
                                                                                  Ruezinsky DM,
                                                                                                                                                                                                                            Example 7; Page 31; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.0%;
    98US-0101939.
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99US-0146461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-APR-2000; 2000WO-US10368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ccgcgggctcacagtggt 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccgcggccgcacaatggt 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC61924 standard; DNA; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lassner MW,
                                                                                    Emig RA,
                                                                                                                             WPI; 2000-303447/26.
                                            (CALJ ) CALGENE LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CALJ ) CALGENE LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200063391-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis sp
    25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAR-2001
                                                                                    Lassner MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Savidge B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC61924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC61924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
    δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primers AAV42720-21 were used to amplify human furin cDNA (see AAV42731). The amplified product is used in the retroviral vector of the invention to encode a cell bound prodrug convertase for ablation therapy. The specification describes a gene delivery vehicle which directs expression of a non-immunogenic selectable marker or molecule which is capable of activating a previously inactive compound. Vectors expressing the markers and a heterologous sequence are useful in gene therapy. The vectors can be used to deliver a molecule into a target area where it may cause the activation of a previously inactive substance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana acyltransferase ATAT7 PCR primer, SEQ ID NO:173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Non:immunogenic pro:drug activating enzyme(s) and selectable marker(s) - are used in gene therapy for the treatment of a wide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.0%; Score 13.2; DB 19; Length 31; 83.3%; Pred. No. 1.1e+03; ive 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acyltransferase; lipid synthesis; recombinant expression; membrane fluidity; cold resistance; transgenic plant; baculovirus expression; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31 BP; 5 A; 12 C; 10 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 8; Page 53; 121pp; English
human; furin; ablation therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                           Moore MD
                                                                                                                                                                                                                            98US-0038339.
97US-0035473.
97US-0038339.
                                                                                                                                                                                      98WO-US00715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US22231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            geggeteacagtggteg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 gtgggctcacagagggcg 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA37483 standard; DNA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          variety of disorder(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                         Chada S, Jolly DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-399153/34
                                                                                                                                                                                                                                                                                                             (CHAD/) CHADA S.
(JOLL/) JOLLY D J.
(MOOR/) MOORE M D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200018889-A2
                                                                                                                                                                                                                                                                                                           (CHAD/) CHADA
                                                                                                                                                                                                                            13-JAN-1998;
14-JAN-1997;
27-FEB-1997;
                                                             Homo sapiens
                                                                                                   WO9830709-A2
                                                                                                                                                                                      14-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-AUG-2000
                                                                                                                                              16-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-APR-2000
                                        Synthetic.
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AAA37483;

AAA37483 RESULT

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Gaps

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Indels

Length 39;

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Oligonucleotides can be used to alter the profile of the blood factor without significantly altering its activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Page 54; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                AAA72106 standard; DNA; 44 BP.
                                                                                                                                        64.0%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JAN-2000; 2000WO-US00456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JAN-1999; 99US-0115404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                       Query Match
Best Local Similarity 87.59
                                                                                                                                                                                                                                    2 cgcgggctcacagtgg 17
                                                                                                                                                                                                                                                                              19 egegtgeteagagtgg 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-465959/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wild CT, Weiss CD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (WILD/) WILD C T.
(WEIS/) WEISS C D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200040616-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA72106;
                                                                                                                                                                                                                                                                                                                                                       10
                                                                                                                                                                                                                                                                                                                                                                          AAA72106
                                                                                                                                                                                                                                                                                                                                                       RESULT
  SS \times S
                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                          PCR primers AAC61924-25 were used to amplify DNA encoding a prenyltransferases designated ArPT1. ATPT2. ATPT3. ATPT3. ATPT5. ATPT6. ATPT7. ATPT7. ATPT8. ATPT9. ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                      to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Factor VIII analogue is sufficiently mutated from the original gene that it is not recognised by blood Abs of the patient. The analogue is composed of human FVIII but carries the B-domain of human FV in place of the FVIII B-domain.
                                                                    sequence encoding prenyltransferase used increase the production of tocopherols -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide carrying mutation for factor VIII gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New hybrid DNA encoding hybrid procoagulant proteins - prepd. by modifying DNA encoding human factor VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 13.2; DB 21;
Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ٠<u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 50 BP; 9 A; 16 C; 14 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.16
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                        Example 2; Page 26; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.0%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89WO-0005049.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human factor VIII analogue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88US-0270882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ04938 standard; DNA; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ccgcgggctcacagtggt 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cegeggeegeaaatggt 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; ; pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENETICS INST INC.
                                                                    An isolated nucleic acid
                                                                                          transform plant cells to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaufman RJ, Pittman DD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                     WPI; 2000-647519/62.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Simi
Matches 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
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The invention relates to raising a neutralising antibody response to a broad spectrum of HIV (human immunodeficiency virus) strains and isolates, comprising the administration of a peptide which corresponds to or mimics highly conserved portions of the gp41 envelope glycoprotein which are important in mediating the process of viral entry into host cells. Such peptides can correspond to or mimic the coiled coil solution structure of the N-helical domain (the heptad repeat region), or can correspond or mimic the C-helical domain (the transmembrane-proximal amphipathic alpha-helical segment), or the gp41 core 6-helical domains of three gp41 proteins. The peptides can be administered either singly or as a combination of N-helical and C-helical peptides), and can be administered either singly or as a combination of N-helical and C-helical domain peptides can be altimized. For example, N- and C-helical domain peptides can be altimized together to form a peptide which mimics the core alternately linked together to form a peptide (s) generates a humoral response, with the production of antibodies against gp41 structures involved in viral entry. As these portions of gp41 are well conserved,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Raising neutralizing antibody response to human immunodeficiency virus, comprises administering a polypeptide capable of forming a stable coiled-coil solution structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV-1; gp41; N-helical domain; heptad repeat region; C-helical domain; gp41 transmembrane-proximal amphipathic alpha-helical segment; core 6-helix buddle; viral entry inhibition; immunogenic; antibody; humoral response, broad spectrum vaccine; anti-HIV; envelope glycoprotein; prophylaxis; therapy; PCR primer; ss.
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                   ö
                                                                                                                                                    Length 39;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                               Score 12.8; DB 11;
Pred. No. 1.8e+03;
0; Mismatches 2;
Sequence 39 BP; 9 A; 11 C; 11 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV-1 gp41 C-helical domain 5' PCR primer.
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Pred. No. 2.2e+03;

78.98;

Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ribonucleotide reductase R1; tumourigenicity modulation; therapy; neoplastic cell; tumour growth; tumour regression; PCR primer; mouse; ss.
such antibodies may be effective against a broad range of HIV strains and isolates. The peptide compositions may be administered as a prophylactic or therapeutic vaccine to generate antibodies which reduce or inhibit the ability of HIV to infect uninfected cells. A composition comprising polyclonal or monoclonal antibodies can be administered to entry-relevant gp41 structures may also be used therapeutically and as tools to further elucidate the mechanism of HIV cell entry. Sequences AAA72104-A72107 represent PCR primers used in an exemplification of the invention to construct DNA (AAA72102) encoding a protein construct (AAB14603) comprising the N- and C-helical domains of HIV-1 gp41 separated by a short peptide linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a PCR primer for the mouse ribonucleotide reductase R1 (RRR1) gene. The gene and the protein it encodes can be used in the methods of the invention for modulating tumourigenicity of neoplastic cells in a mammal. The RRR1 can slow tumour growth and cause tumour regression and reduction of tumourigenicity and metastatic
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of ribonucleotide reductase R - for modulating the tumourigenicity and metastatic potential of neoplastic cells in a mammal, particularly for inhibiting tumour growth
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                                                                                                                                                                                                                                                                           Score 12.8; DB 21; Length 44; Pred. No. 1.8e+03;
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer for ribonucleotide reductase R1 coding sequence.
                                                                                                                                                                                                                           Sequence 44 BP; 13 A; 10 C; 15 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29 BP; 3 A; 11 C; 7 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Page 21; 56pp; English.
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                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 87.5%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV59089 standard; DNA; 29
                                                                                                                                                                                                                                                                                                                                                              cgcgggctcacagtgg 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wright JA, Young AH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-520956/44.
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19-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV59089;
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
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Score 12.6; DB 19; Length 29;

63.0%;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for cancer causitively associated
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                         Sense primer for methylthioadenosine phosphorylase gene exons 5-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sense primer is designed for the PCR amplification of exons
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                                                                                                                                                                                                                                                                                        Chromosome 9p21; human; cancer; tumour; diagnosis; prognosis; methylthloadenosine phosphorylase; MTAP; gliona; melanoma; primary lymphoid malignancy; non-small cell lung cancer; head and neck cancer; ovarian cancer; bladder cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12.6; DB 21; Length 32;
Pred. No. 2.2e+03;
); Mismatches 4; Indels
 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lung cancer, melanoma, head and neck cancer, obladder cancer or a chondrosarcoma (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 32 BP; 8 A; 9 C; 6 G; 9 T; 0 other;
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnosing and determining prognosis with derangements of chromosome 9p21
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0
                                                                                                                                                                                                                                                                                                                                                               chondrosarcoma; PCR primer; ss.
                                                                                                                                                       BP.
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78.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US13981.
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                                 1 ccgcgggctcacagtggtc 19
                                                                 2 cctcgagctgacagtcgtc 20
                                                                                                                                                    AAZ35374 standard; DNA; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccgcgggctcacagtggtc 19
                                                                                                                                                                                                                       27-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 63.0°
Best Local Similarity 78.9°
Matches 15; Conservative
15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schmid M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-126650/11.
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9967634-A1.
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                                                                                                                                                                                     AAZ35374;
 Matches
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Ets-2; human; transcription factor; chromosome 21q22.3; cancer; invasion; metastasis; skeletal abnormality; Down's syndrome; expression inhibition; phosphorothioate; antisense; ss.
                                                      Human Ets-2 phosphorothioate antisense oligonucleotide, SEQ ID NO:40.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense compound, 8-30 nucleobases in length, inhibiting the expression Ets-2 is useful for treating cancer and detecting Ets-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Column 40; 31pp; English.
                   21-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                     Baker BF, Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-338495/29.
                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                               25-JUN-1999;
                                                                                                                                                                                                                                                                                                25-JUN-1999;
                                                                                                                                                                                            US6054316-A.
                                                                                                                                                                                                                               25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression
     The invention relates to a mammalian PG1 gene and protein, and a set of used biallelic markers. The PG1 polynucleotide and biallelic markers are used in a hybridisation assay, a sequencing assay, or in an allele-specific amplification assay for determining the identity of a nucleotide at a PG1-related biallelic marker. The methods can be used to detect and to assess the risk of developing cancer or prostate specific antigen (PSA) dosage. However, the effectiveness of this is limited auffections of the organ. A need exists for both a reliable diagnostic procedure which would enable early-stage diagnosis, and for preventative procedure which would enable early-stage diagnosis, and for preventative detection of prostate cancer, and the risk of developing it in the
                                                                                                                                                                                                                                         PG1 gene; biallelic marker; PCR primer; PG1-related biallelic marker; cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                future, and can also be used to determine therapies for the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of a prostate cancer associated gene and biallelic markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 47;
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Pred. No. 2.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 47 BP; 14 A; 9 C; 14 G; 10 T; 0 other;
                                                                                                                                                                                                           Probe for human PG1 biallelic marker 4-50-293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chumakov I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 328; 385pp; English.
                                                                                   AA201125
ID AA201125 standard; DNA; 47 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-IB02133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0099658
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19 CTGAGGTCTCATAGTGGTC 1
                                                                                                                                                                        27-SEP-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-405178/34.
                                                                                                                                                                                                                                                                                PSA; human; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blumenfeld M,
                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                               WO9932644-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-SEP-1998;
22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1999
                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                      AAZ01125;
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99US-0344579.

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Sequences AAA38349-A38388 represent antisense oligonucleotides targetted to the human Ets-2 gene, which inhibit its expression. The antisense oligonucleotides were designed to target different regions of the human class. RNA, and were analysed for their effect on Ets-2 mRNA levels by quantitative real-time PCR. The Ets-domain transcription factors are a family of proteins which are involved in controlling key cellular events such as proliferation, differentiation and development. The Ets domain is a DNA-binding domain shared by all members of this family. Through this motif, Ets family members bind to the promoter regions of various genes at a GCA consensus sequence, thereby acting as either repressors or activators of the gene. All but one Ets family protein bind to DNA as monomer. Ets-2 has been implicated in the regulation of cellular proliferation and differentiation. The Ets-2 gene is located at chromosome 21q22.3, which is within a region known to undergo translocations associated with malignancies. Ets-2 has been found to be upregulated in several cancers, including lymphoblastic leukaemia. It may also play a role in the cancer phenotype, as it activates the urokinase plasminogen activator to epidermal growth factor (EGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stimulation. High levels of upA and metalloproteinases are associated with tumour invasion and metastasis in breast cancers. As the Ets-2 gene is located on chromosome 21, which is triplicated in Down's syndrome, it is also thought to be responsible for the skeletal abnormalities present in this condition. The antisense oligonucleotides of the invention are useful for the treatment or prophylaxis of conditions associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 12.2; DB 21;
Pred. No. 3.4e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 BP; 1 A; 5 C; 9 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ets-2 expression, especially cancer.
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82.4%;
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Best Local Similarity 82.4
Matches 14; Conservative
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ò a AAA38381 standard; DNA; 18 BP.

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AAA38381 RESULT

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AAA38381;

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AAA29335-38 are oligonuclectide primers used to synthesize the alpha and beta chain cDNA for a MAGE-1 specific T cell receptor from the CD8 positive cytotoxic T lymphocyte (CTL) clone 82/30. Novel immune cells with predefined specificity, are produced by either complexing the cells with an antigen specific MHC-restricted TCR or transfecting the cells on thigher specific MHC-restricted chimaric TCR gene. The antigen-specific MHC-restricted chimaric TCR gene. The antigen-specific MHC-restricted for complexed with lymphocytic cells for treatment of a tumour. Alternatively, the autologous climents of a transfected with an antigen specific MHC-restricted for in antigen associated with the tumour and a segment encoding a single chain TCR (scFv-TCR) which binds to an antigen associated with the tumour and a segment encoding a signal transducing element of an immune cell. Compositions comprising the manner cells may be used for the treatment of cancer (especially melanomas, if the TCR binds to the MAGE-1 antigen), infectious diseases, autoimmune disease and/or graft rejection.
                                                                                                                                    human leukocyte antigen; HLA-A1; melanoma; neoplastic; MAGE-1; TCR; MHC; soluble; major histocompatability complex; antigen; T cell receptor; lymphocyte; tumour; cytostatic; anti-microbial; immunosuppressive; primer; alpha chain; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immune cells with predefined specificities useful for treating melanoma
                                                                                               Primer V-beta-3 for MAGE-1 specific TCR-alpha chain cloning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29 BP; 4 A; 10 C; 11 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bolhuis RLH, Eshhar Z, Willemsen RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 29; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         (YEDA ) YEDA RES & DEV CO LTD (BOLH/) BOLHUIS R L H.
                                                                                                                                                                                                                                                                                                                                                                99WO-IL00622
                                                                                                                                                                                                                                                                                                                                                                                                      98IL-0127142
                                                     12-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-451678/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and immune diseases
                                                                                                                                                                                                                                                                             WO200031239-A1
                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                              18-NOV-1999;
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                                                                                                                                                                                                                                                                                                                       02-JUN-2000
                  AAA29338;
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Query Match 61.0%; Score 12.2; DB 21; Length 29; Best Local Similarity 82.4%; Pred. No. 3.4e+03; Matches 14; Conservative 0; Mismatches 3; Indels ( ò

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Search completed: October 2, 2001, 16:18:33 Job time: 15477 sec

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Sequence:

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Result No.

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Sequence 1
   Sequence
                                                                                                                                                                                                                                                                                                                                          FACUL NO. 0133031
APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT PILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 33
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FAPLICATION NUMBER: US/09/377,310B
CURRENT FAPLICATION NUMBER: 2.9
SOFTWARE: PATENTING PATE: 1999-08-19
SOFTWARE: PATENTING PATE: 2.0
                                                                                                                                                                                                                    Sequence
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US-08-467-023-105
US-08-198-431-14
US-08-158-431-14
US-08-537-874-14
US-08-621-859-14
US-09-099-015-14
US-09-099-015-14
US-08-05-198-431-13
US-08-564-955-13
US-08-564-955-13
US-08-621-859-13
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Mismatches
                                                                                                                                                                                                                                                          ALIGNMENTS
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; OTHER INFORMATION: antisense sequence
US-09-377-310-33
                                                                                                                                                                                                                                                                                                                      ; Sequence 33, Application US/09377310B
; Patent No. 6133031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 13, Application US/09377310B
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Best Local Similarity
Matches 15; Conserv
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US-09-377-310-33
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US-09-377-310-13
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10.8
   SEQ ID NO 13
LENGTH: 20
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                                                                                      Search time 417.38 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-377-310-13
US-08-45-467B-28
US-08-459-568-11
US-08-399-411-11
US-08-516-859A-11
US-08-937-271-39
US-09-087-232A-2
US-09-116-498-16
US-07-884-811-10
US-08-087-238A-10
US-08-087-238A-10
US-08-087-238A-10
US-08-087-238A-10
US-08-435-501-9
US-08-435-501-9
US-08-435-764-9
US-08-435-764-9
US-08-435-764-9
US-08-435-764-9
US-08-435-764-9
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US-08-271-942A-7
US-08-779-916A-7
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US-08-961-083-272
US-08-832-985-49
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                                                                                     2001, 16:03:55
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Maximum Match 100%
Listing first 45 summaries
                                                             OM nucleic - nucleic search, using sw model
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431
431
431
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Match
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Score 12.4; DB 1; Length 27; Pred. No. 1.3e+02;
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Fatent No. 5831008
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ADDRESSEE: ADDRESSEE: 4370 La Jolla Village Drive, Suite 700
      Retinoblastoma Protein - Interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/459,568
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
TITLE OF INVENTION: Retinoblastoma Protein - Interpreted of INVENTION: Zinc Finger Proteins NUMBER OF SEQUENCES: 93
CORRESSONDENCE ADDRESS: ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,315
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELERAX: (619) 535-901
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/399,411
FILING DATE: 06-MAR-1995
FLASSIFCATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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92.9%;
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Best Local Similarity 92.9
Matches 13; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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California
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US-08-399-411-11/c
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Sequence 28, Application US/08462467B
Patent No. 6210899
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rosenbaum, Jan S
TITLE OF INVENTION: Complex for Screening Bone Metabolism Actives and Cells TITLE OF INVENTION: Complex for Screening Bone Metabolism Actives and Cells TITLE OF INVENTION: Complex for Screening Bone Metabolism Actives and Cells TITLE OF INVENTION: BMP Receptor
TITLE OF INVENTION: BMP Receptor
TITLE OF INVENTION: BMP Receptor
CORRESPONDENCES: 39
CORRESPONDENCES: 39
CORRESPONDENCES: The Procter & Gamble Company
STREET: 11810 East Miami River Road
                                                                                                                                                                                                                                 ö
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                                                                                                                                                                  100.0%; Score 15; DB 3; Length 20; 100.0%; Pred. No. 4.1;
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red. No. 56;
Mismatches 0; Indels
                                                                                                                                                                                                                                 0; Indels
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COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/462,467B
                                                                                                                                                                                                                                 0; Mismatches
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APPLICATION ...
FILING DATE:
FLING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HETEKO, BAIT S.
REGISTRATION NUMBER: 32,572
REGISTRATION NUMBER: 5474R
TELECOMMUNICATION INFORMATION:
TELEFAN: (513) 627-0260
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
LENGTH: 21 base pairs
TELEGOMMUNICATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TELEGOMMUNICATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TWPE: INUCLE CALCULATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TWPE: INUCLE CALCULATION FOR SEQ ID NO: 28:
THE COLOR OF THE CALCULATION FOR SEQ ID NO: 28:
THE CALCULATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
THE CALCULATION FOR SEQ ID NO: 28:
THE CA
         ; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-377-310-13
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Patent No. 5811304
GENERAL INFORMATION:
APPLICANT: Huang, Shi
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US-08-462-467B-28
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
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MEDIUM TYPE: Floppy
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US-08-459-568-11/c
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      FEATURE:
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Sequence 2, Application US/09087232A
Patent No. 6153431
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
              Gaps
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Pred. No. 1.3e+02;
0; Mismatches 1; Indels
            Indels
                                                                                                                                                                                                                                               APPLICANT: Dale, James B.
APPLICANT: Lederer, James W.
TITLE OF INVENTION: RECOMBINANT MULTIVALENT M PROTEIN
TITLE OF INVENTION: VACCINE
NUMBER OF SEQUENCES: 40
CORRESPONDER SED and BERRY
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA.
              ;
            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Rosenman, Stephen J.
REGISTRATION UNBER: 43,058
REFERENCE/DOCKET NUMBER: 481112.405C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/937,271
FILING DATE: 15-SEP-1997
CLASSIFICATION: 424
                                                                                                                                                                                      Sequence 39, Application US/08937271 Patent No. 6063386 GENERAL INFORMATION:
          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.7%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Rosenman, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 82.7
Best Local Similarity 92.9
Matches 13; Conservative
          13; Conservative
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                                                  1 tggcttatcttcag 14
                                                                        27 TGGCTTTTCTTCAG 14
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                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-09-087-232A-2/c
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TOPOLOGY:
US-08-937-271-39
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COUNTRY:
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          Matches
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Patent No. 6069231

GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: 2inc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITTLE California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                               Score 12.4; DB 2; Length 27; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 27;
                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/516,859A
FILING DATE: 18-AUG-1995
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 12.4; DB 3;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1776
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGHH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
NAME: Campbell, Cathryn A.
REGISTRATION HUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 555-9001
FIELEPHONE: (619) 555-904
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                          82.7%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.7%;
92.9%;
                                                                                                                                                                                                                                                                                                            Query Match 82.7
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-516-859A-11/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 92122
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Sequence 10, Application US/07884811
Fatent No. 5316921
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 22;
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                                                                                                                                                                                                                                                                                       Score 11.8; DB 4;
Pred. No. 2.7e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 11.8; DB 1;
Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC-DOS/MS-DOS SOFTWARE: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA: FILLING DATE: 19920518
REFERENCE/DOCKET NUMBER: 1049-1-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SED ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 16: US-09-116-498-16
                                                                                                                                                                                        LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 75:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.7%;
86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.78;
86.78;
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NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 78.7
Best Local Similarity 86.7
Matches 13; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 tggcttatcttcagt 15
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 in
COMPUTER: IBM PC COM
                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: NO
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY:
US-07-884-811-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-884-811-10
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Unutnat, Derga
Ramanii, Vincet N.K.
FITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                               CURRENT APPLICATION BATENERS

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/087,232A
FILING DATE: 28 MAY 1998
CLASSIFICATION ATA:
APPLICATION NUMBER: 06/048,057
FILING DATE: 30 MAY 1997
APPLICATION DATA:
APPLICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATORNEY/AGENT INFORMATION:
NAME: KOLE, LISA B.
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: 35,225
REFERENCE/DOCKET NUMBER: 36,268
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELEPHONE: (212) 408-2628
TELEFRAX: (212) 765-2519
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TENTOR THE TENTOR TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/09/116,498
FILING DATE: 16-Jul-1998
CLASSIFICATION: CURROWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.0%; Score 12; DB 3; L6
100.0%; Pred. No. 2.1e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "PRIMER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/09116498 Patent No. 6251582 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Littman, Dan R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 21 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floor
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US-09-116-498-16
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Sequence 10, Application US/08194088B
Patent No. 5580963
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Generach, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 11.8; DB 1;
Pred. No. 2.8e+02;
0; Mismatches 2;
                                                                              MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIE: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                        CURRENT APPLICATION (Generatech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,783A
FILING DATE: 13-Jul.1993
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/884811
FILING DATE: 18-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/885971
FILING DATE: 18-MAY-92
ATTONNEY,AGENT INFORMATION:
NAWE: MASCHARQ, DIANE L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: 35,600
REFERENCE/DOCKET NUMBER: 35,600
REFERENCE/DOCKET NUMBER: 90755779P1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,088B
FILING DATE: 09-FEB-1994
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CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/884811
FILING DATE: 18-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: GAllegos, R. Thomas
REGISTRATION NUMBER: 32,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 415/225-5416
415/952-9881
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 78.7
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 30 base pairs
Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 tggcttatcttcagt 15
                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY:
US-08-087-783A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-194-088B-10
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Sequence 10, Coker, Nathalie A. Mark, Melanie R. TITLE OF INVENTION: HEATOCYTE GROWTH FACTOR PROTEASE DOMAIN VARIANTS
NUMBER OF SEQUENCES: 21
CORRESPONDESS: 21
CORRESPONDESS: 21
STREET: 460 Point San Bruco Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER: DAM PRESS: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
COMPUTER: SYSTEM: PC-DOS/MS-DOS
COMPUTER: CALIFA: COLORS STATES COMPUTER: COLORS SYSTEM: COLORS SYSTE
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   Gaps
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Sequence 10, Application US/08087783A

Patent No. 5547856

GENERAL INFORMATION:
APPLICART: Godowski, Paul J., Lokker, Nathalie A., Mark, Melanie R., TITLE OF INVENTION: HEPATOCYTE GROWTH FACTOR VARIANTS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
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      Indels
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Pred. No. 2.8e+02;
0; Mismatches 2;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,971
FILING DATE: 19920518
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TELECOMUNICATION INFORMATION:
TELEPHONE: 415/25-3216
TELERA: 910/31-716
ILELRA: 910/31-716
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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ilarity 86.7%;
Conservative
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ATTORNEY/AGENT INFORMATION:
13; Conservative
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7 TGACATATCTTCAGT 21
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Best Local Similarity
Matches 13; Conserv
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US-07-885-971-10
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Pred. No. 2.8e+02;
0; Mismatches 2; Indels
78.7%; Score 11.8; DB 1; Length 30; 86.7%; Pred. No. 2.8e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08435764
Fatent No. 5763584
Fatent No. 5763584
GENERAL INFORMATION
TITLE OF INVENTION: Receptor Activation
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genertech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Prancisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,764
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PRICATION NUMBER: 05/06/453,77
PRICASIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/884811
FILING DATE: 18-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/885971
FILING DATE: 18-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/950572
FILING DATE: 21-SEP-1992
ATTORNEY/AGENT INFORMATION:
WANTE: DESCRIPTION CALLORS OF THE CA
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REFERENCE/DOCKET NUMBER: 775
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.78;
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 86.7
Matches 13; Conservative
                                                                 Conservative
                                                                                                                               1 tggcttatcttcagt 15
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STRANDEDNESS: single
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                                Best Local Similarity
Matches 13; Conserv
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US-08-435-764-9
      Query Match
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US-08-435-501-9
Sequence 9, Application US/08435501
Setent No. 5684136
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Paul J. Godowski
TITLE OF INVENTION: Receptor Activation
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,501
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APPLICATION NUMBER: 07/84811
FILING DATE: 18-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/885971
FILING DATE: 18-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/950572
FILING DATE: 12-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
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                                                                              TELEFAX: 415/952-9881
TELEX: 910/371-7168
INPORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 bases
TYPE: nucleic acid
STRANDEDNESS: single
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                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-2614
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
   REFERENCE/DOCKET NUMBER:
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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US-08-194-088B-10
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US-08-435-501-9
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Primer used to gen PCR 5' primer for Retinoblastoma gen

Primer deltaK3 huH

genomic marker

Human SIV/HIV

Perfect score:

Sequence:

OM nucleic

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Run

Scoring table:

Searched:

Minimum DB s Maximum DB s

Database

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New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human focal adhesion kinase antisense sequence #31.
                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                    AAA66237
AAQ52624
AAX15645
                                                                                     AAV27482
AAV84748
AAQ55632
AAQ29005
                                                                                                                                                                                                                                                         AAQ32816
AAQ57839
AAQ76318
                                                     AAT12845
AAT11444
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AAQ26930
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AAT62465
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AAV12309
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  (ISIS-) ISIS PHARM INC.
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Homo sapiens
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PCR primer for Cel
Human focal adhesi
PCR primer for mou
Antisense primer f
PCR primer used to
Human gene single
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Streptococcus pyog
CCR5/CCR2b PCR pri
HIV-1 co-receptor
                                                                                      (without alignments)
10.740 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                         Search time 876.95 Seconds
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                730101 seqs, 313950809 residues
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                                                                         2, 2001, 16:18:48
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Listing first 45 summaries
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                                                                                      AAC65545;
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                   The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New DNA encoding cotton cellulose synthase proteins - useful for controlling cellulose synthesis in prokaryotic or eukaryotic cells
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                                                                                                                                          22; Length 15;
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                                                                                                                                                                                                                                                                                                                               PCR primer for Cellulose synthase coding sequence.
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                                                                                                                                           DB
22;
                                                                                                          Sequence 15 BP; 2 A; 3 C; 3 G; 7 T; 0 other;
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Pred. No. 22;
; Mismatches
                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                   Cellulose synthase; cotton; PCR primer; ss.
                                                                                                                                          Score 15;
Pred. No.
 Claim 15; Column 25; 30pp; English.
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100.0%;
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                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
Gossypium hirsutum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of mammals etc
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The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                       Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BMP type II receptor kinase-3; BRK-3; bone morphogenetic protein; primer; PCR; polymerase chain reaction; ss.
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                                                                                                                                                     Human focal adhesion kinase antisense sequence #11.
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100.0%; Pred. No. 22;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 5 A; 3 C; 4 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Column 23; 30pp; English.
                                                                                                                                                                                                                                                          antisense; phosphorothioate; ss.
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AAC65545 standard; DNA; 20
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ID AAT28037 standard; DNA; 21
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This primer corresponds to the sequence of plasmid pSPORTI/N89-5, and is the reverse complement of nucleotides 968-948 in a gene encoding mouse bone morphogenetic protein (BMP) receptor type-II kinase-3 (BRK-3), which induces cellular differentiation in response to BMP. The primer may be used with anchor primer AAT27331 in 5'-rapid amplification of CDNA ends (5'-RACE), to isolate 600 bp at the 5'-end of the BKR-3 gene, by PCR amplification of NIB373 mouse embryo fibroblast (ATCC CRL 1658) cDNA. To reduce background, a 2nd round of PCR is performed using nested primer AAT27232 with the anchor primer. This results in isolation of 600 bp from the 5'-end of the gene, which may be used to assemble a full-length clone (AAT27225) by PCR using primers AAT2723-4 and cloning in phage Bluescript-II-SK(-) in Escherichia coll DH5-alpha. The receptor and antibodies against the may be used in diagnostic assays for BMP disorders, or in the beautiful coll by the anchor the may be used in diagnostic assays for BMP disorders, or in the beautiful coll by the BMS and antibodies against the may be used to assays for BMP disorders, or in the beautiful coll by the BMS and antibodies against the may be used to assays for BMP disorders, or in the beautiful coll by the BMS and antibodies against the may be used to assays for BMP disorders, or in the base and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope; PCR primer; ss.
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                                                                nsed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy to bind or scavenge BMPs. In addition, expression of the BMR-3 gene along with a reporter gene under the control of a hormone-responsive element in a cell culture may be used to screen compounds for BRK-agonist or -antagonist activity, by monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.7%; Score 13; DB 17; Length 21; 100.0%; Pred. No. 2.8e+02; ive 0; Mismatches 0; Indels
                                                          Isolated bone morphogenic protein receptor kinase protein determine if a test cpd. is capable of binding to, or is (ant)agonist of BMP receptor kinase protein transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR primer used to amplify an ORF of Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 other;
                                                                                                                                            Example 9; Page 30; 87pp; English.
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Matches 13; Conservative
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Chlamydia pneumoniae.
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                     WPI; 1996-251762/25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A PCR primer (AAT28037) Includes the reverse complement of a partial cDNA clone isolated from NIBT3 mouse embryonic fibroblasts. It was used with an anchor primer (AAT28038) to amplify the 5' end of mouse bone morphogenetic protein (BMP) type receptor kinase protein-3 (BRK-3) cDNA. Following further PCR amplification and cloning into pUT6, a cDNA clone (AAT28020) coding for full-length murine BRK-3 (AAR55224) was obtd. The PCR primer is the reverse complement of nucleotides 968-948 of this clone.
                                                                                                                                                                                                                                                                                                                                 Assays for bone morphogenetic protein activities - using complex of BMP type I receptor kinase protein and BMP receptor kinase protein BRK-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense primer for mouse BRK-3 gene 5'-end amplification.
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                                                                                                                                                                                                                             (PROC ) PROCTER & GAMBLE CO
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Matches 13; Conservative
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                                                                                                                                                                                                                                                                  Rosenbaum JS;
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                                      WO9614579-A1
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Synthetic.
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                                                                                                  frames and other nucleic acid sequences from the genome of Chlamydia pneumoniae (see AAX91990). C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be contributing factor in heart disease, sarcoidosis, sinusitis, purulent otits media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAX3684-AAX36879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as
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polymorphism; vascular disease; coronary artery disease; forensics;
myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
pulmonary embolism; paternity test; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and
                                                                                   AAX91991-X97517 represent PCR primers used to amplify open reading
                                                                                                                                                                                                                                                                                  immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of {\tt C.} pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/standard_name= "single nucleotide polymorphism"
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                              Score 12.4; DB 20;
Pred. No. 6e+02;
); Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                 Sequence 20 BP; 3 A; 4 C; 6 G; 7 T; 0 other;
Genome sequence of Chlamydia pneumoniae
                                          Page 1688; Disclosure; 1912pp; English.
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92.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-SEP-2000; 2000WO-US24503.
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2000US-0225724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Best Local Similarity 92.9
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atherosclerosis -
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16-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-SEP-1999;
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                     In an individual, involving determining the sequence at various polymorphic sites within the human thrombospondin 1 and thrombospondin 4 genes. The sequences at a number of polymorphic sites are also provided in the specification. In particular, the method can be used in the diagnosis of atherosclerosis, myocardial infarction, coronary heart disease, stroke, peripheral vascular diseases, venous thromboembolism and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also useful in forensics, paternity testing, genetic analysis and phenotype correlations to diseases. The present sequence is an example of one of the human gene SNPS shown in the specification.
present invention provides a method of diagnosing a vascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a PCR primer for the rat retinoblastoma (RD) interacting zinc finger (RIZ) protein (AMB12028). RIZ is a nuclear phosphoprotein that acts as a cell differentiation factor. RIZ can modulate cell growth by binding to RD protein, which is involved in regulating cell proliferation. In addition, RIZ can act to regulate transcription. RIZ functions to maintain cells in the GI phase of the cell cycle, by interacting with RD through the cr2 domain of RIZ. RIZ protein is a PR domain protein and is present primarily in the cell
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transcription requiator; breast cancer; gene therapy; melanoma;
neuroblastoma; leukaemia; Parkinson's disease; Huntingdon's disease;
Alzheimer's disease; paralysis; motor neurone disorder; PCR primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rb-interacting zinc finger; RIZ; retinoblastoma; heart disease; rat;
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Pred. No. 6.1e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21 BP; 3 A; 6 C; 4 G; 8 T; 0 other;
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ilarity 92.9%;
Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat RIZ PCR primer # 1.
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Matches 13; Conserv
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nucleus. RIZ gene mutations may be implicated in various cancers such as melanoma, neuroblastoma, leukaemia and breast cancer, and so the RIZ gene may be used in gene therapy for these disorders. Since RIZ protein is implicated in cell cycle arrest, inhibition of RIZ activity may be useful in neurodegenerative disorder therapy e.g. for Parkinson's, useful in neurodegenerative disorder therapy e.g. for Parkinson's, disorders, or cardiac disorders e.g. heart disease, where the ability to induce neural, cardiac disorders proliferation would be useful. The present sequence was used in the construction of vectors which were used to clone
                                                                                                                                                                                                                                                                                     mammalian RIZ coding sequences.
         8888888888888
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Sequence 27 BP; 9 A; 7 C; 9 G; 2 T; 0 other;

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Gaps
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0
Score 12.4; DB 21; Length 27;
Pred. No. 6.2e+02;
0; Mismatches 1; Indels (
 82.7%;
92.9%;
                         Conservative
                                              1 tggcttatcttcag 14
                                                            Best Local Similarity
Matches 13; Conserv
 Query Match
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Streptococcus pyogenes M19 gene PCR primer, SEQ ID NO:39. AAA57918 standard; DNA; 30 BP. (first entry) 10-OCT-2000 AAA57918; σ AAA57918 

Multivalent hybrid M protein; group A streptococcus; serotype; immunogenic; sero-specific antibody; streptococcal infection; cross reactivity; vaccine; acute rheumatic fever; ARF; rheumatic heart disease; streptococcal pharyngitis; strep throat; pneumonia; PCR primer; ss.

Streptococcus pyogenes.

16-MAY-2000

US6063386-A.

92US-0945954. 97US-0937271. 15-SEP-1997; 16-SEP-1992;

(UYTE-) UNIV TENNESSEE RES CORP.

Dale JB; Lederer JW,

WPI; 2000-364475/31.

New immunogenic recombinant hybrid M protein comprising amino-terminal peptide fragments of streptococcal M protein useful as vaccine against rheumatic fever and infections leading to rheumatic fever Disclosure; Column 13-14; 62pp; English.

The invention relates to multivalent immunogenic hybrid group A streptococcal M proteins comprising N-terminal peptide fragments of M proteins that elicit opsonic antibodies against multiple serotypes of group A streptococci (e.g., Streptococcus pyogenes). The antibodies generated using the hybrid proteins are against one or more M protein serotypes, where at least one of the serotypes is Mi, M3, M18 or M19. The invention also encompasses a recombinant DNA molecule comprising a nucleotide sequence that encodes a multivalent hybrid M protein; and a method for immunisteng a mammal against streptococcal infections, comprising administering an immunogenic multivalent hybrid M protein to the mammal. The multivalent hybrid M proteins are useful for eliciting opsonic or protective antibodies to the M proteins of different

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serotypes of group A streptococci, and may therefore be used as vaccines to protect against and control infection by type A streptococci Type A streptococci are not only responsible for streptococcal pharyngitis (strep throat), forms of pneumonia and a condition resembling toxic shock, but are also involved in the development of acute rheumatic fever (ARF) and rheumatic heart disease. In a patient with ARF, antibodies formed during a group A streptococcal infection are also cross-reactive with heart tissue, which indicates that the streptococci and host tissue contain similar antigenic motifs. The new multivalent vaccines are capable of raising sero-specific antibodies against various serotypes of group A streptococci which are not cross-reactive with human heart tissue. Sequences AAA57903-A57904 and AAA57903-A57904 represent PCR primers used in the generation of DNA (AAA57803-A57902) encoding multivalent hybrid Streptococcus pyogenes M proteins (AAB03113-B03117, multivalent.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method of surveying the CC (beta) chemokine receptor (CCR) genotypes in a population. The method is particularly applied to the human CCRS and CCR2 genes located on chromosome 3p21-22, which encode co-receptors for HIV-1. The method involves obtaining genomic DNA samples from a representative number of individuals within a population; combining each sample with experimental and control primer combinations to produce primer-annealed DNA; amplifying the DNA to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Surveying CC beta chemokine receptor (CCR) genotypes in population, involves amplifying genomic DNA of individuals with experimental and control primer combinations, size-separating amplicons and determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCR5/CCR2b PCR primer, SEQ ID:18, used to genotype HIV susceptibility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC chemokine receptor; beta chemokine receptor; CCR; human; CCR5; CCR2, polymorphism; genotyping; HrV-1 transmission; infection susceptibility; AIDS; acquired immunodeficiency syndrome; disease progression; chromosome 3p21-22; PCR primer; ss.
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Pred. No. 6.3e+02;
0; Mismatches 1;
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92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 82.7
Best Local Similarity 92.9
Matches 13; Conservative
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Wed Oct

Individuals homozygous for the

to the wild-type allele.

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produce amplicons; separating the amplicons by size; determining the genotype based upon the presence of CCR alleles; and compiling the genotypes determined. The method is particularly applied to the human CCRS and CCRS are associated with a variation in the susceptibility of an individual to infection by HIV-1, or with a variation in the disease c progression of AIDS after infection. The invention specifically claims the experimental PCR primers AAF76119, and the control PCR primers AAF76119-AAF76119, and the control PCR primers AAF76119-AAF76119, and of the invention fulfils a longstanding need for the development of a rapid and informative genotyping strategy that can readily applied to analyse CCRS, CCR2 and related genetic variants, and disease progression. The present sequence represents a human and disease progression. The present sequence represents a human and disease progression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19 BP; 6 A; 4 C; 5 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 nvention.
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ő Length 19; 0; Indels DB 22; 1e+03; Query Match 80.0%; Score 12; DB Best Local Similarity 100.0%; Pred. No. 1e+Matches 12; Conservative 0; Mismatches 2 gecttatcttca 13 ö

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Gaps

HIV-1; CCR5; CCR5-delta32; co-receptor; infection; diagnosis; AIDS; gene therapy; human; PCR; primer; ss. HIV-1 co-receptor CCR5-delta32 variant PCR primer delta-32 inv. AAV84128 standard; DNA; 21 BP. 15-MAR-1999 (first entry) 15 GCCTTATCTTCA 4 AAV84128; 셤

98WO-EP03437. Homo sapiens. WO9854317-A1 29-MAY-1998; 03-DEC-1998 Synthetic 

97US-0048057 30-MAY-1997;

(MOND-) FOND MONDIALE RECH & PREVENTION SIDA.

Braun J, Quillent C; Beretta A, Arenzana Siesdedos F, WPI; 1999-059835/05.

This is the nucleotide sequence of a claimed DNA primer, designated delta-32 inv, which can be used for the amplification of HIV-1 CCRS co-receptor nucleic acids. It corresponds to nucleotide 955 of wild-type CCRS cDNA (see AAV84126). 4 Pairs of primers (see AAV84127-34) are provided. These can be used in claimed methods for detecting and identifying the presence of a CCRS variant in a sample. Primer pair delta-31 inv and delta-32 sens (see AAV84127) are particularly useful in detecting the presence of variant CCRS-delta32 (see AAV84159) that contains a 32 bp deletion when New CCR5 variant protein of the HIV-1 co-receptor - useful in developing resistance of CCR5-expressing cells to HIV-1 infection Claim 7; Page 8; 55pp; English.

ö TATA-box binding protein; epitope-tagged TBP; transcription complex; TAF; TBP associated factor; TAF-interaction factor; gene expression regulator; Gaps variant allele show resistance to HIV-1 infection. The detection of CCR5 variants may be used to identify individuals at lower risk of infection relative to the general population who, if infected, may exhibit slower progression to AIDS. ; 0 80.0%; Score 12; DB 20; Length 21; 100.0%; Pred. No. 1e+03; ive 0; Mismatches 0; Indels Primer for Transgene for epitope tagged TBP protein. BP; 7 A; 6 C; 5 G; 3 T; 0 other; 80.00, 100.0%; Pre-BP. AAV08563 standard; DNA; 21 Conservative 2 ggcttatcttca 13 13 GCCTTATCTTCA 2 Local Similarity nes 12; Conserv 12-FEB-1999 Sequence 21 AAV08563; Query Match Best Loca Matches RESULT 12 AAV08563/ 888888 ò ρp 

Transgenic animal expressing epitope-tagged TATA-box binding protein - for isolating higher-order transcription complexes and specific factors that associate with the protein, useful as potential WPI; 1999-001394/01. therapeutic agents

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Polites

Meisterernst M,

Berglund E, Kirschbaum B,

(FARH ) HOECHST AG.

98EP-0109516. 97EP-0108433

26-MAY-1998; 26-MAY-1997;

PCR primer; ss

Homo sapiens.

Synthetic.

EP881288-A1 02-DEC-1998. Example 4; Page 11; 38pp; English.

This sequence is a PCR primer for DNA encoding an epitope-tagged TATA-box binding protein (TBP) that is expressed by the transgenic non-human binding protein (TBP) that is expressed by the transgenic non-human can mimals are used to produce TBP. TBP is used to isolate and characterise higher-order transcription complexes (from different tissue and cell types, optionally at different developmental stages). It is also used to identify new and/or specific. TBP associated factors (TAFS, e.g. transcription factors, activators or inhibitors) and TAF-interaction factors, and to raise antibodies against TBP. The TAFS may be useful for regulating gene expression.

Ce.g. disease-related genes, so are potential pharmaceuticals, also for identifying human analogues for use in drug screening. The antibodies are used for affinity purification of TBP and its complexes. TBP can isolate transcription complexes from a wide variety of different tissues and calls (contrast known methods that are limited to isolation from a

Sequence 21 BP; 6 A; 4 C; 8 G; 3 T; 0 other;

4 tggcttatcatcaat 18

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RESULT 1
AAA66237/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This primer corresponds to a region 550 bp downstream of the ATG initiation codon of human Bob (see AAX0732), a new HIV/SIV traslocation codon of human Bob (see AAX0732), a new HIV/SIV traslocation promoter agent which acts with CD4 to serve as a receptor for retroviral entry. It was used with an upstream primer (see AAX07297) in the RT-PCR amplification of lymphocyte RNA. Bob mRNA was detected in PHA stimulated peripheral blood monounclear cells (PMBC), purified T cells, and weakly in monounclear genes (see AAX0728994) encoding 2 receptors, termed Bonzo macaque genes (see AAX0728994) encoding 2 receptors, termed Bonzo and Bob (see AAW97783-88), that are associated with retroviral entry into cells have been identified. Diagnostic and therapeutic uses of these novel translocation promoting agents are provided, and unitial agents for treatment
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding the human translocation promoter Bonzo used to screen for potential agents for treating acquired immune deficiency syndrome
                                                                                                                                                                                                         SIV receptor; HIV receptor; Bob; translocation promoting agent; Bonzo; G protein coupled receptor; chemokine receptor; AIDS; infection; virus transmission; PCR; primer; ss.
                      ö
Length 21;
                      Indels
Score 11.8; DB 20;
Pred. No. 1.3e+03;
3; Mismatches 2;
                                                                                                                                                                                      Human SIV/HIV receptor Bob downstream PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                  Kewalramani VN, Littman DR, Unutmaz D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22 BP; 6 A; 5 C; 4 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 51; 97pp; English.
                     ;
                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIV- and HIV-induced AIDS.
78.78;
86.78;
                                                                                                                                                                                                                                                                                                                                                                            (UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                       97US-0896155
                                                                                                                     AAX07298 standard; DNA; 22
                                                                                                                                                                (first entry)
                     Conservative
                                            tggcttatcttcagt 15.
                                                     WPI; 1999-132164/11.
          Similarity
                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                      WO9903888-A1
                                                                                                                                                                                                                                                                                                                                  17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                       17-JUL-1997;
                                                                                                                                                                21-MAY-1999
Query Match
Best Local Simi
Matches 13;
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                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                           AAX07298;
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                                                                                                 RESULT 13
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                                                                                                            AAX07298
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The present invention describes a radiation hybrid map of the dog (Canine familiaris) genome comprising the genome location of a marker selected from AAA6619 to AAA6692. The radiation hybrid map is useful for identifying and localising dog genes, since it covers approximately 80 % of the dog genome and provides a dense map integrating different types (i.e. Type I and Type II) of markers. The map and the dog genome markers (or complementary sequences) are especially useful to identify genes responsible for phenotypic and behavioural traits in dogs, to identify morbid genes, to analyse diseases and identify implicated genes in such diseases and their alleles, and to study dog pedigrees. They may also be useful for isolating corresponding human gene sequences e.g. genes involved in genetic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New radiation hybrid map of the dog, Canine familiaris, genome, useful for e.g. identifying genes implicated in phenotypic and behavioral traits or in genetic diseases and for studying dog pedigrees
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                   Dog; genome; genomic marker; radiation hybrid map; identification; chromosome location; gene marker; polymorphic microsatellite marker; phenotype; behaviour; pedigree; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                    Dog genomic marker oligonucleotide sequence SEQ ID NO:99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23 BP; 10 A; 6 C; 5 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 57; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CNRS ) CNRS CENT NAT RECH SCI.
  BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.78;
86.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-IB01907.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0108193.
AAA66237 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ52624 standard; DNA; 30
                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 86.7°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 tggcttatcttcagt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 TGGCTTGTTTTCAGT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Galibert F, Andre C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer deltaK3 huHGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-387821/33.
                                                                                                                                                                                                                                                                                                                                   Canis familiaris.
                                                                                                                                                                                                                                                                                                                                                                                    WO200029615-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-1998;
                                                                                                          09-0CT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAY-2000
                                                      AAA66237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ52624;
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Gaps

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Indels

78.7%; Score 11.8; DB 20; 86.7%; Pred. No. 1.3e+03; tive 0; Mismatches 2;

Query Match
Best Local Similarity 86.7'
Matches 13; Conservative

1 tggcttatcttcagt 15

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Length 22;

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Polymerase chain reaction; PCR; amplify; primer; pRK 5.1 huHGF; human hepatocyte growth factor; huHGF; varient; E. coli; human; fetal; kidney 293 cells; hepatocyte; ligand; receptor; activation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences given in AAQ52616-28 are primers which were used in the generation of pRK 5.1 human hepatocyte growth factor (huHGF) varient molecules. The amplification products from these reactions were cloned in E. coil cells and were then used to transfect human fetal kidney 293 cells. The expressed proteins were used to study the ability of huHGF to induce DNA synthesis of hepatocytes in primary culture. The expressed proteins may be used as first and/or second ligands in a conjugate for receptor activation. These conjugates may be used to activate the respective receptors and thereby mimic the biological activity of the corresponding native ligand.
                                                                                                                                                                                                                                                                                                                                                                                                            Activation of receptors, partic. of growth factors - using conjugate of two ligands capable of binding to receptors, for mimicking biological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 11.8; DB 14; Length 30;
Pred. No. 1.3e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30 BP; 7 A; 7 C; 4 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 49; 103pp; English.
                                                                                                                                                                                                                             92US-0884811.
92US-0885971.
92US-0950572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 78.7%;
Best Local Similarity 86.7%;
Matches 13; Conservative
                                                                                                                                                                                             93WO-US04717.
                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-386581/48.
                                                                                                                                                                                            17-MAY-1993;
                                                                                                                                                                                                                                                  18-MAY-1992;
22-SEP-1992;
                                                                                                                                                                                                                               18-MAY-1992;
                                                                                                                     W09323550-A.
                                                                                                                                                          25-NOV-1993.
                                                                                                                                                                                                                                                                                                                                         Godowski PJ;
                                                                                   Synthetic.
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Search completed: October 2, 2001, 16:18:49 Job time: 15493 sec

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Gaps

Appl Appl Appl Appl Appl

Sednence Sed

Sequence Sequence Sequence Sequence

Sequence

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GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase;
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT APPLICATION NUMBER: 43
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/09377310B
Fatent No. 6133031
GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
      US-08-473-503-87

US-08-473-503-87

US-08-720-420A-87

US-08-714-017-87

US-08-75-680-87

US-08-906-517-69

US-08-906-517-69

US-08-482-882-100

US-08-483-389-100

US-08-483-389-100

US-08-483-399-100

US-08-483-399-100

US-08-483-932-100

US-08-720-420A-100

US-08-720-420A-100

US-08-720-420A-100

US-08-720-420A-100

US-08-720-420A-100

US-08-73-6882-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 15; DB 3; 100.0%; Pred. No. 4.1;
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                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF EGG ID NOS: 43
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                    CTHER INFORMATION: antisense sequence US-09-377-310-31
                                                                                                                                                                                                                                                         ; Sequence 31, Application US/09377310B
; Patent No. 6133031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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  1 tacccaggtgagtct 15
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Matches 15; Conserv
US-09-377-310-31
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SEQ ID NO 31
LENGTH: 15
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LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
FEATURE:
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Sequence 15, Appl
Sequence 6, Appli
Sequence 6, Appli
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6.804 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                   Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-377-310-31

US-09-377-310-11

US-08-137-310-11

US-08-117-952-668

US-09-101-886B-71

US-08-988-728-15

US-08-988-71-119

US-09-237-510-6

US-09-488-57-119

US-09-015-876-20

US-08-015-876-20

US-08-015-876-20

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US-08-477-989B-78
US-08-477-989B-79
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US-08-483-389-87
         GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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                                                                                                                                                                                   324599 segs, 94655562 residues
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                                                                    2001, 16:03:54
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Maximum Match 100%
Listing first 45 summaries
                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                               Gapop 10.0 , Gapext 1.0
                                                                                                                                tacccaggtgagtct 15
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                                                                                                          US-09-757-100B-31
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                                                                                                                                                     IDENTITY_NUC
                                                                    October 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0 Maximum DB seq length: 50
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Match
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100.8
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Perfect score:
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Length 15; Indels

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                                                                                                                                                                                                             CA
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US-08-117-952-668
                                                                                                                                                                                                                                                                                         COMPUTER:
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Pred. No. 1.3e+02;
3; Mismatches 1; Indels
                                                                            Score 15; DB 3; Length 20; Pred. No. 4.2;
                                                                                                                                                                                                                                                     Sequence 7, Application US/08136118
Patent No. 5580969
GENERAL INFORMATION:
APPLICANT: HOKE, Glenn D
APPLICANT: BRADLEY, Matthews O
APPLICANT: HILLIAMS, Taffy J
APPLICANT: LEE, Che-Hung
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES DIRECTED
TITLE OF INVENTION: AGAINST HUMAN ICAM-1
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRATT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,118
                                                                                                                                                                                                                                                                                                                                                                                                                                 Naval Medical Res. & Dev. Cmd
                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Spevack, A. David
REGISTRATION NUMBER: 24,743
REFERENCE/DOCKET NUMBER: N.C. 75,776
TELECOMMUNICATION INFORMATION:
         OTHER INFORMATION: antisense sequence US-09-377-310-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,259
FILING DATE: 24-UL-1992
ATTORNEY/AGENT INFORMATION:
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                                                                            100.0%;
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92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202) 295-6759
TELEFAX: (202) 295-1022
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                            Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                            l tacccaggtgagtc 14
| |||||||||||||||
18 TTCCCAGGTGAGTC 5
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO
                                                                                                                                                                                                                                         US-08-136-118-7/C
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US-08-136-118-7
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FEATURE:
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Gaps
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Pred. No. 1.3e+02;
); Mismatches 1; Indels
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US-09-101-886B-71
Sequence 71, Application US/09101886B
SEQUENCE THOMAS
APPLICANT: DILERENUD, OLE K
APPLICANT: NILSSEN, OIVIND
TITLE OF INVENTION: GENETIC TEST FOR ALPHA-MANNOSIDOSIS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
Sequence 668, Application US/08117952
Patent No. 5851760
GENERAL INFORMATION:
APPLICANT: Evans, Glen A.
APPLICANT: Smith, Michael W.
TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
                                                                                                                                                                 NUMBER OF SEQUENCES: 797
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,952
FILING DATE: 07-SEP-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
APPLICATION DATA:
APPLICATION NUMBER: US/08/078,471
FILING DATE: 15-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUITE 701E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: BARBARA G. ERNST
STREET: 555 13TH STREET, NW
CITY: WASHINGTON
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Reiter, Stephen E. REGISTRATION NUMBER: 31,192 REFERENCE/DOCKET NUMBER: P4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.78;
92.98;
                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 82.7
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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RESULT

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Gaps
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Pred. No. 2.9e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: R. J. Rodrick, Becton Dickinson and Company STREET: 1 Becton Drive CITY: Franklin Lakes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08865675
Patent No. 5928869
GENERAL INFORMATION:
APPLICANT: Nadeau, James G.
APPLICANT: Pitner, James B.
APPLICANT: Carl P.
APPLICANT: Schram, James L.
TITLE OF INVENTION: PLORESCENCE QUENCHING
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/865,675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 11.8; DB 2;
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); Mismatches
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; Patent No. 5958700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32,135
                                            LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-988-128-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,13:
REFERENCE/DOCKET NUMBER: P.
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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86.78;
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86.78;
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Best Local Similarity 86.7
Matches 13; Conservative
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Best Local Similarity 86.7
Matches 13; Conservative
                            SEQUENCE CHARACTERISTICS:
      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                             16 TACCCAGCTGTGTCT 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: NJ
COUNTRY: US
ZIP: 07417
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US-09-237-510-6/C
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US-08-865-675-6
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Fatent No. 5994505
GENERAL INFORMATION:
APPLICANT: Ting, Jenny Pan-Yung
APPLICANT: Chin, Keh-Chin
TITLE OF INVENTION: No. 5994505el Forms of Class II MHC
TITLE OF INVENTION: Transactivator (CIITA)
TUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Myers Bigel Sibley & Sajovec, P.A.
STREET: P.O. Box 37428
CITY: Releigh
STATE: No. 5994505th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 11.8; DB 4; Length 20;
Pred. No. 2.8e+02;
0; Mismatches 2; Indels
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MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

SOFTWARE: PAPLICATION DATA:

APPLICATION NUMBER: US/08/988,128

FILING DATE: 10-DEC-1997

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: B1swas, SOCIO11n1 J.

REGISTRATION NUMBER: 39,111

REFERENCE/DOCKET NUMBER: 5470-136

TELECOMMONICATION: NOWER: 54710-10
                                                                           SOPTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                     APPLICATION NUMBER: US/09/101,886B
FILING DATE: 29-JANUARY-1998
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/00109
FILING DATE: 12-JAN-1997
ATTONNEY/AGENT INFORMATION:
NAME: ERNSY, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1181-240
TELECOMMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION 18-06140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.7%;
86.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 78.7
Best Local Similarity 86.7
Matches 13; Conservative
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US-09-101-886B-71
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Sequence 34, Application US/08123702; Patent No. 5604131
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NAME: Paber, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: TSII:
TELECHONICATION INFORMATION:
TELEPHONE: (404)-873-8794
INFORMATION FOR SEQ ID NO: 381:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Wadsworth, Samuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.0%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 76.0
Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS: ADDRESSE: Patrea L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
3 cccaggtgagtct 15
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                                      15 CCAAGGTGAGTCT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: DNA US-08-123-702-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30309-3450
                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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US-09-015-876-20
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Patent No. 6187545
GENERAL INFORMATION:
APPLICANT: INFORMATION:
APPLICANT: Madeline M. Butler
APPLICANT: Jacqueline Wyatt
APPLICANT: Jacqueline Wyatt
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-CYTOSOLIC EXPRESSION
FILE REFERENCE: RTS-0123
CURRENT FAPLICATION UNBER: US/09/488,671A
CURRENT FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 177
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Pred. No. 3e+02;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.0%; Score 11.4; DB 4; Length 20; 92.3%; Pred. No. 4.8e+02; live 0; Mismatches 1; Indels
              APPLICANT: Nadeau, James G.
APPLICANT: Pitner, James B.
APPLICANT: Linn, Cames B.
APPLICANT: Linn, James B.
APPLICANT: Schram, James L.
APPLICANT: Schram, James L.
TITLE OF INVENTION: PEUCNESCENCE QUENCHING
NUMBER OF SEQUENCES: 9
CORRESPONDENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: R. J. Rodrick, Becton Dickinson and Company
STREET: 1 Becton Drive
                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/237,510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Antisense Oligonucleotide US-09-488-671-119
                                                                                                                                                                                                                                                         COUNTRI.

ZIP: 07417
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
PC COMpatible
PC-DOS/MS-DV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.78;
86.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 78.7
Best Local Similarity 86.7
Matches 13; Conservative
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US-09-237-510-6
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Matches 12; Conserva
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                      STATE: N. COUNTRY:
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LENGTH: 20
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APPLICANT: Snyder, Benjamin
APPLICANT: Reddy, Vermuri, B.
APPLICANT: Red, Chamer
TITLE OF INVENTION: A cDNA Genomic Hybrid Sequence Encoding APP770
Patent No. 5604131
TITLE OF INVENTION: Containing a Genomic DNA Insert of the KI and OX-2 Regions
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Patent No. H001825
GENERAL INFORMATION:
APPLICANT: ROMANO, JOSEPH W
APPLICANT: RUNTLIFF, ROXANNE
APPLICANT: WILLIAMS, KIMBERLY G
TITLE OF INVENTION: ISOTHERMAL TRANSCRIPTION BASED ASSAY
TITLE OF INVENTION: FOR THE DETECTION OF HTLV I AND HTLV II
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 11.4; DB 1; Length 30;
Pred. No. 4.9e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,702
FILING DATE: 17-SEPT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                         ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
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APPLICANT: MARANADA. TARESHAL
APPLICANT: MASATO
TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
TITLE OF INVENTION: SELECTAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
FILE REFERENCE: Q-53599
CURRENT APPLICATION NUMBER: US/09/273,565A
CURRENT FILING DATE: 1999-03-22
EARLIER APPLICATION NUMBER: 09/055,699
EARLIER APPLICATION NUMBER: 09/055,699
EARLIER PILING DATE: 1997-03-19
EARLIER PILING DATE: 1997-03-19
EARLIER PILING DATE: 1997-03-19
EARLIER FILING DATE: 1997-03-19
EARLIER FILING DATE: 1997-03-19
SARLIER FILING DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PATENTIN VET: 2.1
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                        1064/41979CP4
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979C;
TELECHONE: (202) 628-8800
TELECHONE: (202) 628-8804
INFORMATION FOR SEQ ID NO: 53:
SEDURINE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: NUCLEC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 86, Application US/09273565A Patent No. 6166190
                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: DNA (genomic) US-08-609-443B-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: FUJIWARA, TSUTOMU
APPLICANT: WATANABE, TAKESHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 73.3
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                             linear
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US-09-273-565-86/c
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Patent No. 5840693
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: ALITALO, Kari
APPLICANT: ALITALO, Kari
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
STREET: 1200 & Street, N.W., Suite 700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.3%; Score 11; DB 1; Length 20; 100.0%; Pred. No. 8.1e+02; ive 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
ADDRESSEE: AKZO NOBEL PATENT DEPT.
STREET: 1300 PICCARD DRIVE, SUITE 206
CITY: ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DAIR:
APPLICATION NUMBER: US/08/609,443B
FILING DATE: 01-MAR-1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 01-MAR-1995
PRIOR APPLICATION UMBER: US 08/397,651
FILING DATE: 01-MAR-1995
                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,876
                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 100.
Matches 11; Conservative
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MOLECULE TYPE: DNA
                                                               MARYLAND
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                                                                                                                                                                                                            SOFTWARE:
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                                                                                   COUNTRY:
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Search completed: October 2, 2001, 16:03:55 Job time: 14599 sec
APPLICATION NUMBER: US/09/067,908
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           Sequence 4, Application US/08456103
Sequence 4, Application US/08456103
Sequence 4, Application US/08456103
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: INFLAMMATION-INDUCED EXPRESSION OF A
TITLE OF INVENTION: RECOMBINANT GENE
NUMBER OF SEQUENCES:
COMPRESSE: Annold, White & Durkee
STREET: P.O. Box 4433
COMPTRY: United States of America
STATE: Texas
COMPTRY: United States of America
STATE: Texas
COMPTRY: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
FILING DATE: Submitted Herewith
SAPPLICATION NUMBER: US/08/456,103
FILING DATE: Submitted Herewith
APPLICATION: APPLICATION ADATA

APPLICATION: APPLICATION ADATA

APPLICATION NUMBER: US/08/456,103
FILING DATE: Submitted Herewith
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Fatent No. 5851822
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: INFLAMMATION-INDUCED EXPRESSION OF A TITLE OF INVENTION: RECOMBINANT GENE NUMBER OF SEQUENCES:
ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
COUNTRY: United States of America STATE: Texas
COUNTRY: United States of America SIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 73.3%; Score 11; DB 1; Length 28; Best Local Similarity 100.0%; Pred. No. 8.3e+02; Matches 11; Conservative 0; Mismatches 0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: KİECHGIL, BADDARA S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSD:406/KIT
TELECOMMUTCATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4 SEQUENCE CHARACTERISTICS: LENGTH: 28 base pairs TYPE: nucleic acid
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                                                                                                                                                                                                                       UTSD:406/KIT
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/456,103
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 18-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-09-067-908-4
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Oligonucleotide ca
VEGF-B186 exon 5 b
VEGF-B167 exon 5 b
Human VEGF-B186 ex
Human eukaryotic i
                                                            Skeletal muscle sp
GATA-1 locus splic
Primer used to amp
Humanised antibody
Humanised antibody
Humanised LO-CD2a
Humanised LO-CD2a
PCR primer used to
PCR primer used to
HUV-1 LTR (long te
Human ICAM-R CDNA
Human ICAM-R CDNA
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Primer for antibod
Chimeric ICR-1,1 a
                                                                                                                                                                                                                                3' VH primer VHTP3
Bacillus thuringie
                                                                                                                                                                                                                                                    Oligonucleotide #6
Human vascular end
Humanised 340 Vh a
                                                                                                                                                                                                                                                                                   Human VEGF-3 3' PC
Human hAPO8 RACE p
                                                                                                                                                                                                                                                                                                        PCR primer FOG1VHF
                                                                                                                                                                                                            Humanised ICR-1.1
Humanised murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                    Human ICAM-R
                                                                                                                                                                                                   PCR primer 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human focal adhesion kinase antisense seguence #29.
                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
AAA72481
AAQ04939
                                                                                                                                   AAV22892
AAZ10191
                                                                                                                                                                                                           AAA08308
AAZ24334
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AAT44073
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AAA15752
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AAX21887
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                                                                                  AAV22641
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 AAC65563 standard; DNA; 15
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 (ISIS-) ISIS PHARM INC.
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                                                                                          AAC65563;
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 RESULT
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ICAM-1 antisense o
Human ICAM-1, E-se
Chromosome 11 (loc
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Target oligonucleo
Mouse PEPCK-cytoso
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Blackcurrant rever
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Human focal adhesi
                                                                     Search time 876.95 Seconds (without alignments)
10.740 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                          /SIDSB/gcgdata/geneseq/geneseqn/NA1989.DAT:
/SIDSB/gcgdata/geneseq/geneseqn/NA1990.DAT:
/SIDSB/gcgdata/geneseq/geneseqn/NA1990.DAT:
/SIDSB/gcgdata/geneseq/geneseqn/NA1991.DAT:
/SIDSB/gcgdata/geneseq/geneseqn/NA1993.DAT:
/SIDSB/gcgdata/geneseq/geneseqn/NA1994.DAT:
/SIDSB/gcgdata/geneseq/geneseqn/NA1995.DAT:
/SIDSB/gcgdata/geneseq/geneseqn/NA1995.DAT:
/SIDSB/gcgdata/geneseq/geneseqn/NA1995.DAT:
/SIDSB/gcgdata/geneseq/geneseqn/NA1998.DAT:
/SIDSB/gcgdata/geneseq/geneseqn/NA1998.DAT:
/SIDSB/gcgdata/geneseq/geneseqn/NA1998.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:*/SIDS8/gcgdata/geneseq/geneseqn/NA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                /SIDS8/gcgdata/geneseq/geneseqn/NA1983.DAT:*/SIDS8/gcgdata/geneseq/geneseqn/NA1984.DAT:*/SIDS8/gcgdata/geneseq/geneseqn/NA1985.DAT:*/SIDS8/gcgdata/geneseq/geneseqn/NA1986.DAT:*/SIDS8/gcgdata/geneseq/geneseqn/NA1987.DAT:*/SIDS8/gcgdata/geneseq/geneseqn/NA1987.DAT:*/SIDS8/gcgdata/geneseq/geneseqn/NA1987.DAT:*/SIDS8/gcgdata/geneseq/geneseqn/NA1988.DAT:*/
                                                                                                                                                                                                                                                                                                                  /SIDS8/gcgdata/geneseq/geneseqn/NA1980.DAT:*/SIDS8/gcgdata/geneseq/geneseqn/NA1981.DAT:*/SIDS8/gcgdata/geneseq/geneseqn/NA1982.DAT:*
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                          hits satisfying chosen parameters:
                                                                                                                                                                                      730101 seqs, 313950809 residues
                                                                        ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                      2001, 16:18:48
                                                                                                                                                                                                                                                             Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                 - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT58077
AAV38613
AAQ82668
AAY28523
AAV28523
AAV15506
AAV15506
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AAC65543
                                                                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                  1 tacccaggtgagtct 15
                                                                                                           US-09-757-100B-31
15
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Maximum DB seq length: 50
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Match
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Score

Result Š. 11.8 11.8 11.4

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Post-processing:

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Database

Total number of

Searched:

Scoring table:

Perfect score:

Title:

Sequence:

OM nucleic

Run on:

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Antisense; pre-mRNA; mature mRNA; vascular defect; tissue defect; human intercellular adhesion molecule-1; ICAM-1; inflammation; adult respiratory distress syndrome; multiple organ failure; GM1594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anti-sense oligo:nucleotide(s) for blocking ICAM-1 mRNA translation - for treating septic shock, adult respiratory distress syndrome
                                                                                                                                                                          ICAM-1 antisense oligonucleotide #7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Column 21; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bradley MO, Hoke GD, Lee C,
                                                                                                                                                                                                                                                                                                                                                                           93US-0136118.
92US-0918259.
                                                                                                                                                                                                                                                                                                                                                    92US-0918259
                                                                              077/c
AAT58077 standard; DNA; 21
                                                                                                                                               (first entry)
 1 tacccaggtgagtct 15
             (USNA ) US SEC OF NAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-033603/03.
                                                                                                                                                                                                                                           septic shock; ss
                                                                                                                                               18-MAR-1997
                                                                                                                                                                                                                                                                                                                                                  24-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                             12-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                        24-JUL-1992;
                                                                                                                                                                                                                                                                                            US5580969-A.
                                                                                                                                                                                                                                                                                                                        03-DEC-1996
                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                     AAT58077;
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ID AAV386
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                                                                  RESULT
AAT58077/ID AAT5
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                       The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a number of phosphorothicate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated
                                                 is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in cancer, particularly colon, breast and oral tumours, embryonic development disorders, anglogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing;
                                                                                                                                                                                                    .;
0
                                                                                                                                                                          22; Length 15;
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Human focal adhesion kinase antisense sequence #9.
                                                                                                                                                                                                 ;
                                                                                                                                                                        DB
15;
                                                                                                                               Sequence 15 BP; 3 A; 4 C; 4 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 other;
                                                                                                                                                                                                 Mismatches
                                                                                                                                                                        Score 15;
Pred. No.
Claim 15; Column 25; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; Column 23; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                       antisense; phosphorothioate; ss.
                                                                                                                                                                                                 ö
                                                                                                                                                                       100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                        BP.
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                                                                                                                                                                                                                                                                                                                     AAC65543 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antisense sequences, inclu
treatment of all of these.
                                                                                                                                                                     Ouery Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                          tacccaggtgagtct 15
                                                                                                                                                                                                                                         (ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monia BP, Gaarde WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-006141/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                           12-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6133031-A
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Williams TJ;

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The sequences given in AAT58071-85 represent oligonucleotides which are
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              transcript of human intercellular adhesion molecule-1 (ICAM-1). These oligonucleotides may be used for treating septic shock and the manifestations of septic shock, e.g. inflammation, and vascular and rissue defects. They are also useful in the treatment of septic shock associated diseases, e.g. adult respiratory distress syndrome,
                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                 Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ICAM-1, E-selectin, VCAM-1 antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                 Score 12.4; DB 18;
Pred. No. 4.7e+02;
); Mismatches 1;
                                                                                                                                                                                                  Sequence 21 BP; 5 A; 9 C; 5 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                 82.7%;
92.9%;
                                                                                                                                                       multiple organ failure etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV38613 standard; DNA; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                 Query Match 82.7
Best Local Similarity 92.9
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 1 tacccaggtgagtc
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Gaps

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100.0%; Score 15; DB 22; Length 20; 100.0%; Pred. No. 16; 0; Mismatches 0; Indels

Query Match 100. Best Local Similarity 100. Matches 15; Conservative

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Sequences were determined from the ends of chromosome 11-specific cosmids by automated sequencing without intermediate subcloning.
A sample of 371 DNA sequence fragments were determined and of these, 277 were suitable for STS primer prediction by computer these, 277 were mapped by in situ hybridisation, somatic cell hybrid analysis (using the "primer" program available from E.Lander, MIT).
The STSS and cosmids were mapped by in situ hybridisation, somatic cell hybrid analysis to both. Using this method, 370 STSS specific for human chromosome 11 were generated and most of them were regionally mapped. This procedure illustrates a novel method for sequencing complex genomes, designated "sequence sampled mapping method is useful for the completion of high dennisty sequence—based maps, and ultimately, for the complete sequencing of genomic DNA directly from cosmid clones.
See AAQ82001-Q82706 and AAQ91325-Q91358 for STS primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pathogen; yeast; intergenic spacer region; IGS1; PCR primer; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel assemblage useful for discriminating among pathogenic yeasts,
                                                                                                                                                           Sequencing complex genomes, present as fragments in a cosmid
library - by sequencing end-specific nucleotides of each clone
then correlating with spatial relationship of cosmid, esp. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 12.4; DB 16;
Pred. No. 4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C neoformans strain discrimination probe #30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22 BP; 8 A; 5 C; 4 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                       (SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                                                            Example 4; Page 92; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF98212 standard; DNA; 33 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.7%;
92.9%;
93US-0117952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-SEP-2000; 2000WO-US26758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENE-) GENETIC VECTORS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McCabe M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 82.7
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cryptococcus neoformans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                          mammalian chromosomes.
                                                                               Smith MW;
                                                                                                                     WPI; 1995-036508/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 acccaggtgagtct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FELL/) FELL J.
(DIAZ/) DIAZ M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200123616-A2
07-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-2001
                                                                               Evans GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF98212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          φ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is that of an antisense oligonucleotide which is substantially complementary to at least a portion of the preor mature RNA transcript of human intracellular adhesion molecule (ICAM), E-selectin or vascular cell adhesion molecule (VCAM). It can be used to inhibit expression of these proteins forms the basis for treatment of conditions and diseases that have an inflammatory component, e.g. acne, psoriasis, arthritis, organ rejection, wounds, burns, septic shock or inflammatory complications of septic shock.
                                 vascular cell adhesion molecule-1; antisense; inflammatory; disease; treatment; septic shock; psoriasis; wounds; burns; acne; arthritis; organ rejection; inhibition; expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                ICAM-1; intracellular adhesion molecule-; E-selectin; VCAM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense oligonucleotides to ICAM-1, E-selectin or VCAM-1 - for treating diseases having an inflammatory component, e.g. psoriasis, wounds and septic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.7%; Score 12.4; DB 19; 92.9%; Pred. No. 4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chromosome 11 (locus LDHC) STS primer LDHC-Z.
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                                                                                                                                                                                                                                                                                                                                                                               Williams TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Page 40; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                  Lee C,
                                                                                                                                                                                                                                                          96WO-US19194
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                          (DYAD-) DYAD PHARM CORP.
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                                                                                                                                                                                                                                                                                                                                                                             Bradley MO, Hoke GD,
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-333253/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCCCAGGTGAGTC
                                                                                                                                    Homo sapiens
                                                                                                                                                                              WO9824797-A1
                                                                                                                                                                                                                                                          02-DEC-1996;
                                                                                                                                                                                                                                                                                                  02-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-1993;
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                                                                                                                                                                                                                    11-JUN-1998
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                                                                                                                   Synthetic.
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Length 22; Indels SS.

AAQ82668;

RESULT 5 AAQ82668/c

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Query Match

us-09-757-100b-31.szlim50.rng

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Sequence 32 BP; 6 A; 11 C; 9 G; 6 T; 0 other;
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 SSSSSXS
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                                                         The present invention describes an assemblage comprising two primers, each of which can be used to amplify the intergenic spacer region IGS1 from one of various strains of the yeast Cryptococcus neoformans. A number of primers and probes are provided, as are the sequences of the IGS1 for 91 C. neoformans strains. This is useful in the discrimination of pathogenic yeasts, and the sequences can be used to construct a database having the same purpose. The present sequence is a probe or
comprises two universal primers adapted for nucleic acid amplification
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer 5 and primer 6 (see AAV28524) are designed to amplify a 481 nucleotide DNA fragment initiating 265 nucleotides upstream of the polyA tail of RNA2 of a blackcurrant reversion vitus (BRV) Finnish isolate genome (see AAV28525). They were used with primer 1,2 (see AAV28521-22), designed to amplify a 210 nucleotide fragment, to detect different isolates of BRV originating from widely different geographic locations. Primer pair 1,2 amplified the expected virus-specific fragments from all tested virus isolates, and the primer pair 5,6 amplified the expected virus isolates, and the nearly all the tested virus isolates, indicating that the viral
                                                                                                                                                                                                                                                                                                                                                                                                                                        Blackcurrant reversion disease; BRV; rna2; diagnosis; Ribes; PCR;
                                                                                                                                                                                                                                                                                                                                                                                                               Blackcurrant reversion virus RNA2 3' proximal fragment primer 5.
                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                         Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing blackcurrant reversion disease in plants e.g. blackcurrant - using reverse transcriptase-PCR with primers amplifying cDNA fragment complementary to fragment of new
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                      Score 12.4; DB 22;
Pred. No. 4.8e+02;
0; Mismatches 1;
                                                                                                                                                                     Sequence 33 BP; 7 A; 6 C; 13 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus1 P;
                                                                                                                                             primer described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 27; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lehto K, Lemmetty A,
                                   Claim 6; Page 18; 88pp; English.
                                                                                                                                                                                                                                                                                                                                         AAV28523 standard; DNA; 20 BP.
                                                                                                                                                                                                        82.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blackcurrant reversion virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       blackcurrant reversion virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-FI00507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96FI-0003474
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                        Query Match 82.7
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                        2 acccaggtgagtct 15
                                                                                                                                                                                                                                                                      (ABOA-) ABOATECH OY AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-193642/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9810100-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                         28-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Latvala S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                  AAV28523;
            protocol
                                                                                                                                                                                                                                                                                                                  RESULT
AAV28523
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                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining whether an individual has metastasised colorectal cancer cells and origin of tumour cells - by detecting presence of heat-stable toxin receptor on cells in a sample
sequences detecting by these primer pairs are well conserved in all 1solates, including the common (E) and strong (R) forms of the reversion disease. The invention provides methods and kits for the diagnosis of blackcurrant reversion disease using RT-PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; heat stable toxin receptor; colorectal cancer; tumour; diagnosis; human; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                Length 20;
                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                             DB 19; L 7.9e+02;
                                                                                                                                                                Sequence 20 BP; 7 A; 5 C; 6 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                             80.0%; Score 12;
100.0%; Pred. No.
Live 0; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; Page 54; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT99528 standard; DNA; 32 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ST receptor PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0016564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waldman SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                Query Match 80.0
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               2 acccaggtgagt 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 acccaggtgagt 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-008454/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ST receptor; heat
metastasis; diagno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carrithers SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09742506-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT99528;
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DB 19; Length 32;

80.0%; Score 12;

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Target oligonucleotides AAV82665-68 were designed to hybridise to the
                                                                                                                           Detector oligonucleotide; hairpin structure; fluorescence; primer extension; hybridization; signal primer; frameshift mutation;
                                                                                                                                                                                                                                                                                                                                                                                                     quenched dyes - where dyes become fluorescent when region is unpaired, useful for detection and amplification of target nucleic
                                                                                                                                                                                                                                                                                                                                                                                       New detector oligo:nucleotide having base-paired region carrying
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 12; 20pp; English.
                                                                                                                                                                                                                                                                                                                                     Nadeau JG, Pitner BJ,
            AAV82665/c
ID AAV82665 standard; DNA; 48 BP.
                                                                                                                                                                                                                                                                                                           (BECT ) BECTON DICKINSON & CO.
                                                                                                  Target oligonucleotide JN5
                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-001406/01.
                                                                          25-FEB-1999
                                                                                                                                                                                                                                                        28-MAY-1998;
                                                                                                                                                                                                                                                                                  30-MAY-1997;
                                                                                                                                                                                                                                02-DEC-1998.
                                                                                                                                                                                                       EP881302-A2.
                                                                                                                                                                             Synthetic.
                                                 AAV82665;
                                                                                                                                                                                                                                                                                                                                     Linn PC,
                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence was used in the development of a novel system, comprising an adeno-associated virus (AAV) vector containing a foreign DNA, and the rep 68/78 sequence of AAV, the expression of which is delayed. The components may be present in cis (in a single agent) or in trans (in separate agents).

The system is used for production of AAV vectors, particularly for gene therapy. The foreign DNA may encode a therapeutic protein, e.g. interferon, interleukin, growth factor, coagulation factor or metabolic enzyme, particularly one that increases the immunogenicity of tumour cells, and/or a diagnostic protein. The system produces AAV vectors on a large scale. It is based on the discovery that the rep68 and 78 proteins interfere with replication of AAV DNA, and that this interference is overcome by delaying
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    System of adeno-associated viral vector and rep 68/78 sequence of this virus - expression of which is delayed until replication of viral DNA has started, provides large scale production of vectors for gene therapy
                        ;
                        Indels
                                                                                                                                                                                                                                        AAV; vector; rep 68/78; PCR primer; gene therapy; ss.
         Pred. No. 8.1e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 34 BP; 4 A; 13 C; 9 G; 8 T; 0 other;
                                                                                                                                                                                                                Primer for adeno-associated virus DNA.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
Ö
                                                                                                                                     AAV15506 standard; DNA; 34 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Page 7; 20pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of these proteins.
                                                                                                                                                                                                                                                                                                                                                           97WO-DE01333
                                                                                                                                                                                                                                                                                                                                                                                     96DE-1025188
                                                                                                                                                                                       11-JUN-1998 (first entry)
                      12; Conservative
                                                                                                                                                                                                                                                                               Adeno associated virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bogedain C, Hallek M,
                                                                                                                                                                                                                                                                                                                                                                                                              (MEDI-) MEDIGENE GMBH.
                                             3 cccaggtgagtc 14
                                                                      12 cccaggtgagtc 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-086641/08.
                                                                                                                                                                                                                                                                                                                                                                                                                            (MEDI-) MEDIGENE AG
         Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                        W09749824-A1
                                                                                                                                                                                                                                                                                                                                                          24-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                   24-JUN-1996;
                                                                                                                                                                                                                                                                                                                                 31-DEC-1997.
                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                               AAV15506;
                                                                                                                         AAV15506
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Schram JL;

98EP-0109682. 97US-0865675,

(first entry)

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detector oligonuclectied of the invention. The detector oligonuclectied of the invention. The detector oligonuclectied of the invention. The detector oligonuclectied comprises a single-stranded target-binding region and an intramolecularly base-paired secondary structure linked to two dyes (donor and acceptor fluorophores). In the secondary structure, fluorescence of the donor is quenched, but when it is linearised or unfolded a change in some fluorescence parameter becomes detectable. A target nucleic acid is detected by hybridizing it to a detecteor oligonuclectide in which the secondary structure is 5' to the target binding region, primer extension to produce a complementary strand using the secondary structure as template, resulting in linearization or unfolding of it and detecting a change in fluorescence. The detector oligonuclectide are used to detect (by primer extension and hybridization) and amplify (as signal primer) target sequences, e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse PEPCK-cytosolic antisense oligonucleotide ISIS 113360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.7%; Score 11.8; DB 20;
86.7%; Pred. No. 1.1e+03;
ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 48 BP; 15 A; 8 C; 10 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                          detecting frameshift mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF62963/c
ID AAF62963 standard; DNA; 20 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 78.7
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 TACTCAGATGAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 tacccaggtgagtct
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Gaps

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78.7%; Score 11.8; DB 19; Length 34; 86.7%; Pred. No. 1.1e+03; ive 0; Mismatches 2; Indels (

Conservative

Best Local Similarity Matches 13; Conserv

Query Match

1 tacccaggtgagtct 15 

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RESULT

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Sequences AAA72437, AAA72449-A72461, AAA72468 and AAA72474-A72477

represent cDNAs encoding novel plant isoflavone synthases (AAB21052 and AAB21071). Also discibsed is the soybean cytcohrone P450

concoxygenase CYP93C1, encoded by a known sequence (AAA7444, NCBI No. 2799005), which was identified in the present invention as having isoflavone synthase earlivity. The invention also relates to expression constructs, transformed host cells, and transgenic plants and seeds conscribing the novel cDNA sequences of the invention. The invention also encompasses methods of altering isoflavone synthase expression in a host cell, altering isoflavoned in a pint, and identifying nucleic acids encoding other plant isoflavone synthases. Isoflavone synthase catalyses cell, altering isoflavonoid levels in a plant, and identifying nucleic acids encoding other plant isoflavone synthases. Isoflavone synthase catalyses cells as Ney Toll in the biosynthesis of isoflavonoids. Isoflavonoids are catas of secondary metabolites mainly produced in leguminous plants by a branch of the phenylpropanoid pathway. Isoflavone synthase catalyses the first step in the branch of this pathway that commits metabolic intermediates to the synthesis of isoflavonoids. Isoflavonoids

consumption of legumes and rhizobial bacteria which eventually result in nodulation and nitrogen fixation. They have also been shown to act as artibiotics, repellents, attractants, and signal compounds, and consumption of legume isoflavonoids synthases, and nucleic acids encoding them, are useful for altering the levels of isoflavonoids produced in legumes such as soybean, and for the production of isoflavonoids in them, are useful for altering the levels of isoflavonoids produced in legumes such as soybean, and for the production of isoflavonoids cannot begunes and haltering the levels of isoflavonoids produced in legumes such as soybean, and for the production of isoflavonoids cannotic cannotification of the invention to ampility DNA encoding synthases.
                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding isoflavonoid synthases, useful for producing transgenic plants with increased production of isoflavonoids which are involved in defense against phytopathogenic microorganisms -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 11.4; DB 21; Length 25;
Pred. No. 1.7e+03;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide carrying mutation for factor VIII gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25 BP; 6 A; 7 C; 5 G; 7 T; 0 other;
                                                                                                                                                                                                                              Fader GM, Jung W, McGonigle B, Odell JT,
                                                                                                                                                                       (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 14; Page 52; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human factor VIII analogue; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ04939 standard; DNA; 46 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.0%;
92.3%;
                                                       99US-0117769.
99US-0144783.
99US-0156094.
26-JAN-2000; 2000WO-US01772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-OCT-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phenylpropanoid pathway).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 cccaggtgagtct 15
                                                                                                                                                                                                                                                                                WPI; 2000-543395/49.
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                                                       27-JAN-1999;
20-JUL-1999;
24-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 nucleobases in length that are capable of inhibiting the expression of anotheronal pyruvate carboxykinase-cytosolic (PEPCK cytosolic). The antisense compounds are useful for inhibiting the expression of PEPCK-cytosolic in cells or tissues. They are commonly used as research reagents and in diagnostics, e.g. to elucidate the function of particular genes. They are also useful for distinguishing between functions of various members of a biological pathway and for research use. The antisense compounds are also useful prophylactically, e.g. to prevent or delay infection, inflammation or tumour formation. The present sequence is a chimeric phosphorothioate oligonucleotide with 2'-MOE wings and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence is one of a number of antisense compounds of up to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense compound capable of modulating the expression of phosphoenol pyruvate carboxykinase-cytosolic, useful for preventing or delaying infection, inflammation or tumor formation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soybean; chalcone reductase; phenylpropanoid pathway; isoflavone synthase; isoflavonoid biosynthesis; defence response; attractant; repellant; signal compound; antibiotic; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                       Mouse; antlinflammatory; cytostatic; antisense gene therapy; phosphoenol pyruvate carboxykinase-cytosolic; PEPCK-cytosolic; infection; inflammation; tumour formation; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 11.4; DB 22; Length 20; Pred. No. 1.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soybean chalcone reductase PCR primer, SEQ ID NO:65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Butler MM, Wyatt J, Cowsert LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 17; Column 44; 64pp; English.
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92.3%;
                                                                                                                                                                                                                                                                                                                21-JAN-2000; 2000US-0488671
                                                                                                                                                                                                                                                                                                                                                                  21-JAN-2000; 2000US-0488671
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Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          (ISIS-) ISIS PHARM INC.
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                                                                                                                                            Mus musculus.
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AAT ANT37933-T37946 represent the intron/exon boundaries for the human vascular endothelial growth factor (VEGF) proteins of the invention (see AAW04829, and AAW04831), which promote endothelial or mesodermal cell proliferation. VEGF is also a glycosylated cationic dimer, and is sometimes referred to as vascular permeability factor (VPF). VEGF has diverse effects, depending on the specific biological context in which it is found. VEGF is a potent endothelial cell mitogen, and directly contributes to induction of angiogenesis in vivo by promoting endothelial cell growth during normal embryonic development, wound healing, and tissue regeneration/recognisation. The VEGF proteins of the invention share the angiogenic and other properties of VEGF, but are distributed and expressed in tissues differently to VEGF. The proteins can therefore be used to accelerate angiogenesis in wound healing. Antibodies against the proteins can be used for inhibiting angiogenesis. The antibodies can also be used diagnostically to quantitively detect vEGF-B. Primers complementary to the coding sequences for the proteins of the invention can also be used to detect VEGF-B coding sequences. Quantification of VEGF-B in cancer biopsy specimens may be useful as an influence of metastatic risk. VEGF-B expression in a cell can be retarded using antisense sequences direct against the VEGF coding sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endothelial cell; proliferation; vascular endothelial growth factor; VPF; VEGF; endothelium; mesodermal cell; cationic dimer; tissue regeneration; vascular permeability factor; cell mitogen; anglogenesis; cell growth; embryonic development; wound healing; tissue reorganisation; antibody; cancer; metastatic risk; tumour cell; human; ss.
                                                                                                                              Vascular endothelial growth factor VEGF-B proteins - useful to accelerate angiogenesis in wound healing, also related nucleic acid and antibodies for cancer diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
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                                            Olofsson B, Pajusola K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.3%; Score 11; DB 17; I 100.0%; Pred. No. 2.9e+03; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 other;
    (UYHE-) UNIV HELSINKI LICENSING LTD OY.
                                                                                                                                                                                                               Example 7; Page 28; 107pp; English.
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Best Local Similarity 100.
Matches 11; Conservative
                                              Alitalo K, Eriksson U,
                                                                                      WPI; 1996-412582/41.
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01-MAR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Factor VIII analogue is sufficiently mutated from the original gene that it is not recognised by blood Abs of the patient. The analogue is composed of human FVIII but carries the B-domain of human FV in place of the FVIII B-domain.
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Pred. No. 1.8e+03;
0; Mismatches 1;
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                                       Location/Qualifiers
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92.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; ; pp; English.
                                                                                                                                                                                                                                                                                             (GENE-) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 76.0
Best Local Similarity 92.3
Matches 12; Conservative
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01-MAR-1995;
06-JUN-1995;
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Synthetic.
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AAT37933-T37946 represent the intron/exon boundaries for the human vascular endothelial growth factor (VBGF) proteins of the invention (see AAW04829, and AAW04831), which promote endothelial or mesodermal cell proliferation. VBGF is also a glycosylated cationic dimer, and is sometimes referred to as vascular permeability factor (VPF). VBGF has diverse effects, depending on the specific biological context in which it is found. VBGF is a potent endothelial cell mitogen, and directly contributes to induction of anglogenesis in vivo by promoting contributes to induction of anglogenesis in vivo by promoting healing, and tissue regeneration/reorganisation. The VBGF proteins of the invention share the anglogenic and other properties of VBGF, but are distributed and expressed in tissues differently to VBGF. The proteins can therefore be used to accelerate anglogenesis in wound healing. Antibodies against the proteins can be used for inhibiting anglogenesis. The antibodies can also be used diagnostically to quantifactively detect VBGF. Became as a sequence of the proteins can be used to detect VBGF. Became of the proteins can be used the detect VBGF. Became of the proteins can be used to detect VBGF. Became of the proteins can be used the detect VBGF. Became of the proteins can be used the detect VBGF. Became of the proteins can be used the detect VBGF. Became of the proteins can be used the detect VBGF. Became of the proteins can be used the detect VBGF. Became of the coding sequences for the proteins can be used the detect VBGF. Became of the coding sequences for the proteins can be used to detect VBGF. Became of the coding sequences for the proteins can be used to detect VBGF. Became of the coding sequences for the proteins can be used to detect VBGF. Became of the coding sequences for the proteins can be used to detect VBGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vascular endothelial growth factor VEGF-B proteins - useful to accelerate angiogenesis in wound healing, also related nucleic acid and antibodies for cancer diagnosis
                                                                                                                                                                                                                                                                                                                       Alitalo K, Eriksson U, Olofsson B, Pajusola K;
                                                                                                                       (LUDW-) LUDWIG INST CANCER RES. (UYHE-) UNIV HELSINKI LICENSING LTD OY.
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95US-0469427.
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06-JUN-1995;
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Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 other;

Gaps ö Ouery Match 73.3%; Score 11; DB 17; Length 20; Best Local Similarity 100.0%; Pred. No. 2.9e+03; Matches 11; Conservative 0; Mismatches 0; Indels

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5 caggtgagtct 15 ò

8 caggtgagtct 18

Search completed: October 2, 2001, 16:18:48 Job time: 15492 sec

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APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE GAALGE, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 20
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Best Local Similarity
Matches 15; Conserv
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US-09-377-310-30
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US-09-377-310-10
TYPE: DNA
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Sequence 486, App
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Sequence 486, App
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6.804 Million cell updates/sec
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Sequence 487,
Sequence 486,
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Sequence 487
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. /cgn2_c/ptodata//ina/5B_COMB.seq:*
. /cgn2_c/ptodata/1/ina/6A_COMB.seq:*
. /cgn2_c/ptodata/1/ina/6B_COMB.seq:*
. /cgn2_c/ptodata/1/ina/PCTUS_COMB.seq:*
. /cgn2_c/ptodata/1/ina/PCTUS_COMB.seq:*
. /cgn2_c/ptodata/1/ina/PCTUS_COMB.seq:*
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-377-310-10

US-08-485-286-44

US-08-12-389-486

US-08-171-389-486

US-08-171-389-486

US-08-173-936-487

US-08-175-228A-487

US-08-475-228A-487

US-08-475-228A-487

US-08-475-228A-487

US-08-475-228A-487

US-08-482-080A-486

US-08-482-080A-486

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US-08-482-080A-487

US-08-482-080A-5

US-08-88-25-88A-5

US-08-88-25-88A-5

US-08-88-25-88A-5

US-08-88-21-88A-5

US-08-88-21-88A-5

US-08-88-21-88A-5

US-08-88-21-88A-5

US-08-88-31-31-88-26

US-08-88-31-31-88-26

US-08-482-115-8-26

US-08-482-115-8-26

US-08-482-115-8-26

US-08-482-115-8-26
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US-08-834-655-15
US-09-363-574-15
US-08-479-614-21
US-08-479-852-12
                                                                                                                                                                                                     Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                    324599 segs, 94655562 residues
                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                   2, 2001, 16:03:54
                                                 - nucleic search, using sw model
                                                                                                                                                                Gapop 10.0 , Gapext 1.0
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                                                                                                      US-09-757-100B-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match Length
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DB seq length: 50
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111.8
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Maximum I
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Sequence 30, Application US/09377310B

Patent No. 6133031

GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389

CURRENT APPLICATION NUMBER: US/09/377,310B

CURRENT FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 30

LENGTH: 15
        Sedinence Sedine
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US-08-479-852-64
US-08-479-852-78
US-08-462-646-12
US-08-462-646-12
US-08-462-646-12
US-08-462-646-78
US-09-013-406-12
US-09-013-406-92
US-09-013-406-92
US-09-013-406-92
US-09-13-406-92
US-09-13-406-92
US-08-343-682-12
US-08-343-682-12
US-08-951-822-13
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Mismatches
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; Patent No. 6133031
; GENERAL INFORMATION:
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MORGAN, ALICE ER
APPLICANT: HEY, TIMOTHY D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 93.3.
                              TITLE OF INVENTION: RIBO
TITLE OF INVENTION: DEECTITLE OF INVENTION: USIN
UNMER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGIH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
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ZIP: 94111-3834
                                                                                                                                                                                                          46268
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                   APPLICANT:
                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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US-08-378-761A-45/C
Sequence 45, Application US/08378761A
SEMENAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: WALSH, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
COUNTY: US
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                                                                                    DB 3; Length 20;
                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
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                                                                                                                    Mismatches
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Pred. No. 72;
                                                                                    Score 15;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
              ; OTHER INFORMATION: antisense sequence US-09-377-310-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 45, Application US/08485286
Patent No. 5646026
Patent No. 5646026 5646119
GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFO TATOR IN NAME: BORUCKI, ANDREA TREGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 3827
RELECOMMUNICATION INFORMATION:
TELEHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
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                                                                                  100.0%;
100.0%;
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93.3%;
                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 taagcagctgccatt 15
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US-08-485-286-45/c
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US-08-378-761A-45
FEATURE:
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RIBOSOME-INACTIVATING PROTEINS, INACTIVE
PRECIRSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
USING
81
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Patent No. 6033663
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids Encoding GDP-Fucose;
TITLE OF INVENTION: Pyrophoshorylase
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,964
                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BORUCKI, ANDREA T
REGIGSTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                   ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CIITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 45:
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93.3%;
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Pred. No. 5.8e+02;
0; Mismatches 2; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
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RELOR APPLICATION DATA:
APPLICATION NUMBER: 40 08/123,936
FILING DATE: 17-SEP-193
RELOR APPLICATION DATA:
APPLICATION NUMBER: 05 07/996,783
FILING DATE: 23-DEC-1992
RICH APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-UN-1991
PRIOR APPLICATION NUMBER: US 08/081,070
APPLICATION NUMBER: US 08/081,070
RELING DATE: 22-UN-1993
FILING DATE: 22-UN-1993
ATTORNEY/AGENT INFORMATION:
   REGISTRATION NUMBER: 33,875
REFERNCE/DOCKET NUMBER: 4600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 486:
SEQUENCE CHARACTERISTICS:
LENGHT: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.7%;
86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 78.7
Best Local Similarity 86.7
Matches 13; Conservative
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// INDIVIDUAL ISOLATE:
US-08-171-389-486
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US-08-171-389-487
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US-08-17-389-486
US-08-17-389-486
Sequence 486, Application US/08171389
Patent No. 5578444
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
TITLE OF INVEWTION: Sequence-Directed DNA Binding
TITLE OF INVEWTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.0%; Score 12; DB 3; Length 29, 100.0%; Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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ZIP: 94063
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
                                                                                                                                                        NAME: Bastian, Kevin L.
REGISTARION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 014137-009910US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-UNN-1991
PRIOR APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-UNN-1993
ATTORNEY/AGENT INFORMATION:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/015,241
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 80.0
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fabian, Gary R.
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    3 agcagctgccat 14

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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Gaps

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                                                           Human T-cell Lymphotropic virus type
III (HIV-1)
                                                                                                                                                                Score 11.8; DB 1; Length 50;
Pred. No. 5.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
TITLE OF INVENTION: Screening Assay for the Detection of NUMBER OF SEQUENCES: 640
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDIVIDUAL ISOLATE: Aids-associated retrovirus INDIVIDUAL ISOLATE: (arv-2;proviral) US-08-123-936-487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.7%; Score 11.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 05 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-UN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/123,936 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 487, Application US/08123936
; Patent No. 5726014
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                78.7%;
86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                   Best_Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 50 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                             1 taagcagctgccatt 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy COMPUTER: IBM PC COMP
                                                     ; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-123-936-486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: RNA
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                   HYPOTHETICAL: NORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: NORIGINAL SOURCE:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94063
                                                                                                                                                                                                                                                                                                                                                                  US-08-123-936-487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                 Length 50;
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Patent No. 5726014
GENERAL INFORMATION:
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Andrews, Beth M.
TITLE OF INVENTION: Screening Assay for the Detection of TITLE OF INVENTION: DAM Blinding Molecules
NUMBER OF SEQUENCES: 640
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                       TOPOLOGY: linear HAW (Genomic)
HAYDOTHETICAL: NO ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Aids-associated retrovirus
INDIVIDUAL ISOLATE: (arv-2;proviral)
US-08-171-389-487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                             Score 11.8; DB 1;
Pred. No. 5.8e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 486:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genelabs Technologies, Inc. STREET: 505 Penobscot Drive CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION UDHBER: US 07/723,618
APPLICATION UNBER: US 07/723,618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/123,936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                 TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 487:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                             78.78;
86.78;
                                                                                                                                                                                                                                                                                                                                             Query Match 78.7
Best Local Similarity 86.7
Matches 13; Conservative
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LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                              1 taagcagctgccatt 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Redw
STATE: CA
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US-08-123-936-486
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                                                                                                                                                                                                    GENERAL INCORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Challes R.
APPLICANT: Cantor, Challes R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TILLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 50;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,228A
FILING DATE: 06-JUN-1995
PRIOR APPLICATION NUMBER: US 08/123,936
FILING DATE: 10-58P-1993
PRIOR APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-58P-1993
PRIOR APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION NUMBER: US 08/081,070
FILING DATE: 27-JUN-1991
PRIOR APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/COCKET NUMBER: 34,444
REFERENCE/COCKET NUMBER: 33-40880
TELECHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aids-associated retrovirus (arv-2; proviral)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 11.8; DB 2;
Pred. No. 5.8e+02;
0; Mismatches 2;
                                                                                                                                                         Sequence 487, Application US/08475228A Patent No. 5869241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: RNA (genomic)
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TELEPAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 487
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
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    1 taagcagctgccatt 15
                                               24 TAAGCAGCTGCTTTT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-475-228A-487
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Best Local Similarity
Matches 13; Conserv
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                                                                                                                     RESULT 11
US-08-475-228A-487
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                            Gaps
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Sequence 486, Application US/08475228A

GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDIVIDUAL ISOLATE: Human T-cell Lymphotropic virus type
INDIVIDUAL ISOLATE: III (HIV-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 78.7%; Score 11.8; DB 2; Length 50; Best Local Similarity 86.7%; Pred. No. 5.8e+02; Matches 13; Conservative 0; Mismatches 2; Indels
  Pred. No. 5.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: FLORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,228A
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 3-DEC 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 2-3-DEC 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 2-2-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 4600-0175.21/G19P3D2
TELECOMMUNICATION NUMBER: 4600-0175.21/G19P3D2
TELECOMMUNICATION NUMBER: 4600-0175.21/G19P3D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Genelabs Technologies, Inc. 505 Penobscot Drive
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TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 486:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: RNA (genomic)
86.78;
  Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 50 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                   1 taagcagctgccatt 15
                                                                                                                24 TAAGCAGCTGCTTTT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 505 Penobs. CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                   RESULT 10
US-08-475-228A-486
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Sequence 487, Application US/08482080A
Patent No. 6010849
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Auriews, Beth M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: 664
NUMBER OF SEQUENCES: 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORTANTOS SISIEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,080A
FILING DATE: US/08/482,080A
FILING DATE: US/08/482,080A
FILING DATE: US/08/482,080A
FILING DATE: US/08/11,389
FILING DATE: US 08/171,389
FILING DATE: US 08/171,389
FILING DATE: US 08/123,936
FILING DATE: US 08/123,936
FILING DATE: US 08/123,936
FILING DATE: US 08/123,936
FILING DATE: US 07/996,783
FILING DATE: US 08/081,070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 4600-0175.20/G19F3D1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genelabs Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 505 Penobscot Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 60
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RESULT 13
US-08-482-080A-487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human T-cell Lymphotropic virus type
III (HIV-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.7%; Score 11.8; DB 3; Length 50; 86.7%; Pred. No. 5.8e+02; ive 0; Mismatches 2; Indels
                                                                                                                                               APPLICANT: Edwards, Cynthia A. APPLICANT: Cantor, Charles R. APPLICANT: Andrews, Beth M. APPLICANT: Andrews, Beth M. APPLICANT: ALVIN, Lisa M. APPLICANT: Fry, Kirk E. TITLE OF INVENTION: Sequence-Directed DNA Binding TITLE OF INVENTION: Molecules, Compositions and Methods NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: FLOPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,080A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: US 07/23,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1991
PRIOR APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Brady, John F.
REGISTRATION NUMBER: 39-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
                                                      Sequence 486, Application US/08482080A Patent No. 6010849 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 505 Penobscot Drive
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INFORMATION FOR SEQ ID NO: 481
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 86.7
Matches 13; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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ZIP: 94063
                       US-08-482-080A-486
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Gaps ö Length 50; Indels Aids-associated retrovirus (arv-2;proviral) Score 11.8; DB 3; Pred. No. 5.8e+02; 0; Mismatches 2; 78.7%; 86.7%; Best_Local Similarity 86.7 Matches 13; Conservative 1 taagcagctgccatt 15 24 TAAGCAGCTGCTTTT Query Match à QQ

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Search completed: October 2, 2001, 16:03:54 Job time: 14598 sec
Redwood City
CA
                                    COUNTRY: US
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III (HIV-1)
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                                                                                                                               TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetabs Technologies, Inc.
STREET: 505 Penobscot Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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Molecules, Compositions and Methods
                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12388
FILING DATE:
CLASCITTORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 5.8e+02;
0; Mismatches 2
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GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Sequence-Directed DNA in TITLE OF INVENTION: Molecules, Composition: CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17 SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                          Sequence 486, Application PC/TUS9312388 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INPORMATION FOR SEQ ID NO: 486:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA (genomic)
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86.78;
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Best Local Similarity 86.7
Matches 13; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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24 TAAGCAGCTGCTTTT 38
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PCT-US93-12388-486
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HYPOTHETICAL: N
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PCT-US93-12388-487
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                                                                                                                                                                                                                                                                               STATE: CA
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                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: PCT/US93/12388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aids-associated retrovirus (arv-2;proviral)
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Pred. No. 5.8e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-193
PRIOR APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: RNA (genomic)
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86.7%;
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Best Local Similarity 86.7
Matches 13; Conservative
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PCT-US93-12388-487
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USA
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Human T-cell lymph Aids-associated re HIV-1 TATA region

Test sequence from Test sequence from

AIDS-associated re

Polymorphic fragme IGF-I oligonucleot IGF-I oligonucleot IGF-I oligonucleot Human PRO1555 reve

PCR primer used to PCR primer used to Primer #141 used i

Human epidermal gr

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EGFR oligonucleoti
EGFR oligonucleoti
Native Pseudomonas
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Soybean chlorophyl
RNA component of h
Human telomerase R
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Human IL-8 recepto
PCR primer pRDS1 u
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human focal adhesion kinase antisense seguence #28.
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                          AAT64199
AAV65660
AAX17486
AAX17487
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AAX79550
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AAX77812
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AAT35689
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                                                                 AAA04041
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99US-0377310.
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(ISIS-) ISIS PHARM INC
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RESULT
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PCR primer for hum
Human GDP-fucose p
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Human flt1 VEGF re
HIV-1 promoter fra
HIV-1 TATA region.
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Human focal adhesi
                                                                        (without alignments)
10.740 Million cell updates/sec
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                                                              Search time 876.95 Seconds
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                                                                                                                                                                                                                                                                                                                                                                  /SIDSB/gcgdata/geneseq/geneseq/NA1999.DAT:
/SIDSB/gcgdata/geneseq/geneseq/NA1990.DAT:
/SIDSB/gcgdata/geneseq/geneseqn/NA1990.DAT:
/SIDSB/gcgdata/geneseq/geneseqn/NA1991.DAT:
/SIDSB/gcgdata/geneseq/geneseqn/NA1994.DAT:
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                     hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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AAX36327
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AAT96994
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AAK67939
AAV65645
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Gapop 10.0 , Gapext 1.0
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PCR primers AAX36327-28 were used to amplify human FAK cDNA, in the course of the invention. The specification describes a method for altering the tumorigenicity or malignancy of brain cancer cells by changing the activity of glycosyltransferase in the cell so that glycosylation of cellular proteins is modified. The method is applied to glicom or meningiona, for prevention or treatment of brain tumours. Measuring the level of glycosyltransferase expression in brain cells is used to detect or predict their tumorigenicity.
                                                                                                                                                                                                                                                                                                                                                                                Human; tumorigenicity; glycosyltransferase;
malignancy; brain cancer cell; protein glycosylation; glioma;
meningioma; brain tumour; FAK; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Altering tumorigenicity and malignancy of brain cancer cells
                                                                                                                                                                                                                                                                                                                              Sense primer used to amplify human FAK cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 34; 83pp; English.
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     1 taagcagctgccatt 15
                               3 taagcagctgccatt 17
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                                                                                                                                                                                                                                AAX36327;
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Matches
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AAX36327/
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                                               The present invention describes a number of phosphorothioate antisense sequences to the human focal adhesion Kinase (FKK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a number of phosphorothicate antisense sequences to the human focal adhesion kinase (FAK) protein. This protein is involved in integrin-mediated signal transduction, and is implicated in cancer, particularly colon, breast and oral tumours, embryonic development disorders, angiogenic disorders and wound healing. The antisense sequences, including the one shown here, can be used in the treatment of all of these.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense compounds for inhibiting focal adhesion kinase expression, especially useful for inhibiting retinal neovascularization, or for diagnosing and treating e.g. colon cancer
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; focal adhesion kinase; FAK; signal transduction; cancer; embryonic development disorder; angiogenic disorder; wound healing; antisense; phosphorothloate; ss.
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                                                                                                                                                                                                                                                                                                                              Length 15;
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0
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27;
                                                                                                                                                                                                                                                     Sequence 15 BP; 4 A; 4 C; 3 G; 4 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                              Score 15;
Pred. No.
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Claim 15; Column 25; 30pp; English,
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                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 15; Conservative
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AAC65542
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                                                                                                                                                                                                                                                                               PG1 gene; biallelic marker; PCR primer; PG1-related biallelic marker; cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
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0
                                     22;
                                                              Indels
                                     Length
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                                   Score 14; DB 20;
Pred. No. 1e+02;
Sequence 22 BP; 4 A; 7 C; 5 G; 6 T; 0 other;
                                                              Mismatches
                                                                                                                                                                                                                                                        PCR primer for PG1 gene exon border.
                                                              ;
0
                                     93.3%; 8
100.0%;
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ID AAZ01016 standard; DNA; 27
                                                              Conservative
                                                                                     1 taagcagctgccat 14
                                                                                                     14 TAAGCAGCTGCCAT
                                               Local Similarity
les 14; Conserv
                                                                                                                                                                                                                                                                                              cancer; prostate
PSA; human; ss.
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Gaps

0;

100.0%; Score 15; DB 22; Length 20; 100.0%; Pred. No. 28; 0; Indels ive 0; Mismatches 0; Indels

15; Conservative

Best_Local Similarity Matches 15; Conserv

Query Match

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fibrononectin collagen-binding domain. The amplified sequence was used to construct a collagen-binding physiologically active polypeptide. This polypeptide comprises a peptide from fibronectin ligated to a physiologically active peptide. The polypeptides are used in an agent for enabling topical retention or sustained release of a physiological active peptide or physiological activity-imparting agent. They may be used in gene therapy and in tissue regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This primer is used for the PCR amplification of guanosine 5-diphospho-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guanosine 5-diphospho- beta L-fucose pyrophosphorylase; human; GDPFPP; carbohydrate; donor substrate; GDP-fucose; PCR primer; ss.
                                                                                                                                                                         Collagen-binding active polypeptide for use in an agent for enabling topical retention or sustained release of a physiologically active peptide or physiological activity-imparting agent comprises a fibronectin peptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding GDP-fucose pyro:phosphorylase - useful to synthesise specific carbohydrate structures e.g. to investigate role of carbohydrate(s) in cell surface recognition
                                                                                                                                                                                                                                                                                                                 PCR primers AAA64261-62 were used to amplify cDNA encoding a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human GDP-fucose pyrophosphorylase (GDPFPP) amplifying 5' primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12.4; DB 21;
Pred. No. 8.2e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 49 BP; 12 A; 16 C; 11 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                            Example 1; Page 124; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 24; 33pp; English.
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92.9%;
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99JP-0041913.
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AAT96994/c
ID AAT96994 standard; DNA; 29
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Best Local Similarity 92.9
Matches 13; Conservative
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                                                                                                 Kitajima
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                                                         (TERU ) TERUMO CORP
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19-FEB-1999;
01-NOV-1999;
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                                                                                                 Ishikawa T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a mammalian PC1 gene and protein, and a set of PC1 biallelic markers. The PG1 polynucleotide and biallelic markers are used in a hybridisation assay, a sequencing assay, or in an allele-specific amplification assay for determining the identity of a nucleotide at a PG1-related biallelic marker. The methods can be used to detect and to assess the risk of developing cancer or prostate cancer. Barly stage diagnosis of prostate cancer relies on prostate specific antigen (PSA) dosage. However, the effectiveness of this is limited due to its inability to discriminate between maligiant and non-maligiant affections of the organ. A need exists for both a reliable diagnostic and curative treatments of the disease. The PG1 gene can be used for detection of prostate cancer, and the risk of developing it in the future, and can also be used to determine therapies for the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fibrononectin; collagen-binding domain; sustained release; gene therapy; physiologically active polypeptide; topical retention; PCR primer; tissue regeneration; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                         a prostate cancer associated gene and biallelic markers
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                                                                                                                                                                                                                                                                                               Cohen D;
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                                                                                                                                                                                                                                                                                               Bougueleret L, Chumakov I,
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                                                                                                                                                      98WO-IB02133,
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Matches 13; Conserv
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                                                                                                                                                                                                                                                                                           Blumenfeld M,
                                     Homo sapiens.
                                                                          WO9932644-A2
                                                                                                                                                    22-DEC-1998;
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                Synthetic
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Query Match

AAA64261/c

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Length 49; Indels BP; 6 A; 6 C; 10 G; 7 T; 0 other;

Sequence 29

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beta L-fucose (GDP-fucose) pyrophosphorylase (GDPFPP) cDNA. Cells can be genetically engineered to contain the GDPFPP nucleic acids and produce the protein. GDPFPP enzymes can be used to synthesise carbohydrate molecules of defined structures, useful in investigating the role of carbohydrates as recognition elements on cell surfaces. They are especially useful in producing donor substrates (e.g. GDP-fucose) in reactions of a glycosyl transferase (e.g. fucosyltransferase) with the substrate, an acceptor sugar and a divalent metal cation to allow formation of glycosyl Iningses adding a saccharide to a substrate saccharide. The proteins can also be used to produce antibodies or antisera useful to characterise, detect and isolate proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A 5' primer (AAT997584) and a 3' primer (AAT997585) were used in the PCR amplification of human GDP-fucose pyrophosphorylase (GDPFPP) cDNA (see AAT97583) from Epstein-Barr virus-transformed B lymphoblastoid cell line JY, and were designed to incorporate EcoRV sites at the 5' and 3' termin of the amplified sequence. The amplified GDPFPP CDNA was subsequently incorporated into expression vectors. Recombinant human GDPFPP was expressed in COS, NSO and Spodoptera frugiperda Sf9 cells. The claimed enzyme (see AAW36811) is useful in the synthesis of carbohydrate structures.
                                                                                                                                                                                                        cross-reacting with the GDPFPP protein.
Note: The specification refers to claimed GDPFPP nucleotide and amino acid sequences, neither of which are given in the specification.
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDP-fucose pyrophosphorylase and related coding sequences - useful to synthesise GDP-fucose as substrate for producing specific carbohydrate structures, e.g. to study cell surface recognition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDP-fucose pyrophosphorylase; GDPFPP; human; oligosaccharide; carbohydrate; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                          Length 29;
                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human GDP-fucose pyrophosphorylase cDNA 5' PCR primer.
                                                                                                                                                                                                                                                                                                                                                           1.3e+03;
                                                                                                                                                                                                                                                                                                                                          80.0%; Score 12; DB 18;
                                                                                                                                                                                                                                                                                 Sequence 29 BP; 6 A; 6 C; 10 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                      100.0%; Preu ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT97584 standard; DNA; 29 BP.
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 3 agcagctgccat 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ketcham CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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                                                                                                                                                                                                                                                                                                       Human; variant thrombospondin 1; variant thrombospondin 4; SNP; polymorphism; vascular disease; coronary artery disease; forensics; myocardial infarction; atherosclerosis; stroke; venous thromboembolism; pulmonary embolism; paternity test; ds.
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McCarthy JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids comprising single nucleotide polymorphisms, useful in applications such as forensics, paternity testing, medicine, genetic analysis and phenotype correlations to diseases such as diabetes and atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /standard_name= "single nucleotide polymorphism"
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Length 29;
                                Indels
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               Pred. No. 1.3e+03;
Score 12; DB 18;
                                                                                                                                                                                                                                                                             Human gene single nucleotide polymorphism #19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21 BP; 6 A; 7 C; 4 G; 4 T; 0 other;
        100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (WHED ) WHITEHEAD INST BIOMEDICAL RES. (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers replace(11,T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Examples; Page 48; 242pp; English.
                                                                                                                                                                             AAF95258 standard; DNA; 21 BP.
 80.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-2000; 2000WO-US24503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0153357.
                                                                                                                                                                                                                                             06-JUN-2001 (first entry)
Query Match 80.0
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
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                                                                                    27 AGCAGCTGCCAT 16
                                                              3 agcagctgccat 14
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                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                               AAF95258;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Variation
                                                                                                                                                              AAF95258/C
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HIV-1 promoter fragment used as a target sequence.

(first entry)

16-DEC-1998

AAV65645;

BP.

AAV65645 standard; DNA; 30

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AAV65645
                 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                       Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flx. ADM: hammerhead ribozyme; hairpin ribozyme; cleavage; tumur angiogenesis; psoriasis; rheumatoid arthritis; coular disease; flms-like tyrosine kinase 1; kinase insert domain containing receptor;
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or
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            Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid molecule modulating VEGF receptor(s) gene expmRNA stability - useful for treating e.g. tumour angiogen psoriasis, rheumatoid arthritis, etc., in a human patient
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
                                                                                                                                                                                                                                                                                                                                                                Human flt1 VEGF receptor hammerhead ribozyme #665.
Score 11.8; DB 22;
Pred. No. 1.6e+03;
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          78.78;
86.78;
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95US-0005974.
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                                                                                                                                                                                                                                       AAX67939 standard; RNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR ) CHIRON CORP.
(RIBO-) RIBOZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         foetal liver kinase 1; ss.
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    Query Match 18.7
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                            1 taagcagctgccatt 15
                                                                                                                                 17 TAGGCAGCTGCGATT
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26-OCT-1995;
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This represents a promoter fragment of the HIV-1 genome that is used as a target sequence. The invention provides polyamide DNA-binding ligands for modulating expression of cellular and viral genes. One method comprises identifying a unique target DNA sequence adjacent to the binding site of a minor groove transcription factor protein (MGTFP), choosing a polyamide having subnanomolar affinity for the target DNA and treating the target DNA with the polyamide as transcription inhibition. Methods (1) for inhibiting replication of a pathogen by administering a transcription-inhibiting polyamide; (2) improving binding affinity of polyamide, selected for an identified viral DNA target by replacing a carboxamide binding pair (CBP) that does not include N-methylimidazole carboxamide (IM) with a CBP comprising paired beta-alanine (beta) residues; (3) inhibiting binding of the zinc finger protein TFIIIA to
Polyamide; DNA-binding ligand; modulation; gene expression; CBP; IM; minor groove transcription factor protein; MGTFP; TFIIIA; adenocarcinoma; transcription inhibitor; pathogen; binding affinity; zinc finger protein; carboxamide binding pair; N-methylimidazole carboxamide; bacteria; fungi; 55 ribosomal RNA gene; internal control region; virus; protozoa; HIV-1; human immune deficiency virus; cancer; DNA capture; genomic sequencing; her-2/neu oncogene; gene transcription; DNA cleavage; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modulating expression of genes with poly:amide(s) specific for region near the binding site for transcription factor - for inhibiting replication of pathogen, especially human immune deficiency virus and for treating cancers associated with expression of the her-2/new oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "six basepair sequence bound by the polyamide"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/note= "six basepair sequence bound by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DE;
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/note= "TFIID binding site"
18..23
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                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1.
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97US-0038384.
97US-0038394.
97US-0853022.
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14-FEB-1997;
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Length 27;

Score 11.8; DB 18; Pred. No. 1.6e+03; 0; Mismatches 2;

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78.7%; ilarity 86.7%; Conservative

Query Match Best Local Similarity Matches 13; Conserv

taagcagctgccatt 15

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15 TCATCAGCTGCCATT

9

86.78;

Best Local Similarity

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the SS ribosomal RNA gene internal control region; (4) for treating adenocarcinoma of ovary, endometrium, breast, fallopian tubes and cervix with the polyamide are also provided. Method (1) is applied to viruses, bacteria, fungi and protozoa, especially human immune deficiency virus (HIV)-1, both therapeutically and for treating blood cells in vitro. Method (4) is especially used against cancers that overexpress the her-2,new oncogene. The polyamide can also be used for diagnosis of disease, very generally as therapeutic agents for any disease involving cellular or viral gene transcription, for genomic sequencing, for DNA capture and for DNA cleavage (oxidative or by light). The polyamide has excellent specificity and very high affinity for the target DNA, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATA modulating factor, TMF; transcription; TATA box; promoter; HIV-1; human immunodeficiency virus-1; short arm; human chromosome 3; p12-p21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the TATA region of the HIV-1 LTR from -46 to -1. This region is bound by TATA modulating factor (TMF). TMF is a protein of mol. wt. 123-130 kD which activates transcription in most genes, esp. in human immundeficiency virus-1 (HIV-1) by binding to the TATA box region of the promoter. TMF is encoded by the short arm of human chromosome 3 in the region p12-p21 which is often involved in translocations in patients having lung and other types
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New protein cellular factor - capable of binding double stranded HIV-1 tata region and activating gene expression of HIV-LTR
                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                            Length 30;
                                                                                                                                                                                                    are specific for particular genes, and are cell permeable
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                            Score 11.8; DB 19;
Pred. No. 1.7e+03;
                                                                                                                                                                                                                                        Sequence 30 BP; 7 A; 6 C; 7 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                              0; Mismatches
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV-1 TATA region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A DNA protein-binding assay is provided, useful for screening libraries of synthetic or biological cpds for their ability to bind DNA test sequences. The assay is versatile in that any number of test sequences can be tested by placing the test sequence adjacent to a defined protein-binding screening sequence. Binding of mols, to these test sequences changes the binding characteristics of the protein mol. to its cognate binding sequence. When such a molbinds the test sequence, the equilibrium of the DNA:protein complexes is disturbed, generating changes in the concentration of free DNA probe.
                      Gaps
                                                                                                                                                                                                                                                                          Human T-cell lymphotropic virus type III (HIV-I), target region.
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                                                                                                                                                                                                                                                                                                          DNA protein-binding assay; test sequence; screening sequence; promoter; target; TATA box; Herpes Simplex Virus; HSV; origin of replication; UL9; transcription factor; TFIID: ds.
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                     Indels
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Pred. No. 1.8e+03;
); Mismatches 2;
Pred. No. 1.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceuticals and as molecular reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Edwards CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 28; Page 455; 587pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENELABS TECHNOLOGIES INC
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                                                                                                                                                                         AAQ69736 standard; DNA; 50 BP
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86.7%;
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Best Local Similarity 86.7
Matches 13; Conservative
                     13; Conservative
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                                                        1 taagcagctgccatt
                                                                                        22 taagcagctgctttt
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                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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Indels

taagcagctgccatt 15

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DB 14; Length 46;

78.7%; Score 11.8;

Query Match

Sequence 46 BP; 8 A; 12 C; 11 G; 15 T; 0 other;

Duplex DNA; target region; binding characteristic; DNA binding protein; TFIID; transcription factor; binding site; inhibition; enhance; cancer; inherited genetic disorder; ds.

Human lymphotropic virus type III.

US5578444-A.

26-NOV-1996,

91US-0723618. 93US-0171389. 91US-0723618. 92US-0996783. 93US-0123936

27-JUN-1991;

27-JUN-1991; 23-DEC-1992;

17-SEP-1993;

20-DEC-1993;

Human T-cell lymphotrophic virus type-III (HIV-1) TFIID binding site.

(first entry)

17-MAR-1997

AAT64198;

AAT64198 standard; DNA; 50 BP.

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RESULT 14
                    AAT64198
                                                                        factors (e.g. TFIID), where the target region is typically selected from DNA sequences adjacent to the binding site for the eucaryotic transcription factor. Numerous exemplary test sequences are given: the sequences in AA069251-731 and AA069850 correspond to promoter targets (typically, TATA box-contg. sites) for human genes and the sequences in AA069732-849 correspond to promoter targets for viral genes. The test sequences may also be randomly generated. DNA:protein interaction may be used for screening purposes, e.g. the Herpes Simplex Virus (HSV) origin of replication and UL9 (see AA069851-52, AA069865 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A DNA protein-binding assay is provided, useful for screening libraries of synthetic or biological cpds. for their ability to bind DNA test sequences. The assay is versatile in that any number of test sequences can be tested by placing the test sequence adjacent to a defined protein-binding screening sequence. Binding of mols. to these test sequences changes the binding characteristics of the protein mol. to its cognate binding sequence. When such a mol. binds the test sequence, the equilibrium of the DNA:protein complexes is disturbed, generating changes in the concentration of free DNA probe. One application of this method is to eucaryotic general transcription
                                                                                                                                                                                                                                                   DNA protein-binding assay; test sequence; screening sequence; promoter; target; TATA box; Herpes Simplex Virus; HSV; origin of replication; UL9; transcription factor; TFIID: ds.
                                                                                                                                                                                                                 AIDS-associated retrovirus (arv-2; proviral), target region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Turin LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence-directed DNA-binding molecules - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 50 BP; 8 A; 13 C; 13 G; 16 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 28; Page 455; 587pp; English.
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                                                                                                        AAQ69737 standard; DNA; 50 BP.
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24 taagcagctgctttt 38
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17-SEP-1993;
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                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                                            AAQ69737;
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Altering binding characteristics of DNA binding proteins to duplex DNA - by attaching specific small cpd. to target region close to the protein's binding site, useful in treatment of viral disease, cancer

Claim 6; Column 347-348; 264pp; English.

Turin LM;

Fry KE,

Cantor CR, Edwards CA,

Andrews BM,

WPI; 1997-020402/02.

(GENE-) GENELABS TECHNOLOGIES INC.

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The sequences given in AAT63713-4312 represent duplex DNA's which act as target regions in the method of the invention. The method for altering the binding characteristics of a DNA-binding protein to duplex DNA comprises contacting the duplex DNA with a small molecule which binds sequence-specifically to a target region, where, when the small molecule is bound to the target region, it is adjacent to, but not concentration by more than 4 bp, a binding site for a DNA-binding protein. The small molecule is added at a concentration effective to alter the binding of the DNA binding of the small molecule may inhibit or campounds isolated using this method are potentially useful as the duplex DNA. The binding of the small molecule may inhibit or compounds isolated using this method are potentially useful as the sequence, or inherited genetic disorders etc. The method is suitable for screening large biological or chemical libraries and allows determination of sequence-specific and relative affinities of known DNA-binding agents for different DNA sequences. The design of these duplex DNA's allows a single DNA. PNA binding control or preferential, DNA binding to be used for screening sequence-specific.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to we used tot screening sequence-specific, or preferential, DNA binding proteins that recognise almost any possible sequence (see also AAT49539-74).
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llarity 86.7%; Pred. No. 1.8e+03;
Conservative 0; Mismatches 2;
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mes 13; Conserv
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Indels

78.7%; Score 11.8; DB 15; 86.7%; Pred. No. 1.8e+03; iive 0; Mismatches 2;

Query Match 78.7 Best Local Similarity 86.7 Matches 13; Conservative

1 taagcagctgccatt 15 

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24

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Length 50;

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as target regions in Anion 19713-19712 represent dupter DNA sucretaries at target regions in the method of the invention. The method for altering the binding characteristics of a DNA-binding protein to duplex DNA sequence-specifically to a target region, where, when the small binds sequence-specifically to a target region, where, when the small molecule is bound to the target region, it is adjacent to, but not overlapping by more than 4 bp, a binding site for a DNA-binding protein. The small molecule is added at a concentration effective to alter the binding of the DNA binding protein, pref. TFIID, to its binding site on the duplex DNA. The binding of the small molecule may inhibit or enhance the binding of the DNA-binding protein to its binding site. The compounds isolated using this method are potentially useful as therapeutic agents for treatment of any disease which involves a specific DNA sequence, e.g. cancer, or inherited genetic disorders etc. The method is suitable for screening large biological or chemical libraries and allows determination of sequence-specific and relative affinities of known DNA-binding agents for different DNA sequences. The design of these duplex DNA's allows a single DNA-brotein interaction to be used for screening sequence-specific, or preferential, DNA binding proteins that recognise almost any possible sequence (see also AAT49539-
                                                                                                                                                                                           Duplex DNA; target region; binding characteristic; DNA binding protein; TFIID; transcription factor; binding site; inhibition; enhance; cancer; inherited genetic disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences given in AAT63713-4312 represent duplex DNA's which act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA - by attaching specific small cpd. to target region close to the protein's binding site, useful in treatment of viral disease, cancer
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                                                                                                                                                           Aids-associated retrovirus proviral arv2 TFIID binding site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Column 347-348; 264pp; English.
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                                     AAT64199 standard; DNA; 50 BP.
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91US-0723618.
92US-0996783.
93US-0123936.
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                                                                                                                                                                                                                                                                                 Aids-associated retrovirus
                                                                                                                     (first entry)
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                     AAT64199
RESULT
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Gaps

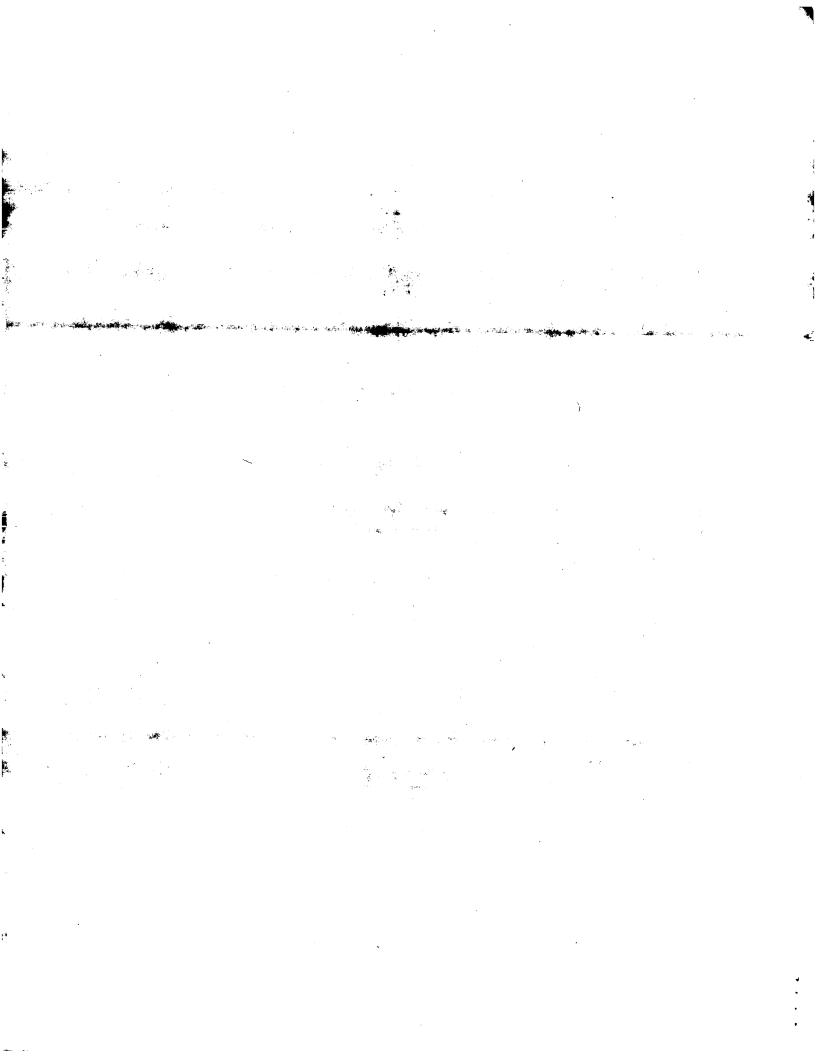
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Best Local Similarity 86.7 Matches 13; Conservative

Query Match

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Search completed: October 2, 2001, 16:18:48
Job time: 15492 sec
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TYPE: DNA
ORGANISM: Artificial Sequence
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US-09-377-310-23
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US-09-377-310-3
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LENGTH: 20
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Patent No. 5190871
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                                                              2001, 16:03:53; Search time 417.38 Seconds
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Sequence 6, 7
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Sequence 25,
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/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
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Compugen Ltd.
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US-09-315-886C-5
US-09-275-680-11
US-09-428-219-86
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US-09-282-996-18
US-08-732-612-11
US-08-161-015-17
US-08-445-2898-25
US-08-445-2898-25
US-08-35-37-8
PCT-US-99-946-8
US-08-34-8
US-08-34-8
US-08-34-8
US-08-31-6-203-9
US-08-31-010-2
US-08-271-880A-50
US-09-249-215-50
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                                                                                                                                                                                     324599 segs, 94655562 residues
GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
                                           - nucleic search, using sw model
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Sequence 4, Appli
Sequence 4, Appli
Sequence 50, Appli
Sequence 50, Appl
Sequence 18, Appl
Sequence 36, Appl
Patent No. 5520913
Sequence 34, Appl
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Fatent No. 6133031
GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
TITLE OF INVENTION: Expression
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION UNMER: US/09/377,310B
CURRENT FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO*23
LENGTH: 15
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APPLICANT: Monia, Brett P.
APPLICANT: Garde, William A.
TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
TITLE OF INVENTION: Expression
FILE REFERENCE: ISPH-0389
CURRENT APPLICATION NUMBER: US/09/377,310B
CURRENT PILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 4.0
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100.0%; Pred. No. 8.6;
ive 0; Mismatches 0
US-08-171-718-51

US-08-468-580-50

US-08-478-087-51

US-08-353-55-4

US-08-643-212-72

PCT-US95-03731-50

US-08-011-745-18

US-08-011-745-18

US-08-18-98-969

US-08-828-533-36

5520913-18

US-08-250-802-34

US-08-250-802-34

PCT-US92-07916-35

US-08-250-802-34

PCT-US92-07916-35

US-08-250-802-34

PCT-US92-07916-35

US-08-250-802-34

PCT-US92-07916-35

US-08-250-802-35

US-08-250-802-34

PCT-US92-07916-35

US-08-250-802-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: antisense sequence US-09-377-310-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09377310B Patent No. 6133031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Loca 15; Conserve
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ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,599
REFERENCE/COCKET NUMBER: 2931:
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELERX: (202) 887-1501
TELEX: 90-4030 MRSNPOERSHEH
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                            78.7%;
86.7%;
                                                                                                                                                                                                                                                                            NAME/KEY: prim_transcript
CCATION: 1.31
COCATION: 1.31
OTHER INFORMATION: /note=
COTHER INFORMATION: designa
US-08-732-612-6
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 78.7
Best Local Similarity 86.7
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 gegggeteacagtgg 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20006-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5 .
US-08-732-612-11
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APPLICANT: MORBEY, MOHAMAD A.

TITLE OF INVENTION: METHODS FOR PRODUCTION OF RECOMBINANT
TITLE OF INVENTION: PLASMIDS
TITLE OF INVENTION: PLASMIDS
TO SEQUENCES: 11
CORRESPONDENCE: 11
CORRESPONDENCE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVE., NW
CITY: WASHINGTON
STRATE: DC.
                                                                                            Length 20;
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                        Sequence 18, Application US/09282996
Fatent No. 6143502
GENERAL INFORMATION:
APPLICANT: Grentramon, Guido
APPLICANT: Gesteland, Raymond F.
APPLICANT: Gesteland, Raymond F.
TILLE OF INVENTION: Dual-Luciferase Reporter System
FILE REFERENCE: T9864. NP
CURRENT FILING DATE: 1999-03-31
EARLIER FILING DATE: 1999-03-31
EARLIER FILING DATE:
NUMBER OF SEQ ID NOS: 18
SOFTWARE: WordPerfect 8.0
SEQ ID NO 18
LENGTH: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                            DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 13.4; D
Pred. No. 63;
0; Mismatches
                                                                                                                               0; Mismatches
                                                                                        Query Match 100.0%; Score 15; Best Local Similarity 100.0%; Pred. No. Matches 15; Conservative 0; Mismatch
                 ; OTHER INFORMATION: antisense sequence US-09-377-310-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/732,612
FILING DATE: 16-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20006-1812
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08732612 Patent No. 5922583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Primer fsAZ2
US-09-282-996-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.3%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 89.3
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                  1 gcgggctcacagtgg 15
                                                                                                                                                                                                   3 gcgggctcacagtgg 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 16
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                        US-09-282-996-18/c
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US-08-732-612-6
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FEATURE:
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Gaps
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Patent No. 5922583
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MORBEY, MOHAMAD A.
TITLE OF INVENTION: METHODS FOR PRODUCTION OF RECOMBINANT
TITLE OF INVENTION: PLASMIDS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVE., NW
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 16-OCT-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 11.8; DB 2;
Pred. No. 4.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                     /note= "downstream primer designated murF2"
NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REPERENCE/POCKET NUMBER: 29,959

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 887-1500
TELEFX: 90-4030 MRSNFORFSWSH
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Gaps
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Pred. No. 7.5e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Jokhadze, George
APPLICANT: Bibliashvilli, Robert
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: Windows95
SOFRWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Oligonuclectide primer US-08-859-998-856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37,620
BER: 09096/002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/859,998 FILING DATE: 21-MAY-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                 RD00003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 856, Application US/08859998
Patent No. 5994076
  NAME: Bade, Annette L. REGISTRATION NUMBER: 37,029 REFERENCE/DOCKET NUMBER: RDITELECOMMUNICATION INFORMATION: 301-231-5520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                      76.0%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,6
                                                                                                                          TELEFAX: 310-810-4...
INFORMATION FOR SEQ ID NO: 2'S SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 76.0 Best Local Similarity 92.3 Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 gggctcacagtgg 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 GGCACACAGTGG 1
                                                                                                                                                                                                                                                                                                                           linear
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US-08-859-998-856/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94025
                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY:
US-08-445-289B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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US-09-161-015-17/c
Sequence 17, Application US/09161015A
Patent No. 5965370
GENERAL INFORMATION:
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF RhoG EXPRESSION
FILE REFERENCE: RTS-0015
CURRENT APPLICATION NUMBER: US/09/161,015A
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-08-445-289B-25/c
Sequence 25, Application US/08445289B
February 25, Application US/08445289B
FEBREAL INFORMATION:
APPLICANT: HU, Mendong
APPLICANT: Hu, Mendong
APPLICANT: Lee, Sunmin
TITLE OF INVENTION: A Mycoplasma PCR Testing System Using A
TITLE OF INVENTION: Set of Mixed and Single Sequence Primers
                                                                                                                                                    Length 39
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                                                                                                                                                                                                       2; Indels
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                                                                                                                                              Score 11.8; DB 2;
Pred. No. 4.6e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 11.4; DB 2;
Pred. No. 7.5e+02;
0; Mismatches 1;
     /note= "downstream primer designated murF4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: American Type Culture Collection
STREET: 12301 Parklawn Drive
CITY: Rockville
STATE: Maryland
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Antisense Oligonucleotide US-09-161-015-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRA.

ZIP: 20852
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

"THER: IBM PC compatible

"THER: TOWN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/445,289B
FILING DATE: 19-MAY-1995
CLESSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                              78.7%;
86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Rele
                                                                                                                                              Query Match 78.7
Best Local Similarity 86.7
Matches 13; Conservative
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Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                          Patent No. 5693467
NUMBER OF SEQUENCES: 2'
CORRESPONDENCE ADDRESS:
ADDRESSEE: American
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17 CGGCGCACAGTG 5
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-732-612-11
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Smith, Richard K.

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                                                                                                                                             sequence 8, Application US/07959946;
sequence 8, Application US/07959946;
patent No. 5408038;
GENERAL INFORMATION:
APPLICANT: Smith, Richard K.
APPLICANT: Woung, Stephen G.
APPLICANT: Witztum, Joseph L.
APPLICANT: Wingtum, Joseph L.
APPLICANT: CALTAS: Linda K.
APPLICANT: CALORESSE: 20
CORRESPONDENCE ADDRESS: 20
CORRESPONDENCE ADDRESSE: Milnamow, Ltd.
STREET: 180 No. 5408038th Stetson, Suite 4700
CITY: Chloago
CITY: Chloago
CONTRY: USA
ZIP. C.
                                                Gaps
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  73.3%; Score 11; DB 2; Length 25; 100.0%; Pred. No. 1.2e+03; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.3%; Score 11; DB 1; Length 31; 100.0%; Pred. No. 1.2e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,946
FILING DATE: 19921008
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,706
FILING DATE: 18-JUN-1992
ATTORNEY/AGENT: 18-DWN-1992
ATTORNEY/AGENT: INFORMATION:
NAME: Gamson, Edward P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08333577 Patent No. 5786206 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: NUCLEIC ACID
STANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (312)616-5400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-959-946-8
Query Match 73.3
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 73.3
Best Local Similarity 100.
Matches 11; Conservative
                                                                                        5 gctcacagtgg 15
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Gaps
                                                                                     TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Smith, Richard K.
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Turis, Linda K.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 31;
                                                                                                                                                                              ADDRESSE: Dressler, Goldsmith, Shore, Sutker & ADDRESSE: Milnamow, Ltd.
STREET: 180 No. 5786206th Stetson, Suite 4700 CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Dressler, Goldsmith, Shore, Sutker & ADDRESSEE: Milnamow, Ltd.
STREET: 180 North Stetson, Suite 4700
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.3%; Score 11; DB 1;
100.0%; Pred. No. 1.2e+0:
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: SCRF 234.0
TELECOMUNICATION INFORMATION:
TELEPHONE: (312)616-5460
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDUUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 8, Application PC/TUS9208634; GENERAL INFORMATION:
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
AAPPLICANT: Witztum, Joseph L.
APPLICANT: Curtiss, Linda K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: DNA (genomic)
US-08-333-577-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 gctcacagtgg 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
PCT-US92-08634-8/c
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APPLICANT: Dalrymple, Michael A
APPLICANT: Prunkard, Donna E
APPLICANT: Foster, Donald C
TITLE OF INVENTION: Production of Fibrinogen in Transgenic
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.0%; Score 10.8; DB 1; Length 24; 85.7%; Pred. No. 1.6e+03; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08371001
Patent No. 5783683
GENERAL INFORMATION:
APPLICANT: MOTISON Ph.D., Richard
TITLE OF INVENTION: Methods and Composition for Treating
TITLE OF INVENTION: Tumor Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE:
STREET: 401 "B" Street, Suite 1700
                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/POCKET NUMBER: 93-15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEPAX: 206-548-2329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/371,001
FILING DATE: January 10, 1995
                                                                                                                                     ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 72.0
Best Local Similarity 85.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                             ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; IMMEDIATE SOURCE:
; CLONE: BLGAMP4
US-08-206-176-10
                                                                                                                                                                          Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                            STATE: WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-08-371-001-2
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STATE:
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Sequence 9, Application US/09166203A

Sequence 9, Application US/09166203A

Patent No. 5968826

GENERAL INFORMATION:

APPLICANT: Bennett, C. Frank

APPLICANT: Condon, Tom P.

APPLICANT: CONDON, TOM P.

TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN 4 EXPRESSION

TITLE REFERENCE: ISPH-0323

CURRENT APPLICATION UNMER: US/09/166,203A

CURRENT FILING DATE: 1998-10-05

WOMBER OF SEQ ID NOS: 60

LENGTH: 18
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 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08634
FILING DATE: 19921009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.0%; Score 10.8; DB 2;
85.7%; Pred. No. 1.6e+03;
tive 0; Mismatches 2;
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                                                                                              CTHER INFORMATION: antisense sequence US-09-166-203-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-206-176-10/c
Sequence 10, Application US/08206176
Patent No. 5639940
GENERAL INFORMATION:
APPLICANT: Garner, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
PCT-US92-08634-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.C
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 72.0
Best Local Similarity 85.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                              TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 gcgggctcacagtg 14
                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 GCTCACAGTGG 9
                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Garner, Ian
APPLICANT: Cottingham, Ian R.
APPLICANT: Temperley, Simon M.
APPLICANT: Temperley, Simon M.
APPLICANT: Sprecher, Condy A.
APPLICANT: Prunkard, Donna E.
TITLE OF INVENTION: PROTEIN C PRODUCTION IN TRANSGENIC
TITLE OF INVENTION: ANIMALS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1201 Eastlake Avenue East
CTTY: Seattle
STATE: WA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/756,506
                                  REGISTRATION NUMBER: 35,461
REGISTRATION NUMBER: 35,461
REFERENCE/DOCKET NUMBER: PO0095USO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 699-3630
TELEPAX: (619) 236-11048
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
NOLECULE TYPE: Other Nucleic Acid
US-08-371-001-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION:

FILING DATE:
CLASSIFICATION: 800
ACTORNEY/AGENT INFORMATION:
NAME: SAW181ak, Deborah A
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 95-2/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
"FILEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/08756506
Patent No. 5905185
GENERAL INFORMATION:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 206-442-00/0
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                Query Match 72.0
Best Local Similarity 85.7
Matches 12; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Query Match
Best Local Similarity 85.7%; Pred. No. 1.6e+03;
Bact Local Similarity 85.7%; Pred. No. 1.6e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 cgggctcacagtgg 15
| | | | | | | | | | | | |
| Db 24 CTGGCTCACAGAGG 11

Search completed: October 2, 2001, 16:03:54
Job time: 14598 sec
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